

# Improving breeding efficiency for quality and yield of sweet potato

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**ABSTRACT.** Sweet potato is one of the most economically important crops in the world. This study obtains information on maternal effect on yield and quality traits of sweet potato under the following designed reciprocal crosses: ‘Nancy Hall’ (NH) × ‘Tainung 27’ (TN27), and ‘Chingshey purple’ (CP) × ‘Tainung 57’ (TN57). The reciprocal crosses were conducted at the same location in different years. Four populations of 119, 112, 200 and 200 plants form NH × TN27, TN27 × NH, CP × TN57, and TN57 × CP crosses, respectively, were used to investigate the inheritance of commercial traits. The correlations between traits were also analyzed. The results indicate that substantial differences of mean and coefficient of variation in the measured traits existed in the F<sub>1</sub> populations. Maternal effects on top weight and root weight between progeny groups have been observed using NH and TN57 as the seed parents. Top weight, storage root weight, and crude protein content of the hybrids were heterotic. The distributions of top weight, weight and number of storage roots were skewed toward low yield characteristics. Significant positive correlations were detected among top weight, weight, and storage root number, between storage root shape and top weight and storage root weight, between skin color and flesh color of storage root, and between starch content and amylose content. Selecting lower starch or amylose content may be useful to improving sugar or crude protein content in view of the significant negative correlation between these traits. Choosing a maternal parent of the breeding hybrid for the yield and quality should effectively improve the selection scheme.

**Keywords:** Maternal effect; Reciprocal cross; Sweet potato breeding.

## INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam) is grown in many countries around the world and ranks fifth as a food crop in developing countries after rice, wheat, maize, and cassava (Food and Agriculture Organization, 2002). It is widely used as food and animal feed and is processed into snacks, starch, liquor, flour, and a variety of other industrial products. Its wide adaptability on marginal land and rich nutritional content have the potential to prevent malnutrition and enhance food security in the developing world (Diaz et al., 1996). Despite its importance, there have been few genetic studies on sweet potato, probably due to its self-incompatibility and high level of cross-incompatibility, polyploidy level (hexaploid), and large chromosome number (2n=6X=90) (Magoon et al., 1970; Ozias-Akins and Jarret, 1994). The *Ipomoea* series *batatas* contains sweet potato and 13-14 other taxa. Nearly 26,000 accessions of *Ipomoea* species are maintained at various genebanks in the world, and 8,000 accessions are sweet

potato cultivars or breeding lines (Nishiyama et al., 1975; Hu et al., 2003). For further improvement of sweet potato, other *Ipomoea* species may play an important role in providing new genes, such as those for flesh color and protein content of the storage roots (Li, 1982). A better knowledge of genetic diversity and relationships between sweet potato and its wild relatives will aid in the development of breeding programs that efficiently utilize wild *Ipomoea* germplasm.

Maternal effects are ubiquitous across plant taxa. Maternal effects can be due to maternal phenotype (Donohue, 1999; Gedye et al., 2005), specific maternal environments (e.g. light, water, nutrient, hormone) (Sultan, 1996; El-Keblawy and Lovett-Doust, 1999; Galloway, 2001; Galloway, 2002), cytoplasmic genes (Shi et al., 1999a, b), or nuclear genes (Wang et al., 1995; Barrett et al., 2002; Zhang et al., 2004). However, studies on the maternal effect of commercial traits in sweet potato are limited. To improve the breeding efficiency for quality and yield of sweet potato, an understanding of the reciprocal crosses of the traits concerned is essential. Thus, the objective of the present study was to determine

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inheritance mode of yield and quality traits that responded differentially to reciprocal crosses in sweet potato. The results would be useful to the selection and breeding of sweet potatoes of high quality and yields for human consumption or animal feed.

## MATERIALS AND METHODS

### Plant materials and reciprocal crosses

Two field experiments with different parents were carried out in different years.

#### Experiment 1: 'NH x TN 27' and 'TN 27 x NH' in 2001

Male and female parents belonging to different incompatible groups can make crosses by hand pollinations. Previous data (Wang, 1982) showed that Tainung 27 (TN 27) and Nancy Hall (NH) belong to the fifth and third group of incompatibility, respectively. In order to produce more flowers on both male and female parents, grafting was applied in May 2001. 'American Yellow Skin', which produces more flowers than other varieties, was used as rootstock, and TN27 and NH were the scions. One month after grafting, the seedlings of grafting were transplanted to the field at Chia-Yi Agricultural Experiment Station (CAES) in July. Twenty plants of TN 27 and NH were then reciprocally cross-hybridized in the field from October to December 2001. Anthers of the male parent were removed before the day of hand crossing. The parents were different in a number of ways. TN 27 produces an extremely high quantity of pollen. NH, introduced from the USA, has high yields of storage root with high levels of  $\beta$ -carotene. Fertile interspecific F<sub>1</sub> hybrid seeds from the controlled crosses were harvested from December 2001 to February 2002. Fifty parents and three hundred F<sub>1</sub> seeds from reciprocal crosses were sown in the nursery at CAES in May 2002. After 45 days, one thousand vine cuttings about 40 cm in length were transplanted 50 cm apart within rows (ridges) spaced 120 cm wide between rows. There were two plots in the field: one for the 119 progenies derived from the cross NH ( $\varphi$ ) and TN27 ( $\delta$ ), and the other plot for the 112 progenies from the reciprocal cross TN27 ( $\varphi$ )  $\times$  NH ( $\delta$ ). Within these two plots, ten plants of each parent were planted. Prior to planting, the field was fertilized with 40, 60, and 100 kg/ha of N, P<sub>2</sub>O<sub>5</sub> and K<sub>2</sub>O, respectively. Six traits were assessed in the parents and F<sub>1</sub> populations at harvest in this experiment: shape, flesh color, skin color, fresh weight and number of storage roots, and fresh weight of tops (leaves and stems). The data were recorded from December 2002 to January 2003 on an individual plant per plot basis. The shape of the storage root was scored visually using a 1 to 3 scale: 1, 2 and 3 were long, round, and oval, respectively. The flesh color and skin color of the storage root were examined according to the Kidgway "Standard Color Chart" rating 1~3 for yellow, red, and purple.

