

DOI: <https://doi.org/10.24297/jaa.v17i.9848>**Main Title: Interaction of gibberellic acid and β -Amylase in regulating dormancy and sprouting of yam (*Dioscorea* spp.) tubers**Michael Akuamoah BOATENG^{1,2,*}, Esther NSEASOM¹, Philip GHANNEY¹, Jerry AMPOFO-ASIAMA³, Wilfred SEFAH⁴, Francis Osei AMOAKO-ANDOH^{1,2,*}¹ CSIR- Crops Research Institute, Biotechnology Seed and Postharvest Division
P. O. Box 3785, AE-0607-9822, Kumasi, Ghana² CSIR College of Science and Technology, Department of Plant Resources Development, Kumasi, Ghana³ University of Cape Coast, Department of Biochemistry, Cape Coast, Ghana⁴ Kumasi Technical University, Department of Food Technology, Kumasi, Ghana**Abstract**

Prolonged tuber dormancy in yam (*Dioscorea* spp.) is crucial for storage and economic benefits but hinders production and improvement efforts. Understanding dormancy regulation is necessary for genetic manipulation and effective postharvest management. This study, using tuber meristematic tissues of three yam cultivars – CRI-*Ahoɔdenfoɔ* (*D. alata*), *Pona*, and *Labreko* (*D. rotundata*), investigated the influence of endogenous gibberellic acid (GA_3) and the enzymes α - and β -amylase on tuber dormancy and sprouting over 90 days of storage. Sprouting occurred at the proximal end of the tubers and coincided with a significant increase in β -amylase activity and maltose levels in the *D. rotundata* and *D. alata* cultivars at 60 and 90 days after harvest (DAH), respectively. Starch content decreased during storage. α -Amylase activity increased initially, peaking at 30 DAH, before declining and then rising again during the later storage period. The study established that yam tuber dormancy could be maintained by keeping GA_3 content below a threshold limit of 1.8 mg/g, and restricting β -amylase activity to less than a 2.5-fold increase compared to harvest values. The results suggest that dormancy is regulated by a combination of GA_3 and β -amylase activity in the meristematic layer of tubers, with GA_3 likely inducing α -amylase synthesis for enhanced glucose generation, and β -amylase producing more maltose.

Keywords: α - and β -amylase activity; dormancy; gibberellic acid (GA_3); sprouting; yam (*Dioscorea* spp.)**Introduction**

Different yam types (*Dioscorea* spp.) are produced as a major staple tuber crop in many tropical countries, particularly in West Africa. In 2023, out of the total global production of 89.3 million metric tonnes (MT), about 85.4 million MT was produced in West Africa, with Nigeria and Ghana accounting for 61.9 million MT and 10.5 million MT, respectively, both representing close to 85% of global production (FAOSTAT, 2025). Yams are an important source of carbohydrate and protein, making them an excellent staple in the production centres (Hamadina & Asiedu, 2015; Tareen et al., 2025).

After harvest, yam tubers stored for continuous use as food over time also importantly ensure appreciation of their market value to maximise economic returns on the unprocessed fresh tubers. Storage also allows yam tubers to be kept as planting material for the subsequent farming season. Dormancy as a fundamental physiological adaptation mechanism generally ensures that yam tubers, compared to other root and tuber crop species, can be stored for relatively longer periods, thereby enhancing food security. Dormancy is a physiological phase of rest during which there are no outward signs of metabolic activity (Considine & Considine, 2016; Craufurd et al., 2001).

