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Amylase Activity and Bio-Chemical Estimation of Different Genotypes of Post-Harvest Banana Corms

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ABSTRACT

Banana corm left in the field reserved high organic content which can nourish the soil as a compost and as a plant material for propagation. Due to less interest shown to these left-over corms their reserved content has never been estimated or used for generating propagules therefore this experiment was conducted to evaluated amylase activity, soluble protein, protein content, soluble sugar and starch of thirty-three corms of different banana genotypes belonging to three different genomic composition. The amylase activity in the corms of the genotypes varied between 0.02 µg in Robusta Clone II (AAA) and 0.80µg in Green Bombay (ABB) of maltose g^{-1} of fresh tissue min^{-1}. The soluble sugar level in the corms of the genotypes varied between 0.99% in Robusta Clone-II (AAA) and 7.5% in Champa-IV (AAB). The starch level in the corms of the genotypes varied 64.63% in Champa-IV (AAB) and 77.06% in Lacaton (AAA). The soluble protein level in the corms of the genotypes varied between 0.11% in Poovan –B9 (AAB) and 2.59% in Lacaton (AAA). The crude protein content in the corms of the genotypes varied between 1.07% in Champa-IV (AAB) and 6.64% in Alpan-Manhar (AAB). This composition state that post-harvest banana corm has sufficient organic content reserved in it which can be used either for promoting propagules or making organic compost.

Keywords Amylase, Corms, Genotypes, Proteins, Sugar, Starch.

INTRODUCTION

Plantain and banana are monocotyledonous plants, belonging to the section Eumusa within the genus *Musa* of the family Musaceae and are grouped according to their "ploidy" and the relative proportion of *Musa acuminata* (A) and *Musa balbisiana* (B) in their genome. Most familiar, seedless cultivars are triploid hybrids (AAA, AAB, ABB) and are typically sterile or have extremely low fertility. Banana produces fruit pulp without pollination and fruits lacking seed. Banana has high fiber content that helps in maintaining the digestive system in good health along with the regular bowel movements thus speeds up the process of digestion (Stewart 2014). A normal size banana provides about 105 calories (Mateljan 2007). Banana is also rich in carbohydrates (22.84 g/100 g), provides energy about 370 kJ/100 (Ranjha *et al.* 2022). Banana residues being organic in nature can be recycled to

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prevent their disposal in environment, thus sustaining the balance between economic development and environmental protection (Memon *et al.* 2012).

Banana corm (rhizome) produces off shoots of young banana plants that grow in clusters around the "mother" plant. These corm act as storage reserve material for nourishing new young sucker. Dormant corm that no longer produce propagules de-compost itself and act excellent source of plant available nutrient and their addition to soil could maintain high microbial populations and activities (Pascual *et al.* 1997). However, amount of these reserved organic content is not known as less interest were shown to these corms left in the field after harvesting of the bunch. With the aim to estimate organic content reserved in post-harvest banana corms the title bio-chemical estimation in post-harvest banana corms of different genotypes were taken into the experiment.

MATERIALS AND METHODS

The experiment was conducted between March 2019 to May 2019. The corms for the experiment were collected from the banana plants raised and maintained at banana plantation garden of AICRP – Fruit Crops, Horticulture Research Station, BCKV, Mandouri Farm, West Bengal. The estimation of soluble protein, amylase activity and soluble sugar and starch content was done in the Nutrio-Physiology Lab, Department of Plant Physiology, BCKV. The estimation of crude protein was done in the Arsenic laboratory at Kalyani Research Building of BCKV, West Bengal.

A total of thirty-three post-harvest banana corms (Table 1) of different genotypes belong to three different genomic groups were evaluated for their amylase activity and bio-chemical content. After harvesting of the bunch, banana trunks left in the field were de-topped just above the juncture of the corm and ariel shoot. These corms were then removed from the soil and clean properly under running tap water to discard dirt and other substances left on the corm. The roots and a layer of the corm was peeled and removed with the help of a knife to remove debris. The starchy corm left was then cut into small pieces and further used for the following estimation :

Estimation	Method followed
Soluble protein	As per Lowry *et al.* (1951)
Soluble sugar and starch	Anthrone reagents as per Yoshida *et al.* (1972)
Enzyme activity of amylase	Dinitrosalycyclic acid (DNSA) assay following bernfeld (1955)
Crude protein	Nitrogen determination as per Kjeldahl Method (1883) followed by multiplication of a factor 6.25

Table 1. Names and the genomic compositions of the banana genotypes.