#### Experiment 2: CPxTN 57 and TN 57xCP in 2003

Twenty plants in the controlled reciprocal crosses were made between Tainung 57 (TN 57) and Chinshey purple (CP) to produce F<sub>1</sub> seeds in September 2003. Fifty parents and three hundred reciprocal F<sub>1</sub> seeds were sown in May, 2004, and grown in the same field under the same cultivation and management conditions as experiment 1. Two hundred plants from each reciprocal cross (TN57  $\times$  CP and CP  $\times$  TN57) and ten plants from each parent (TN57 and CP) were grown in experiment 2. TN 57 was derived from a cross between TN 27 and NH and is one of the most widely grown sweet potato varieties in Taiwan due to its high yield, texture, and flavor. It can be used for human consumption or food processing. CP was a land variety (Taiwan origin) with a purple storage root of high nutritional value. Trait measurement and observation (December, 2004) in this experiment included: fresh weight of tops, skin color, flesh color, fresh weight, number, and contents of crude protein, starch, amylose, and soluble sugar of storage roots. The percentage of starch, protein, amylose and sugar content was measured using the Near Infrared Reflectance Analyzer (Bran-Luebbe 450) on a dry weight basis (Yin et al., 2002). The four sweet potato cultivars used in this study were hexaploidy plants (2n=6X=90) with a base chromosome number of 15.

### Statistical analysis

Statistical analyses and Pearson correlation coefficients between phenotypic and chemical traits in the F<sub>1</sub> population were analyzed using SAS8.2 (SAS Institute Incorporated, Cary, N.C., USA). Different plants as replicates from plots were calculated as average for the traits. The means of top weight, root weight, and root number between the reciprocal crosses were compared using the unpaired-t test. However, the means of root skin color, flesh color, and shape between the reciprocal crosses were compared using Mann-Whitney U test.

## RESULTS AND DISCUSSION

Four F<sub>1</sub> populations of 119, 112, 200 and 200 lines were developed from the interspecific reciprocal crosses among 'NH  $\times$  TN 27' and 'CP  $\times$  TN57'. Table 1 shows that the mean value of top fresh weight for the NH  $\times$  TN 27 (290.0 g, n=119) was significantly higher than that for the TN 27  $\times$  NH (172.3 g, n=112). However, there were no significant differences between the means of each cross in respect to fresh weight, number, skin color, flesh color, or shape of storage roots. These results suggest that the reciprocal effect for the fresh weight of top detected in experiment 1 was caused by maternal effects. Moreover, in Table 2, CP $\times$ TN 57 yielded 419.0 g top fresh weight per plant as compared to 600.2 g per plant from TN 57 $\times$ CP. The average fresh weight of storage roots were 986.9g and 1420.4 g for CP $\times$ TN 57 and TN 57 $\times$ CP, respectively. Significant differences of mean in fresh weight of tops

**Table 1.** Ranges, means, standard deviations (SD) and coefficients of variation (CV) of six traits among F<sub>1</sub> populations generated by reciprocal cross-hybridization. The phenotypic means of the parents TN 27 and NH are included. Comparisons (within reciprocal cross) having the same superscripts did not differ significantly ( $P < 0.05$ ), according to both *t*-test and Mann-Whitney U test.

Trait	♀ NH × ♂ TN 27 (n = 119)			♀ TN 27 × ♂ NH (n = 112)			TN 27 (n = 10)		NH (n = 10)	
	Range	Mean	SD	CV %	Range	Mean	SD	CV %	Mean	Mean
Top fresh weight (g)	8~1300	290.0 <sup>a</sup>	111.1	38.2	10~900	172.3 <sup>b</sup>	94.2	54.6	90.9	163.2
Storage root										
Fresh weight (g)	20~2200	548.3 <sup>a</sup>	301.2	54.5	10~1600	555.0 <sup>a</sup>	299.4	53.8	197.1	84.6
Number	1~16	5.8 <sup>a</sup>	3.0	52.2	1~13	5.6 <sup>a</sup>	2.4	43.1	6.3	6.8
Skin color*	1~3	2.1 <sup>a</sup>	0.7	37.0	1~3	2.3 <sup>a</sup>	0.6	26.5	1.0	1.0
Flesh color*	1~3	2.8 <sup>a</sup>	0.7	25.0	1~3	2.5 <sup>a</sup>	0.3	13.1	1.0	1.5
Shape	1~3	1.8 <sup>a</sup>	0.8	44.0	1~3	1.7 <sup>a</sup>	0.8	48.8	3.0	2.0

\*The flesh color and skin color of storage root were examined according to the Kidgway's 'Standard Color Chart' rating 1~3 for yellow, red and purple.