The storage of yam tubers is accompanied by several biochemical and physiological changes that consequently influence quality (Datir et al., 2024; Makanjuola & Osinfade, 2017). The contents of the tuber, including starch, proteins, and other metabolites, along with the catalytic activity of hydrolytic enzymes, have all been shown to vary significantly during dormancy and sprouting (Haider et al., 2023; Hamadina et al., 2015). A horizontal physiological gradient is reported to exist along the length of the yam tuber, which has been demonstrated to significantly influence the distribution and pattern of changes in the contents of stored metabolites during storage (Degbeu et al., 2025; Hamadina & Asiedu, 2015). Knowledge of the dynamics of tuber metabolite contents during storage can provide insights into the mechanisms of tuber dormancy and sprouting, physiological processes which are energy related. However, there is a dearth of information on the dynamic concentrations of gibberellic acid, a growth hormone implicated in regulating dormancy and sprouting in yam tubers, and its consequential influence on the catalytic activity of starch hydrolytic enzymes. Sprouts are developed from meristematic layers beneath the periderm of yam tubers (Hamadina, 2011; Nwogha et al., 2022). Therefore, this study sought to generate insights into the influence of accumulated endogenous gibberellic acid and the catalytic activity of the starch hydrolytic enzymes – α -amylase and β -amylase, within the meristematic layers of yam tubers on dormancy and sprouting during the storage of three yam cultivars.

Materials and Methods

Production and storage of yam tubers

The tubers of *Dioscorea alata* cultivar – CRI-*Ahooedenfoo* and two *Dioscorea rotundata* cultivars – *Pona* and *Labreko*, were generated by establishing the plants under standard field conditions at Fumesua Station of the CSIR-Crops Research Institute, Ghana, and managed using recommended agronomic practices. Having reached physiological maturity eight months after planting, the tubers were harvested and kept in a barn for 90 days. The daily mean minimum and maximum temperatures recorded in the barn were 23.5°C and 30.1°C, respectively, while the corresponding daily mean minimum and maximum relative humidity were 54.0% and 88.5% during the storage period.

Sample preparation

The tubers were sampled at harvest and then every 30 days until the 90th day of storage. Five tubers of each cultivar were randomly selected, thoroughly cleaned under running tap water, and allowed to air dry at room temperature. The yam tubers were sectioned into the head (proximal), middle and tail (distal) regions to facilitate the assessment of sprouting-related biochemical activities at these distinctive parts of the tuber. After peeling off the skin (periderm), the flesh around the tuber sections was sliced out about 1 cm deep to represent the meristematic layer (Boateng, et al., 2021). Representative samples of the meristematic layers for each cultivar were obtained by pooling the corresponding regions of the five sampled tubers (Karp & Lilley, 2009) and lyophilised before being pulverised and kept at -40°C until analysis.

Gibberellic acid content determination

Gibberellic acid content was determined by the method of Holbrook et al. (1961). About 60 mg of pulverised yam sample in triplicate was thoroughly homogenised in 100 mL of absolute ethanol. Twice 5 mL aliquots of this solution for each replicate were transferred into separate 100 mL volumetric flasks and diluted with 5.0 mL absolute ethanol. The content of one of the flasks was further diluted to 100 mL with 30% hydrochloric acid (sample), incubated in a water bath at 20 ± 1°C for 75 min and the absorbance was immediately measured at 254 nm. To the other flask, 35 mL of 5% hydrochloric acid was added and further diluted to volume with deionised water (blank). The content was briefly mixed and absorbance similarly measured. The blank reading was subtracted from that of the sample and gibberellic acid content was determined using a calibration curve developed from standard GA₃ solutions. Gibberellic acid content was expressed as mg GA₃/g dry weight of sample.

α-Amylase activity assay

The catalytic activity of α-amylase (EC 3.2.1.1) was determined using the Amylase SD method (Megazyme Assay Kit), with modification for a scaled-down approach. Briefly, crude α-amylase was extracted into 1.0 mL buffer solution (1 M sodium malate, 1 M sodium chloride and 40 mM calcium chloride; pH 5.4) by shaking at room temperature for 1 h. The content was centrifuged (Rotina 380R Hettich Zentrifugen) at 11,000 g for 3 min, and 200 µL of the extract at 40°C was added to 50 µL of previously incubated unbuffered Amylase SD Reagent solution at the same temperature. The content was immediately vortexed briefly and incubated at 40°C for 10 min, following which 1 mL of the Stopping Reagent was added and thoroughly mixed. The absorbance values for samples and reaction blank were read against deionised water at 400 nm using a Shimadzu UV-1800 spectrophotometer. Determinations were done on triplicate samples and the catalytic activity of α-amylase expressed as enzyme units per gram (U/g) was determined using the formula below:

$$\frac{\Delta E_{400}}{\text{Incubation Time}} \times \frac{\text{Total Volume in Cell}}{\text{Aliquot Assayed}} \times \frac{1}{\epsilon_{mM}} \times \frac{\text{Extraction Vol.}}{\text{Sample Weight}} \times \text{Dilution}$$

where:

ΔE_{400} = Absorbance (Sample) – Absorbance (Blank)

Total volume in cell (mL) = 1.25

Aliquot assayed (mL) = 0.2

ϵ_{mM} of *p*-Nitrophenol @ 400 nm in tri-sodium phosphate (1% w/v) = 18.1

Extraction volume (mL) = 1.0

Sample weight (g) = - 0.05

β -Amylase activity assay

β -Amylase (EC 3.2.1.2) catalytic activity was determined by the Betamyl-3 method, using the Megazyme Assay Kit, with some modifications. Briefly, crude β -Amylase was extracted from approximately 50 mg pulverised freeze-dried yam sample into 1 mL extraction buffer (1.0 M Tris/HCl buffer: pH 8.0 and 20 mM EDTA) by vortexing at room temperature for 1 h and centrifuging at 2,000 g for 10 min (Rotina 380R Hettich Zentrifugen). A 50 μ L aliquot of the enzyme extract was diluted into 1.0 mL buffer (1.0 M MES buffer pH 6.2, 20 mM EDTA and 10 mg/mL BSA), from which a 20- μ L aliquot (in triplicate) was pre-incubated at 40°C for 5 min before adding 50 μ L of similarly equilibrated Betamyl-3[®] substrate solution. The content was briefly mixed again and then incubated at 40°C for 10 min before 1.0 mL of a stopping reagent was immediately added with brief mixing. The absorbance values for the reaction solutions and reagent blank were read against deionised water at 400 nm. The catalytic activity of β -amylase expressed in enzyme units per gram of sample (U/g) was determined using the formula below:

$$\frac{\Delta A_{400}}{\text{Incubation Time}} \times \frac{\text{Total Volume in Cell}}{\text{Aliquot Assayed}} \times \frac{l}{\epsilon_{mM}} \times \frac{\text{Extraction Volume}}{\text{Sample Weight}} \times \text{Dilution}$$

where:

ΔA_{400}	= Absorbance (sample) - Absorbance (blank)
Incubation time (min)	= 10
Total volume in cell (mL)	= 1.07
Aliquot assayed (mL)	= 0.02 (20 μ L)
ϵ_{mM} <i>p</i> -Nitrophenol	= 18.1 (at 400 nm) in 1% Tris buffer
Extraction volume (mL)	= 1
Sample weight (g)	= 0.05
Dilution	= 0.05 to final volume of 1.05 mL (<i>i.e.</i> , 21-fold)

Flour physicochemical properties determination

About 2.0 g of pulverised freeze-dried yam tuber sample was placed in a tiny cylindrical quartz window-clad cell for scanning with a Near-infrared Spectrophotometer (NIRS), Rapid Content Analyser (RCA) (FOSS NIR Systems, Höganäs, Sweden). A monochromator (XDS 1000, Höganäs, Sweden) was used to gather spectral data to quantify the diffused reflectance (R) of samples in the near-infrared region of the electromagnetic spectrum. The results were recorded as log (1/R) at 2 nm increases and the data processed with the ISscans software package, version 4.2.0 (FOSS NIR Systems, Höganäs, Sweden). The spectral data were analysed and evaluated with the Win ISI II software package, version 1.04 (FOSS NIR Systems, Höganäs, Sweden) using calibration equations developed by Zum Felde et al. (Zum Felde et al., 2009). Determinations were made on triplicate samples for starch, maltose, glucose and protein contents.