Genomic composition	AAA	AAB	ABB
Cultivar name	Srimanti	Chang Monoa CO-1	Cooking III
	Jahaji Clone-I		Kothia
	Jahaji Clone-II	Madhuranga bale	Green Bombay
	Grand naine	Papalou	Baish Chhara
	Giant Governor	Kalibhog	NRCB-08
	Amrit Sagar Clone-I	Sabri	BCB-2
	Amrit Sagar Clone-III	Martaman	
	Robusta Clone-II	MAtta Poovan	
	Lacaton Arunachal	Poovan–B9	
	P. colln	Champa–B11	
		Champa-I	
		Champa-II	
		Champa-III	
		Champa-IV	
		Champa-V	
		Alpan-Mahnar H531	

RESULTS AND DISSCUSSION

Amylase activity of the corms

The amylase activity (µg of maltose mg^{-1} of fresh tissues min^{-1}) of the corms of the genotypes varied between 0.02 µg in Robusta Clone II (AAA) and 0.80 µg in Green Bombay (ABB). Among the genotypes with AAA genomic composition, it ranged between

Table 2. Amylase activity and bio-chemical content of the banana genomic composition AAA.

Genomic composition	Cultivar name	Amylase activity (µg)	Sugar (%)	Starch (%)	Soluble protein (%)	Crude protein (%)
	Srimanti	0.31	2.38	76.58	2.21	2.44
	Jahaji Clone-I	0.30	3.19	75.43	1.26	2.79
	Jahaji Clone-II	0.52	5.00	71.13	2.11	4.52
	Grand Naine	0.23	3.50	71.68	0.17	4.45
AAA	Giant Governor	0.02	2.71	75.42	1.86	3.12
	Amrit Sagar Clone-I	0.37	4.01	71.79	0.94	4.12
	Amrit Sagar Clone-III	0.06	7.50	69.46	0.25	4.96
	Robusta Clone-II	0.02	0.99	76.99	0.23	3.53
	Lacaton	0.10	2.63	77.06	2.59	2.32
	Arunachal *P. colln*	0.24	2.38	76.58	1.19	4.21
	Mean	0.22	3.43	74.21	1.28	3.65
	Range	0.02-00.52	0.99-7.50	69.46-77.06	0.17-2.59	2.32-4.96

0.02 µg and 0.52 µg, the genotypes with AAB genomic composition ranged between 0.09 µg and 0.67 µg, the genotypes with ABB genomic composition ranged between 0.15 µg and 0.80 µg. There appeared to have no pattern in enzyme activity of amylase among the genomic groups: The high, moderate and low values for amylase activity were almost equally distributed among different genomic groups. The amylase activity is considered as an indicator for dormancy status of the rhizomes. The cultivars with very low amylase activity probably are in dormant condition and it shows that rhizomes of such cultivars undergo to dormancy for a certain period after the harvest of the crop. Whereas the genotypes with moderate to high amylase activity probably are not in dormant stage and in cases of them the dormancy stage is either very briefed or non-existence. The β-amylase activity was reported to be enhancing when the physiological process for sprouting was started to initiate (Claassens 2002). The conclusion of amylase to starch breakdown in dormant potato tuber is thought to be less (Bailey *et al.* 1978). Davies (1990) reported that α-amylase is not detectable in dormant tubers. Claassens (2002) found that the activity of

Table 3. Amylase activity and bio-chemical content of the banana genomic composition AAB.

Genomic composition	Cultivar name	Amylase activity (µg)	Sugar (%)	Starch (%)	Soluble protein (%)	Crude protein (%)
	Chang Monoa	0.09	2.23	70.96	1.19	5.52
	CO-1	0.11	4.16	70.15	0.13	4.91
	Madhuranga bale	0.45	4.85	68.31	0.12	6.60
	Papalou	0.14	1.06	76.07	1.72	3.87
	Kalibhog	0.26	6.20	70.92	0.35	4.59
	Sabri	0.26	2.96	73.43	0.98	4.10
	Martaman	0.09	5.50	68.53	0.52	5.39
	Matta Poovan	0.11	1.13	74.48	0.12	4.43
AAB	Poovan –B9	0.51	5.12	70.68	0.11	4.77
	Champa	0.31	4.20	73.76	0.97	4.07
	Champa-I	0.16	2.50	71.41	0.19	6.19
	Champa-II	0.13	1.96	75.02	0.68	4.15
	Champa-III	0.25	7.45	69.66	0.31	4.09
	Champa-IV	0.67	7.50	64.63	0.31	1.07
	Champa-V	0.43	5.42	72.74	0.33	3.64
	Alpan-Mahnar	0.36	2.13	73.02	0.65	6.64
	H531	0.23	2.76	71.10	0.85	6.15
	Mean	0.27	3.95	71.46	0.56	4.72
	Range	0.09-0.67	1.06-7.50	64.63-76.07	0.11-1.72	1.07-6.64

Table 4. Amylase activity and bio-chemical content of the banana genomic composition ABB.