**Table 2.** Ranges, means, standard deviations (SD) and coefficients of variation (CV) of nine traits among F<sub>1</sub> populations generated by reciprocal cross-hybridization. The phenotypic means of the parents TN 57 and CP are included. Comparisons (within reciprocal cross) having the same superscripts did not differ significantly ( $P < 0.05$ ), according to both *t*-test and Mann-Whitney U test.

Trait	♀ CP × ♂ TN 57 (n = 200)			♀ TN 57 × ♂ CP (n = 200)			TN 57 (n = 10)		CP (n = 10)	
	Range	Mean	SD	CV %	Range	Mean	SD	CV %	Mean	Mean
Top fresh weight (g)	10~2700	419.0 <sup>b</sup>	190.2	45.4	10~2250	600.2 <sup>a</sup>	310.0	51.6	940	1390
Storage root										
Fresh weight (g)	160~4220	986.9 <sup>b</sup>	418.9	42.4	60~3000	1420.4 <sup>a</sup>	560.2	39.4	2180	2350
Number	1~20	6.2 <sup>a</sup>	3.0	48.1	1~16	6.4 <sup>a</sup>	2.5	39.7	6.5	7.0
Skin color*	1~2	1.7 <sup>a</sup>	0.4	24.5	1~2	1.6 <sup>a</sup>	0.4	30.6	1.0	2.0
Flesh color*	1~3	2.0 <sup>a</sup>	0.9	50.0	1~3	2.0 <sup>a</sup>	0.9	48.5	1.0	3.0
Starch content (%)	64.6~86.7	78.4 <sup>a</sup>	3.9	4.9	68.8~93.6	79.1 <sup>a</sup>	3.9	4.9	82.4	77.9
Amylose content (%)	32.4~40.5	32.0 <sup>a</sup>	1.4	4.6	33.1~41.1	37.4 <sup>a</sup>	1.4	3.7	38.4	37.5
Sugar content (%)	3.2~17.3	8.3 <sup>a</sup>	2.5	29.8	1.9~16.9	7.3 <sup>a</sup>	2.6	36.2	7.5	9.8
Crude protein content (%)	2.5~7.5	4.4 <sup>a</sup>	0.7	16.5	3.0~6.2	4.4 <sup>a</sup>	0.7	15.6	3.1	3.8

\*The root flesh color and skin color were examined according to the Kidgway's "Standard Color Chart" rating 1~3 for yellow, red and purple.

and storage roots existed among the parents. Nevertheless, maternally-inherited variation in the number, skin color, flesh color, starch content, amylase content, sugar content, and crude protein content of storage roots were not observed in this experiment due to non-significant differences between means in these traits within the crosses (Table 2). Reciprocal crosses were made to determine the pattern of inheritance. Results from Tables 1 and 2 indicate that fresh weight of tops and storage roots showed marked differences using NH and TN57 as the seed parents. Cytoplasmic genes may be influencing these traits.

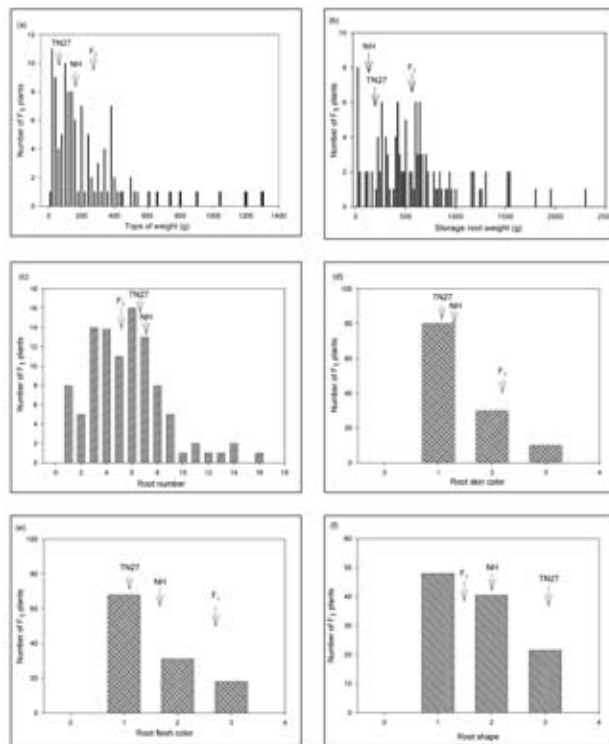
The average root weight of NH×TN 27 was 548.3 g, ranging from 20 g to 2,200 g, and that of TN 27×NH was 555.0 g, ranging from 10 g to 1600 g. In the parents, TN 27 and NH, the mean values were 197.1 g and 84.6 g, respectively (Table 1). In addition to root weight, the average top weight values of NH×TN 27 (290.0 g) and TN 27×NH (172.3 g) were also higher than those of TN 27 (90.9 g) and NH (163.2 g). Therefore, the  $F_1$  populations were heterotic and had substantially higher mean fresh weight of tops and roots than their parents. In Table 2, the percentage of crude protein for the CP×TN 57 population ranged from 2.5 to 7.5, with a mean value of 4.4 on a dry weight basis. In the population developed from TN 57×CP, the range of crude protein was from 3.0 to 6.2% (mean= 4.4). The mean values of % crude protein from both hybrid populations were substantially higher than that from either TN 57 (3.1%) or CP (3.8%). Thus,  $F_1$  populations showed heterotic on % crude protein, and it was possible to select 4.4% of crude protein from 2.5 to 7.5% of crude protein evaluated, so far as this trait was concerned. Fresh weight of tops and roots (Table 1) and crude protein (Table 2) showed heterotic characteristics, suggesting that these three traits can be improved through hybridization of a breeding program. Most likely, dominant genes play an important role in controlling these traits.