Statistical analysis

The data generated were subjected to a one-way Analysis of Variance (ANOVA) using the Minitab 22 statistical software package (Minitab, LLC, Pennsylvania, USA). Significant differences were reported at 95% confidence level using Tukey's test.

RESULTS

Sprouting was exclusively observed at the head region of tubers of the *D. rotundata* cultivars (*Pona* and *Labreko*) at 60 days after harvest (DAH), but at 90 DAH for the *D. alata* cultivar – *CRI-Ahoødenfoø*. At 60 DAH, twice as many *Pona* tubers had sprouted relative to *Labreko*, but at the end of the storage duration of 90 days, a substantial shoot growth was observed in the latter cultivar.

Gibberellic acid content

At harvest, gibberellic acid (GA₃) content of the tuber meristematic layer at various regions along the entire tuber was generally similar for the specific cultivars (Figure 1). The concentrations ranged between 1.83 and 1.92 mg/g dw, except for the tail region of *CRI-Ahoødenfoø* which contained a significantly lower amount of 1.63 mg/g dw. GA₃ content increased significantly by 66.7% - 90.5% within the first 30 days of storage, with *CRI-Ahoødenfoø* peaking at 3.62 mg/g dw. A sudden decrease in GA₃ content to the lowest levels was recorded for all the cultivars at 60 DAH and remained unchanged until the end of the storage studies. The lowest GA₃ levels coincided with sprouting in the *D. rotundata* cultivars – *Pona* and *Labreko*, but not in *D. alata* cultivar – *CRI-Ahoødenfoø* for which sprouting was observed at 90 DAH.