Genomic composition	Cultivar name	Amylase activity (µg)	Sugar (%)	Starch (%)	Soluble protein (%)	Crude protein (%)
	Cooking III	0.30	3.11	76.08	1.06	1.56
	Kothia	0.15	2.10	75.90	1.33	2.18
	Green Bombay	0.80	5.31	68.65	0.83	5.23
ABB	Baish Chhara	0.21	5.25	66.00	0.38	2.44
	NRCB-08	0.44	4.91	74.05	0.16	2.97
	BCB-2	0.51	5.15	71.71	0.48	4.14
	Mean	0.40	4.31	72.07	0.71	3.09
	Range	0.15-0.80	2.10-5.31	66.00-76.08	0.16-1.33	1.56-5.23

alpha amylase is consistently lower than that of beta amylase in dormant micro-tuber. The activity of both enzyme decreases during storage but the activity of beta amylase decreases to larger extents. However, the conclusion to this process increases following the termination of dormancy and as starch break down proceeds (deviation). Among the cultivars with genomic composition AAA (Table 2), Robusta Clone-II, Giant Governor, Amrit Sagar Clone- III and Lacaton was poor in amylase activity and Jahaji Clone- II was rich in amylase activity. Similarly, among the cultivars with genomic composition AAB (Table 3), Martaman, CO-1, Matta Poovan, Champa-II and Papalou was poor in amylase activity and Madhuranga bale, Poovan –B9 and Champa-IV was rich in amylase activity. The cultivars with the genomic composition ABB (Table 4) show moderate level of amylase activity except Kothia with poor activity.

Soluble sugar content of the corms

The soluble sugar content (%) of the corms of the genotypes varied widely between 0.99% in Robusta Clone-II (AAA) and 7.5% in Amrit Sagar Clone-III (AAA) and Champa-IV (AAB). Among the genotypes with AAA genomic composition, it ranged between 0.99% and 7.50%, the genotypes with AAB genomic composition ranged between 1.06% and 7.45% and the genotypes with ABB genomic composition ranged between 2.10% and 5.31%. There appeared to have no pattern in soluble sugar among the genomic groups. The high, moderate and low values for soluble sugar content were almost equally distributed. Among the cultivars with genomic composition AAA (Table 2), Robusta Clone-II was found to have low soluble sugar content and Amrit Sagar Clone-III and Jahaji Clone-II were found to have higher in soluble sugar content. Similarly, among the cultivars with genomic composition AAB (Table 3), Papalou, Matta Poovan and Champa-II were found to have low soluble sugar content and Champa-IV, Champa-III, Kalibhog were found to be higher in soluble sugar content, the cultivars with genomic composition ABB (Table 4) were found to have moderate content of soluble sugar. There no information about soluble level of banana corms. However, Mareček *et al.* (2013) reported that the soluble sugar of potato genotypes generally fluctuated between 0.2% to 1.26%. Mesta *et al.* (2017) reported that different varieties of *Amorphophallus paeoniifolius* (elephant foot yam) was estimated for their total sugar and reducing sugar content and found that it ranged from 1.31%-11.16% and 0.32%-4.28% respectively. Soluble sugar content is a metabolic indicator and may vary depending on its dormancy status and many other factors.

Starch content of the corms

The starch content (%) of the corms of the genotypes varied between 64.63% in Champa-IV (AAB) and 77.06% in Lacaton (AAA). Among the genotypes with AAA genomic composition, it ranged between 69.4% and 77.06%, the genotypes with AAB genomic composition ranged from 64.63% and 76.07%, the genotypes with ABB genomic composition ranged between 66.0% and 76.08%. There appeared to have no pattern in starch content among the genomic groups: The high, moderate and low values for starch content were almost equally distributed. Among the cultivars with genomic composition AAA (Table 2),