Shi et al. (1999a, b) reported that rice nutrient quality traits of protein and lysine contents were found to be simultaneously controlled by seed, cytoplasmic and maternal genetic effects. Zhang et al. (2004) showed significant genetic correlations of maternal additive and maternal dominance between grain characteristics like 100-grain weight, grain length, grain width, grain shape, and the content of mineral elements Fe, Zn, Mn and P in Indica black pericarp rice. In this study, a combination of maternal effect and heterosis of the top weight, root weight and crude protein in the reciprocal crosses (both NH × TN27 and TN57 × CP) could be considered a desirable breeding goal since the female parents NH and TN57 were chosen for crossing. Breeders should pay attention to the direction of crosses in using these parents to increase the top weight, root weight, and crude protein. These results also provide resource material for researchers interested in the genetic and physiological aspects of the yield and quality relationship in sweet potatoes.

The coefficients of variation (CV) for NH×TN 27 ranged from 25% (storage root flesh color) to 54.5% (storage root fresh weight). While in the TN 27×NH, CV in fresh weight of both tops (54.0%) and storage roots (53.8%) were high compared with the other four traits (Table 1). Notably, both flesh and skin color of storage roots had lower CV than other traits in both populations, suggesting that selection for both traits may not be as effective as other traits. The CV% was lower for both skin and flesh color of storage root probably because there were only these values for these traits and therefore less variation was possible. In addition, the CV for number (52.2%), skin color (37.0%) and flesh color (25%) of storage roots showed NH×TN 27 to be more variable than the progeny group from TN 27×NH (Table 1). In contrast, the CV for top fresh weight showed the  $F_1$  population TN 27×NH to be more extended (54.6%) than NH × TN27 (38.2%). In Table 2, the CV for the nine measured traits among  $F_1$  population ranged from 4.6% (amylose content) to 50.0% (storage root flesh color) for CP×TN 57, and from 3.7% (amylose content) to 51.6% (top fresh weight) for TN 57×CP. It is noteworthy that in the TN 57 × CP population, CV of storage root flesh color (48.5%) displayed a twelve-fold greater increase than amylose content (3.7%). Breeding for storage root flesh color may be easier than for amylose content due to its higher CV value.

Figures from 1 to 4 show the distribution of measured traits in the  $F_1$  populations derived from reciprocal crosses among (NH × TN27) and (CP × TN57). Figures 1 and 2 show large differences in the fresh weight of tops and storage root of sweet potato. Furthermore, the distribution of skin color, flesh color, and shape of storage roots was distorted and skewed to yellow and long shape (Figure 1d-f). In Figures 3 and 4, segregation distortions were found in most traits of both populations. Nevertheless, the values for skewness and for kurtosis of the starch content in CP×TN 27 were both close to 0, indicating that starch content tended to be distributed with transgressive segregation (Fig. 4f). Additionally, the distribution of storage root flesh color in both populations (Figures 3e and 4e) was bimodal towards yellow and purple, characteristic of TN 57 and CP parents. Large phenotypic variations in top fresh weight and number, fresh weight, starch content, amylose content, sugar content, and crude protein of storage roots were apparent among the  $F_1$  populations (Figures 1-4). These traits in both reciprocal crosses displayed approximately continuous variations. These variations were likely environmentally based. There is greater genetic differentiation between parents and within parents. Since only ten plants of each parent were grown, we did not know whether  $F_1$  populations displayed more phenotypic variations than the parents. Yield-related traits in sweet potato are generally thought to be quantitative inherited traits significantly affected by variation in environmental factors. Thus, breeding for high yield is restricted due to the complexity of these traits and the sensitivity to environmental changes (Ukoskit and