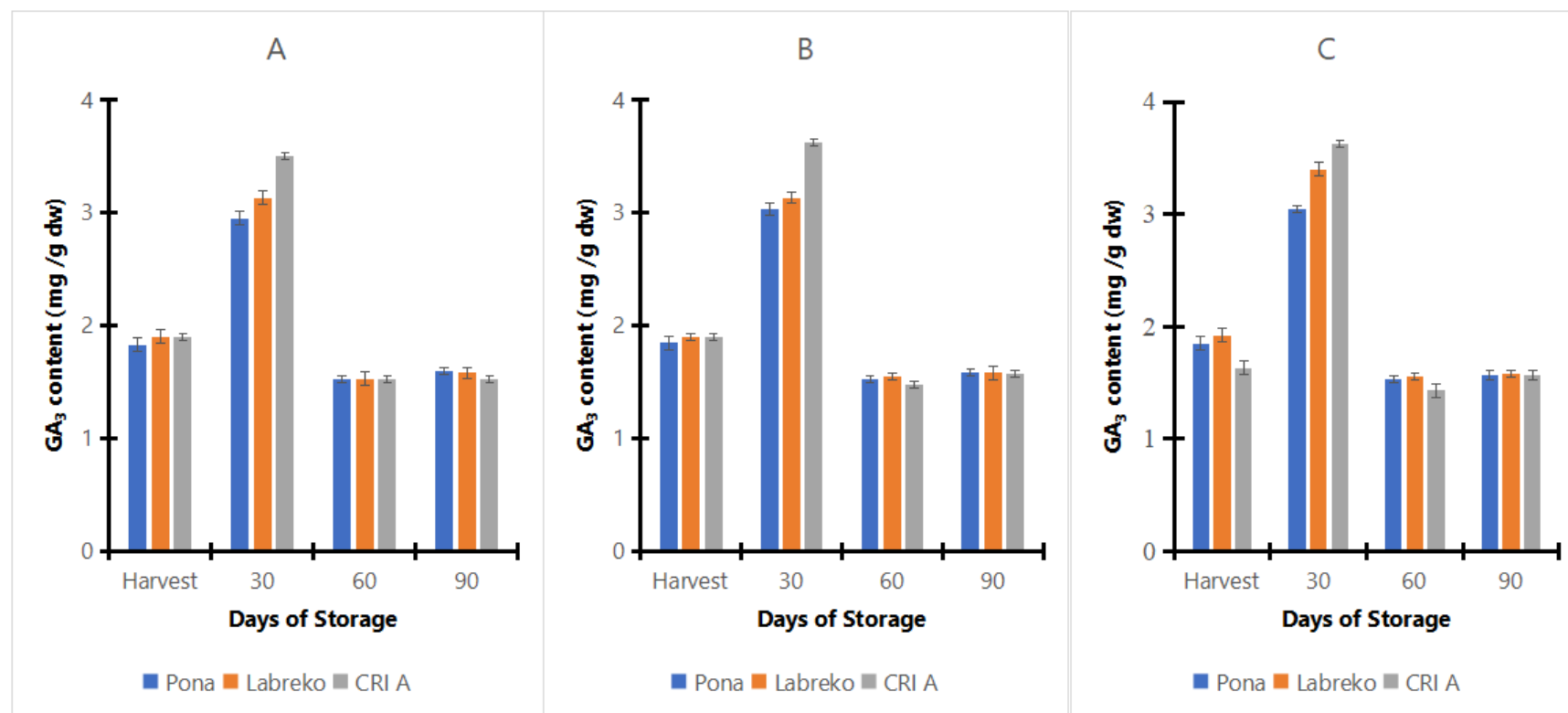


Figure 1: GA₃ content expressed as mg/g dry weight of the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and CRI-*Ahoɔdenfoɔ* ('CRI A') yam cultivars during storage. Values are means \pm SD of triplicate samples

α -amylase catalytic activity

The range of α -amylase catalytic activity at harvest was 0.06 – 0.44 units/g, but it increased significantly (0.88 – 1.09 units/g) at 30 DAH, constituting between 1.7- and 2.9-fold increase; the highest level that was recorded during storage (Figure 2). The enzymatic activity significantly dropped, particularly in the proximal and middle regions along the tuber to 0.03, 0.32 and 0.43 units/g at 60 DAH, respectively in CRI-*Ahoɔdenfoɔ*, *Labreko* and *Pona*. The activity levels in respect of the proximal region remained unchanged ($p > 0.05$) at 90 DAH for *Pona* and CRI-*Ahoɔdenfoɔ*, although there was a significant ($p < 0.05$) increase in *Labreko*. Sprouting which was generally observed at the proximal region coincided with low α -amylase catalytic activity.