Amrit Sagar Clone-III was found to have low starch content and Lacaton, Robusta Clone-II Srimanti and Arunachal *P. colln* were found to have higher in starch content. Similarly, among the cultivars with genomic composition AAB (Table 3), Champa-IV, Madhuranga bale and Martaman were found to have low starch content and Papalou and Champa-II were found to be higher in starch content, the cultivars with genomic composition ABB (Table 4), Baish Chhara and Green Bombay were found to have low starch content and highest in Cooking–III and Kothia. Mesta *et al.* (2017) reported that different varieties of *Amorphophallus paeoniifolius* (elephant foot yam) was estimated for their total starch content and found that it ranged from 33.97% to 69.18%. There is hardly any biochemical analysis for the storage profile of banana corm, at least no report is available. The modified stems of a plants generally are very rich in starch. In *Colocasia esculenta,* total carbohydrate accounts up to 82% of the total dry matter (Mulugeta and Tebeka 2017).

Soluble protein of the corms

The soluble protein content (%) of the corms of the genotypes varied between 0.11 (%) in Poovan–B9 (AAB) and 2.59% in Lacaton (AAA). Among the genotypes with AAA genomic composition, it ranged between 0.17% and 2.59%, the genotypes with AAB genomic composition ranged between 0.11% and 1.72%, the genotypes with ABB genomic composition ranged between 0.16% and 1.33%. Most of the genotypes with higher soluble protein content are in the genomic group AAA. The soluble protein is an indicator of the status of metabolic activity of the corms of the genotypes. In the banana plant the corm is a sink and its sink mode of metabolic activity probably remains dominant at least before harvesting. Among the cultivars with genomic composition AAA (Table 2), Grand Naine, Robusta Clone-II, Amrit Sagar clone- I was found to have low soluble protein content and Lacaton, Srimanti and Jahaji Clone-II was found to have higher in soluble protein content. Similarly, among the cultivars with genomic composition AAB (Table 3), Poovan-B9, Madhuranga bale, Matta Poovan, CO-1 and Champa-I was found to have low soluble protein content and Papalou, Chang Monoa and Sabri was found to be higher in soluble protein content. Similarly, among the cultivars with genomic composition ABB (Table 4), NRCB-08 was to have low soluble protein content and Cooking III and Kothia was found to have low soluble protein content. Ortiz-Medina and Donnelly (2003) studied the total soluble protein in fresh field grown potato tuber and obtained its concentration in the range of 38 to 73 mg g^{-1} dry weight which is not far from the range obtained in the post-harvest corms of banana genotypes.

Crude protein content of the corms

The crude protein (%) of the corms of the genotypes varied between 1.07% in Champa-IV (AAB) and 6.64% in Alpan-Manhar (AAB). Among the genotypes with AAA genomic composition, it ranged between 2.32% and 4.96%, the genotypes with AAB genomic composition ranged from 1.07% and 6.60%, the genotypes with ABB genomic composition ranged from 1.56% and 5.23%. There appeared to have no pattern in the crude protein content among the genomic groups: The high, moderate and low values for this content were almost equally distributed. Crude protein may be one of the determinants of sucker production capability of the corm of the genotypes. Among the cultivars with genomic composition AAA (Table 2), Lacaton, Srimanti and Jahaji Clone-I were found to have low content of crude protein and the rest are in moderate level. Similarly, among the cultivars with genomic composition AAB (Table 3) Champa-IV was found to have low crude protein content and Alpan-Mahnar, Madhuranga bale and Champa-I were found to have higher crude protein content, the cultivars with genomic composition ABB (Table 4), Cooking III was found to have low crude protein content and Green Bombay was found the highest. The underground stems like yam (*Dioscorea spp.*) contained from 6.3 to 13.4% crude protein (Martin and Thompson 1971), *Colocasia esculenta* with 4.5% crude protein (Mulugeta and Tebeka 2017). The range from highest to lowest crude protein contents of the materials present experiment were similar to that was reported by Sjofjan *et al.* (2021) who claimed it to be 3.60%.

CONCLUSION

The enzyme activity of amylase in the post-harvest corms varied among the genotypes which may state

that genotypes with very low amylase activity probably undergo dormancy for a certain period after the harvest of the crop. Whereas dormancy in the genotypes with moderate to high amylase activity is either very briefed or non-existence. The bio-chemical content reserved in the post-harvest corms were also found to be highly variable. This may state that some banana genotypes have sufficient organic content reserved in their corms either for promoting propagules or may use as an organic compost. Banana corm were mostly studied for their conventional vegetative propagation through various application. Therefore, this experiment and its results can be useful for scholars or scientist for utilizing left over banana corm and for further advance research on many aspects.

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