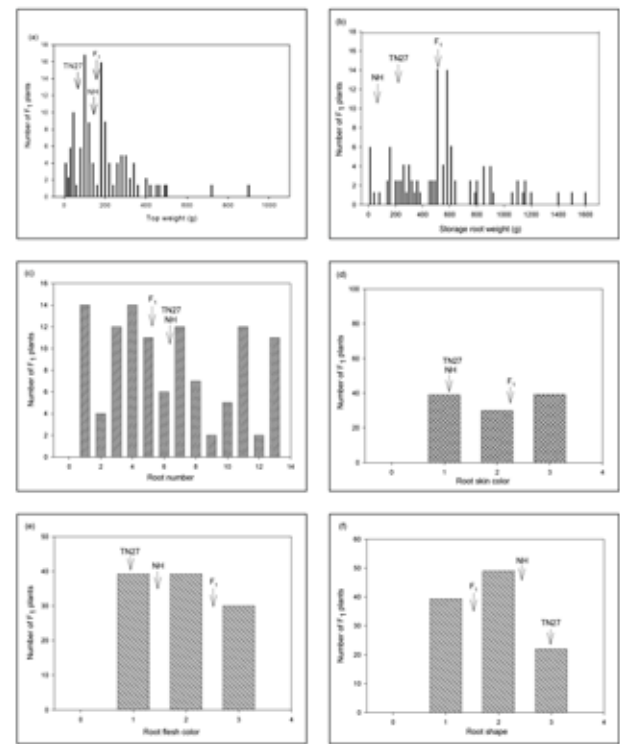




**Figure 1.** Frequency distribution of (a) top fresh weight; (b) storage root fresh weight; (c) storage root number; (d) storage root skin color; (e) storage root flesh color, and (f) storage root shape among  $F_1$  population from TN 27  $\times$  NH. The mean values of parents (TN 27 and NH) and  $F_1$  are shown by arrows.

Thompson, 1997; Huang and Sun, 2000; Hwang et al., 2002; Tseng et al., 2002; Kriegner et al., 2003; Lin et al., 2006; 2007).

Top fresh weight (Figures 1a, 2a, 3a and 4a), fresh weight (Figures 1b, 2b and 3b) and numbers (Figures 1c, 3c and 4c) of storage roots in this study showed a skew towards low-yield characteristics, presumably resulting from the stress of low temperatures during the winters of 2002 and 2004. In general, average day/night temperatures for October, November, and December at CAES were 29/24°C, 23/19°C and 20/14°C, respectively. The sweet potato is native to warm regions and generally injured at low temperatures (Salveit, 2000). It is a plant species resistant to drought stress because its deep-root system accesses moisture. Although sweet potato has been adapted for growth in all seasons and all of Taiwan is subtropical, it is often seriously damaged by chilling currents or cold fronts that frequently occur during each winter season. Low temperature and low irradiance are the primary physiological constraints to production in winter. In our observations, the lower leaves of most of the plants appeared epinastic and senescent during harvest time (photos not shown). Some of the chilling damage was irreversible, but of the damaged parts recovered. Different plants responded differently to chilling stress. In addition to environmental factors, the  $F_1$  population sizes used for this study might not be sufficient to obtain the expected



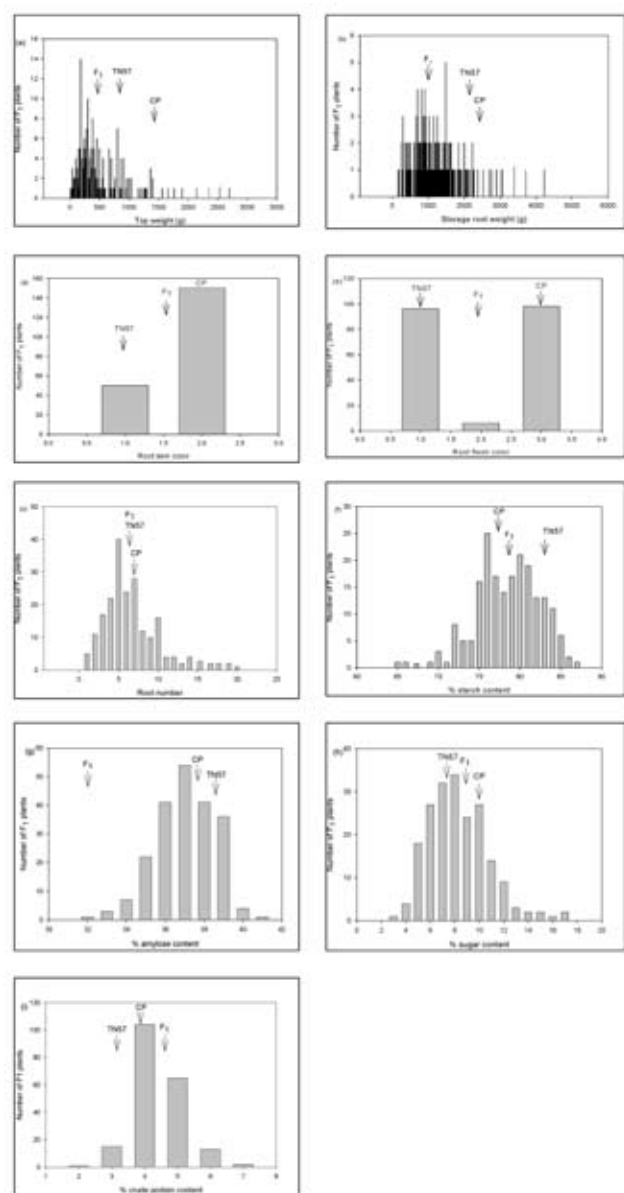
**Figure 2.** Frequency distribution of (a) top fresh weight, (b) storage root fresh weight, (c) storage root number, (d) storage root skin color, (e) storage root flesh color, and (f) storage root shape among  $F_1$  population from NH  $\times$  TN 27. The mean values of parents (NH and TN 27) and  $F_1$  are shown by arrows.

normal distribution in this manner. Correlations existing between these yield-related traits were observed (Tables 3 and 4). In this case, environmental conditions affected one character which then may have interacted with another. Differences in all of the measured traits among and within lines at low temperatures could not be attributed to one major physiological factor, but rather to a combination of responses.