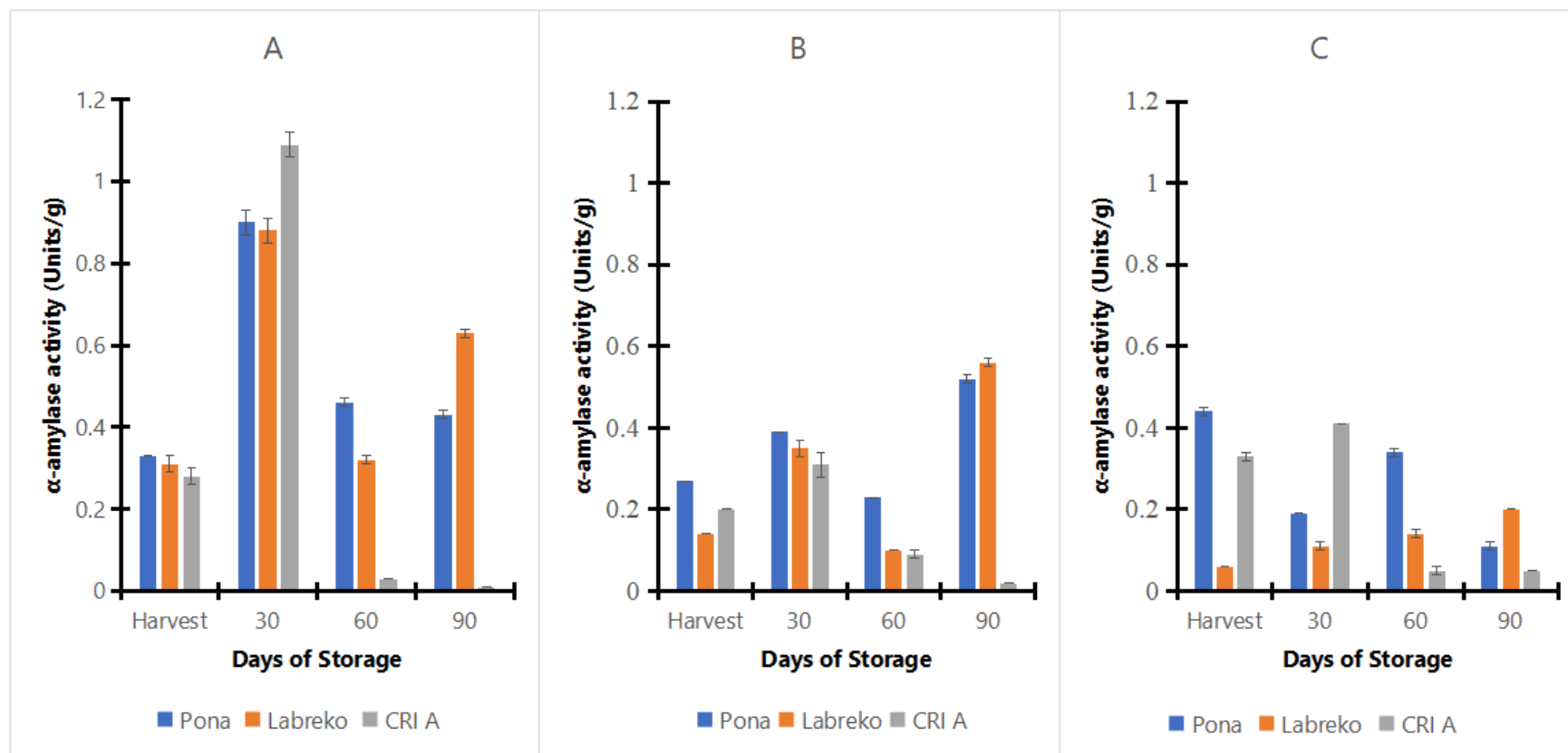


Figure 2: α -amylase activity expressed in enzyme units per gram sample (U/g) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and *CRI-Ahoedenfo* (CRI A) yam cultivars during storage. Values are means \pm SD of triplicate samples

β -amylase activity

The catalytic activity of β -amylase ranged between 2.16 and 10.02 units/g (Figure 3). Catalytic enzyme units for β -amylase were significantly higher than those for α -amylase; approximately ten times higher. β -amylase catalytic activity increased from harvest to its peak levels in all the yam cultivars until dormancy break and sprouting – 60 DAH for *Pona* and *Labreko*, and 90 DAH for *CRI-Ahoedenfo*; following which a reduction was observed. However, a continuously increasing trend in the enzyme activity was observed in the distal (tail) region of tubers until the end of the storage study in all the cultivars.