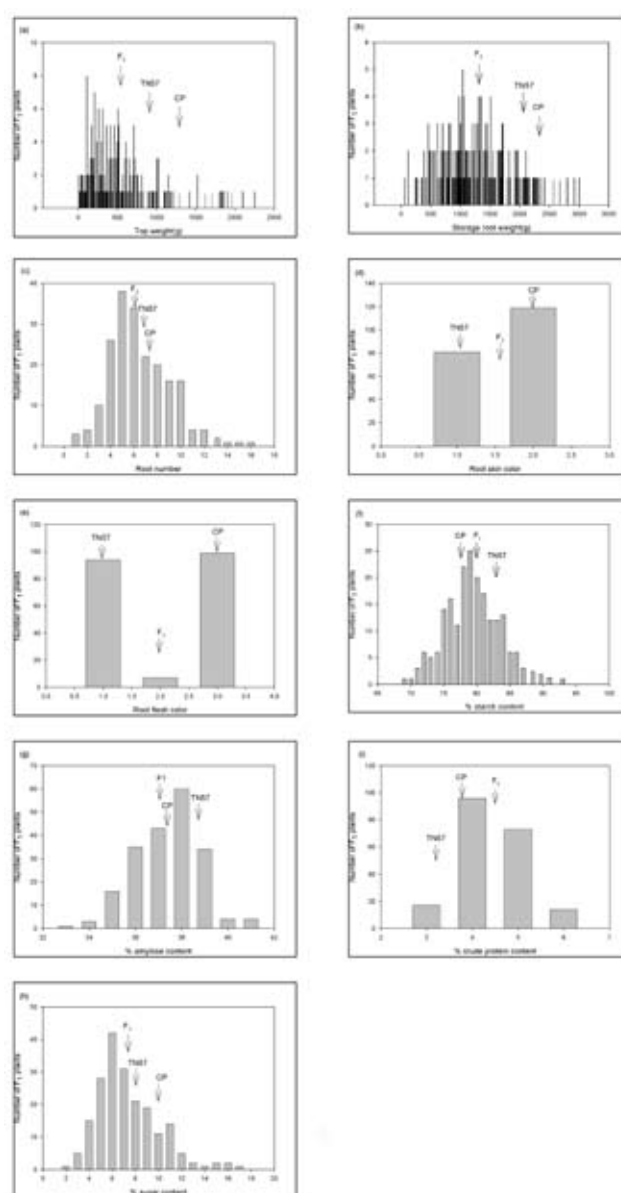
Values for the Pearson correlation coefficients showing the relationship between traits of reciprocal crosses are given in Tables 3 and 4. The top weight of NH $\times$ TN 27 was significantly and positively correlated to fresh weight ( $r=0.68$ ,  $P\leq 0.001$ ), number ( $r=0.22$ ,  $P\leq 0.05$ ), and shape ( $r=0.31$ ,  $P\leq 0.001$ ) of storage root (Table 3a). Positive correlations were also observed between fresh weight and number ( $r=0.56$ ,  $P\leq 0.001$ ) and shape ( $r=0.35$ ,  $P\leq 0.01$ ) of storage roots. Moreover, in the TN 27  $\times$  NH (Table 3b), significantly positive  $r$  values were found between top weight and root weight ( $r=0.65$ ), top weight and root number ( $r=0.36$ ), and root weight and root number ( $r=0.42$ ). However, no significant differences of  $r$  values between the remaining traits were detected in either of the populations. These results indicate that improvement of top weight could be accomplished by indirect selection for fresh weight and number of storage roots regardless of the reciprocal crosses. Similarly, selecting a high root weight tends to increase the root number in both populations.

Thus indirect selection of high fresh weight of both tops and roots could affect the root shape of hybrid progenies from NH×TN 27 (Table 3a). Table 4 displays positive and significant ( $P \leq 0.001$ ) correlations between the fresh weight of tops and storage roots in CP×TN 57 ( $r=0.53$ ) and TN 57×CP ( $r=0.47$ ). With a higher top weight, more storage roots were harvested in both populations. Increasing the root weight seemed to result in an increase in the root numbers in both populations. Meanwhile, the selection of root skin color tended to increase root flesh color in both populations ( $r=0.6$  and  $0.86$ ). Starch content seemed to affect amylose content in TN 57×CP population (Table 4b). On the other hand, significantly negative

correlations of  $-0.71$ ,  $-0.78$  and  $-0.19$  were observed in the CP×TN 57 population between starch content and sugar content, amylose content and sugar content, and amylose content and crude protein content, respectively (Table 4a). Significantly negative  $r$  values were detected between top weight and skin color ( $r = -0.24$ ) and flesh color ( $r = -0.25$ ) of storage root, starch content, and sugar content ( $r = -0.81$ ), and amylose content and sugar content ( $r = -0.83$ ) (Table 4b). No significant correlations emerged between crude protein content or other traits in either population, except that high crude protein would probably be low in amylose content ( $r = -0.19$ ) (Table 4a).



**Figure 3.** Frequency distribution of (a) top fresh weight, (b) storage root fresh weight, (c) storage root number, (d) storage root skin color, (e) storage root flesh color, (f) starch content, (g) amylose content, (h) sugar content, and (i) crude protein content among  $F_1$  population from TN 57 × CP. The mean values of parents (TN 57 and CP) and  $F_1$  are shown by arrows.



**Figure 4.** Frequency distribution of (a) top fresh weight, (b) storage root fresh weight, (c) storage root number, (d) storage root skin color, (e) storage root flesh color, (f) starch content, (g) amylose content, (h) sugar content, and (i) crude protein content among  $F_1$  population from CP × TN 57. The mean values of parents (CP and TN 57) and  $F_1$  are shown by arrows.

**Table 3.** Correlation coefficients among the six traits of  $F_1$  populations from (a) NH×TN 27 (n = 119), and (b) TN 27×NH (n = 112).

Trait	Storage root				
	Fresh weight	Number	Skin color	Flesh color	Shape
(a) ♀ NH × ♂ TN 27 (n = 119)					
Top fresh weight	0.68***	0.22*	0.06 <sup>NS</sup>	0.02 <sup>NS</sup>	0.31**
Storage root					
Fresh weight		0.56***	-0.05 <sup>NS</sup>	-0.07 <sup>NS</sup>	0.35**
Number			0.03 <sup>NS</sup>	-0.03 <sup>NS</sup>	0.11 <sup>NS</sup>
Skin color				0.04 <sup>NS</sup>	-0.14 <sup>NS</sup>
Flesh color					-0.13 <sup>NS</sup>
(b) ♀ TN 27 × ♂ NH (n = 112)					
Top fresh weight	0.65**	0.36**	0.10 <sup>NS</sup>	-0.05 <sup>NS</sup>	0.18 <sup>NS</sup>
Storage root					
Fresh weight		0.42**	0.19 <sup>NS</sup>	0.08 <sup>NS</sup>	0.14 <sup>NS</sup>
Number			0.01 <sup>NS</sup>	-0.05 <sup>NS</sup>	-0.15 <sup>NS</sup>
Skin color				0.11 <sup>NS</sup>	-0.01 <sup>NS</sup>
Flesh color					-0.20 <sup>NS</sup>

\*, \*\*, \*\*\*significant at  $P < 0.05$ , 0.01, 0.001; NS: non-significant difference.

Positively significant correlations between fresh weight of tops and storage root, top weight and root number, and fresh weight and number of roots from both experiments (Tables 3 and 4), suggest that top weight may be used as an indicator for storage root yield (fresh weight and number). Improved top weight would significantly complement storage root yield. Storage root number also could compensate for storage root fresh weight. The economic benefit of improved storage root yield is manifest in increasing both number and fresh weight. It appears unlikely that increased top fresh weight would be accompanied by a significant increase in storage root yield, presumably due to the availability of enough photosynthate from tops to storage roots. The dilution effect resulting from competition for photosynthate was not observed in this study, and high leaves and stems might not have to be sacrificed to obtain high root yields in this range. These yield-related traits could be inherited dependently, and increased storage root yield might be obtained by breeding cultivars with high top fresh weights. This would achieve the breeding goal by indirectly selecting yield traits with a high correlation in different crosses. However, if the significant positive correlations between the yield traits were due to maternal effects, selection for the desired traits could be made on the basis of higher performance of the traits of maternal parents.

Controlling the storage root flesh color of sweet potato has become a goal of breeders and researchers. The flesh color of most sweet potato lines are red and yellow, and deeper root color indicates higher beta-carotene (Li, 1982). In this study, root color was significantly correlated with

skin color in CP×TN 57 ( $r=0.6$ , Table 4a) and TN 57×CP ( $r=0.86$ , Table 4b), but not in the TN 27×NH reciprocal cross. It seems clear that crosses vary to a considerable extent in their colors and that it should be possible through breeding to select new varieties for both skin color and root color. Similarly, root shape was significantly affected by top weight ( $r=0.31$ ) and root weight ( $r=0.35$ ) in NH×TN 27, but not TN 27×NH (Table 3). Thus, top weight and root weight could be effectively applied to the selection of root shape.

Starch, amylose, sugar, and protein are recognized as four important quality characteristics in sweet potato breeding programs for human consumption and food processing. Starch and amylose contents are associated with eating quality. Percentage of starch content was significantly influenced by amylose content ( $r=0.81$ , Table 4b) in TN 57×CP, but not CP×TN 57. Thus, the starch content is immediately available to sweet potato breeders for making modifications to amylose content within traditional hybridization. Negative correlations exist between % sugar and % starch and amylose content in CP ×TN 57 reciprocal cross (Table 4); therefore, concurrent selection for high % sugar, high % starch, and high % amylose might be difficult.

In conclusion, large variations in the  $F_1$  hybrids were found in most of the measured traits. Variation in the maternally-inherited plant genomes effect both top weight and root weight. Selection from the NH and TN57 as female parent would significantly effect these two traits. Meanwhile, top weight, root weight and % crude protein of the  $F_1$  populations also showed heterotic characteristics.