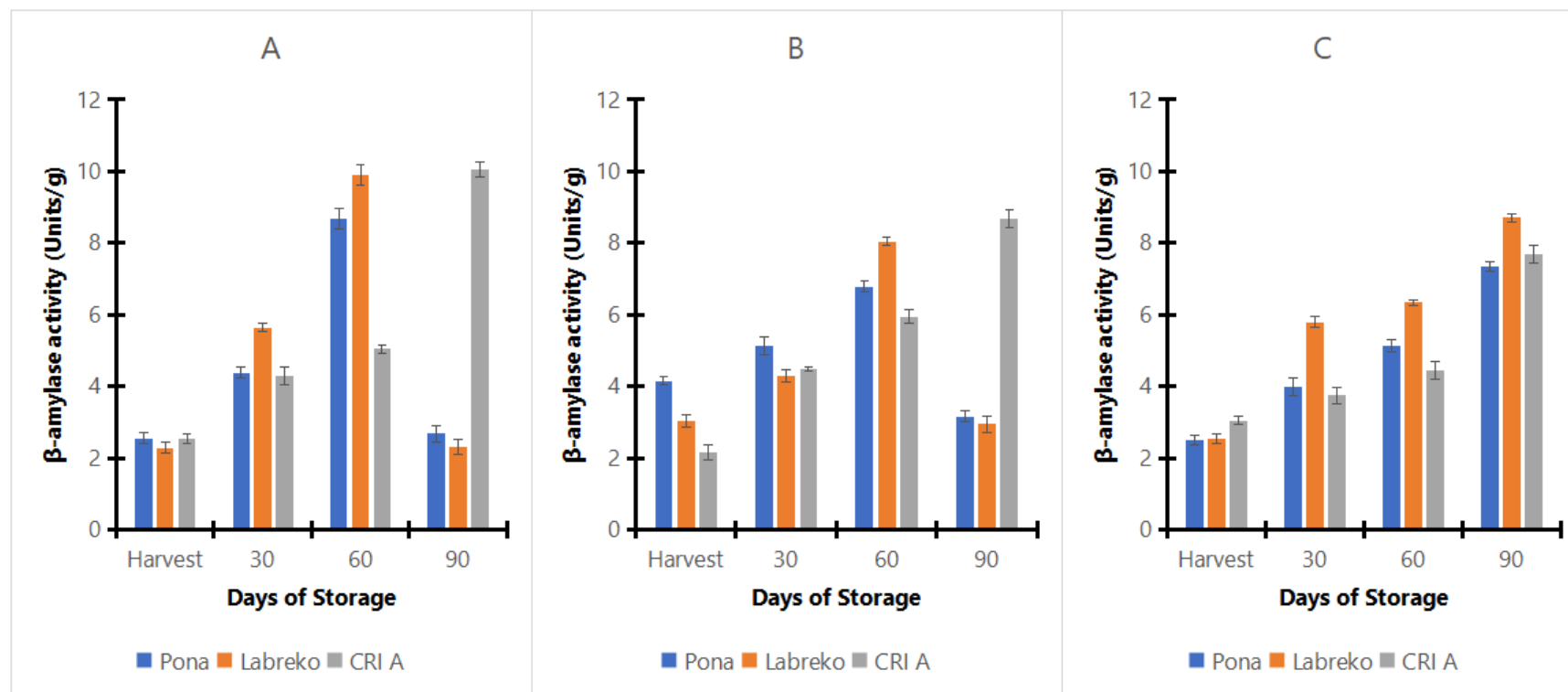


Figure 3: β -amylase activity expressed in enzyme units per gram sample (U/g) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and *CRI-Ahooedenfo* (CRI A) yam cultivars during storage. Values are means \pm SD of triplicate samples

Changes in starch, maltose, glucose and protein contents

Starch

At harvest, starch content did not differ along the tuber, but it varied along this horizontal physiological gradient during storage. Starch content decreased throughout the storage period in all the yam cultivars (Figure 4). Starch levels declined significantly ($p < 0.05$) in the proximal region of *Labreko* and *Pona* - between 7.0% and 7.4%, at 60 DAH, but the reduction (6.1%) was delayed in *CRI-Ahooedenfo* until 90 DAH. The reduction coincided with dormancy break and sprouting.