**Table 4.** Correlation coefficients among the nine traits of F<sub>1</sub> populations from (a) CP×TN 57 (n = 200), and (b) TN 57×CP (n = 200).

Trait	Storage root							
	Fresh weight	Number	Skin color	Flesh color	Content			
					Starch	Amylose	Sugar	Crude protein
(a) ♀ CP × ♂ TN 57 (n = 200)								
Top fresh weight	0.53***	0.27**	-0.04 <sup>NS</sup>	-0.06 <sup>NS</sup>	-0.06 <sup>NS</sup>	-0.09 <sup>NS</sup>	0.04 <sup>NS</sup>	0.01 <sup>NS</sup>
Storage root								
Fresh weight		0.50***	-0.02 <sup>NS</sup>	0.03 <sup>NS</sup>	-0.02 <sup>NS</sup>	-0.02 <sup>NS</sup>	-0.01 <sup>NS</sup>	-0.01 <sup>NS</sup>
Number			0.03 <sup>NS</sup>	-0.02 <sup>NS</sup>	-0.06 <sup>NS</sup>	-0.01 <sup>NS</sup>	0.03 <sup>NS</sup>	0.02 <sup>NS</sup>
Skin color				0.60***	-0.01 <sup>NS</sup>	-0.05 <sup>NS</sup>	0.03 <sup>NS</sup>	0.05 <sup>NS</sup>
Flesh color					0.01 <sup>NS</sup>	-0.03 <sup>NS</sup>	0.04 <sup>NS</sup>	0.06 <sup>NS</sup>
Content								
Starch						0.07 <sup>NS</sup>	-0.71***	0.05 <sup>NS</sup>
Amylose							-0.78***	-0.19**
Sugar								-0.01 <sup>NS</sup>
(b) ♀ TN 57 × ♂ CP (n = 200)								
Top fresh weight	0.47***	0.17*	-0.24**	-0.25**	-0.01 <sup>NS</sup>	0.04 <sup>NS</sup>	-0.01 <sup>NS</sup>	-0.04 <sup>NS</sup>
Storage root								
Fresh weight		0.55***	0.01 <sup>NS</sup>	0.02 <sup>NS</sup>	-0.01 <sup>NS</sup>	-0.03 <sup>NS</sup>	0.11 <sup>NS</sup>	0.04 <sup>NS</sup>
Number			0.01 <sup>NS</sup>	0.03 <sup>NS</sup>	0.06 <sup>NS</sup>	-0.01 <sup>NS</sup>	-0.01 <sup>NS</sup>	0.07 <sup>NS</sup>
Skin color				0.86**	0.01 <sup>NS</sup>	0.03 <sup>NS</sup>	-0.04 <sup>NS</sup>	-0.05 <sup>NS</sup>
Flesh color					0.03 <sup>NS</sup>	0.03 <sup>NS</sup>	-0.05 <sup>NS</sup>	-0.09 <sup>NS</sup>
Content								
Starch						0.81***	-0.81***	0.05 <sup>NS</sup>
Amylose							-0.83***	0.02 <sup>NS</sup>
Sugar								-0.10 <sup>NS</sup>

\*, \*\*, \*\*\*significant at P<0.05, 0.01, 0.001; NS: non-significant difference.

It appears possible to obtain high top weight, high root weight, and root number since these traits were significantly positively correlated. These results may be used to guide indirect selection for nutritional quality and yield of the sweet potato. Sweet potatoes are known to be sensitive to environmental changes. Most of the yield- and quality-related traits were distributed continuously, which is indicative of quantitative inherited characters. Improvement of these traits requires a complex and prolonged breeding process. We currently use the available F<sub>1</sub> segregating populations to identify the molecular marker (i.e. inter simple sequence repeat, ISSR) linked to these important economic traits in sweet potatoes. Using these markers as a selection tool to improve these traits is still being worked out.

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## 改進甘藷品質與產量育種之效益

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甘藷是世界重要經濟作物之一。本試驗藉由甘藷‘台農 27 號’(TN27) × ‘Nancy hall’(NH)及‘台農 57 號’(TN57) × ‘清水紫心’(CP) 兩組正、反交，獲得產量與品質之母系效應資訊。兩組正、反交於同一地點、分兩年完成，調查 TN27 × NH 119 株、NH × TN27 112 株、TN57 × CP 200 株以及 CP × TN57 200 株之經濟性狀之遺傳性、及性狀間之相關性。結果顯示上述 4 個 F<sub>1</sub> 分離族群各性狀之平均值及變異係數均有相當差異。地上部重及塊根重具有母系效應，而地上部重、塊根重及粗蛋白則具有雜種優勢。地上部重，塊根重及塊根數之分布圖則出現偏向低產量特性之歪峰分布。地上部重、塊根重及塊根數之間、塊根形狀與地上部重及塊根重之間、皮色及肉色之間、以及澱粉含量及 amylose 含量之間均呈現顯著正相關。澱粉含量、amylose 含量與糖含量及粗蛋白含量之間有顯著負相關，可藉由選拔低澱粉及 amylose 含量改良糖含量及粗蛋白含量。選用母系親本可以有效改良甘藷品質及產量相關性狀。

**關鍵詞：**母系效應；正反交；甘藷育種。