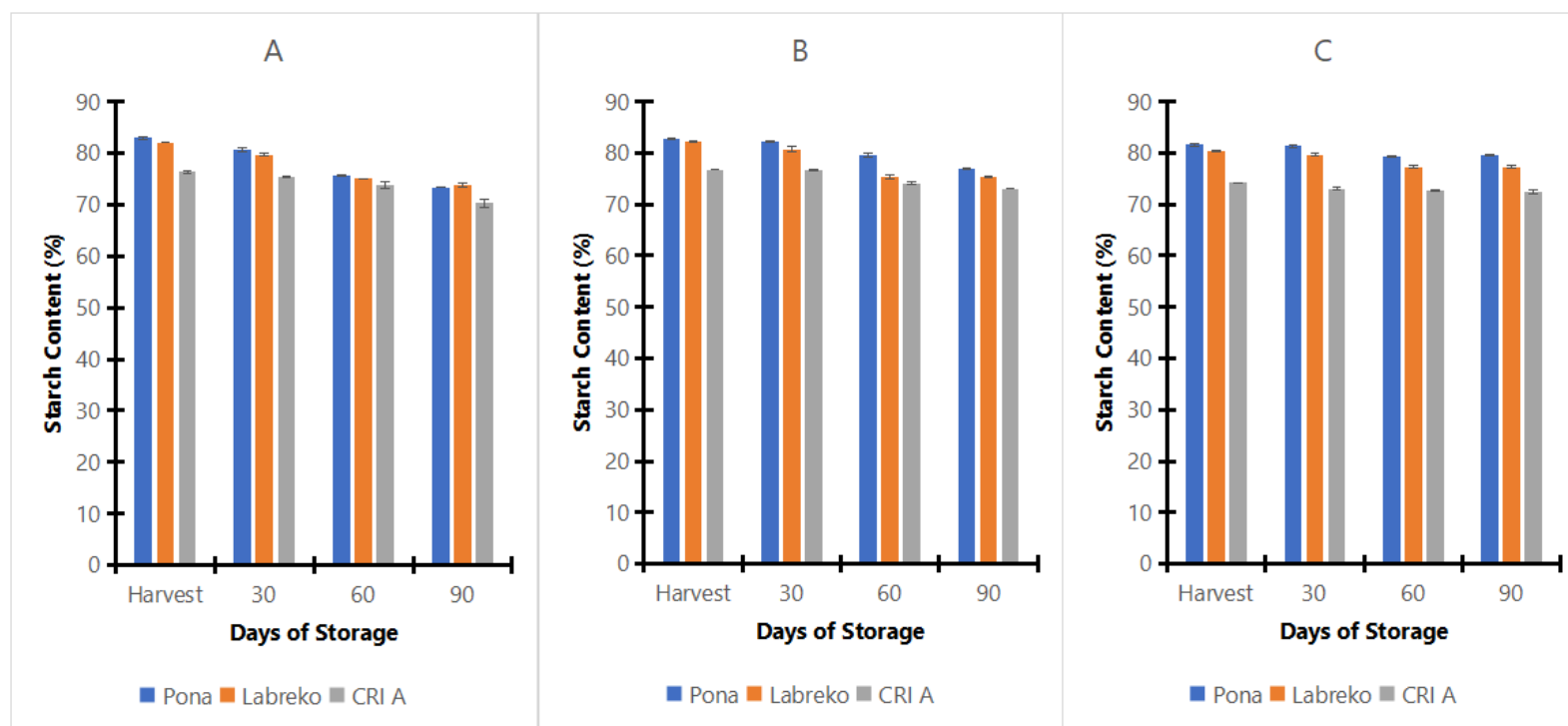


Figure 4: Starch content (%) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and CRI-*Ahoɔdenfoɔ* (CRI A) yam cultivars during storage. Values are means ± SD of triplicate samples

Maltose

Maltose content increased significantly from harvest to its peak respectively at 8.9% and 7.6% in *Pona* and *Labreko* at 60 DAH, but 5.7% at 90 DAH in CRI-*Ahoɔdenfoɔ* (Figure 5). The levels were highest at the proximal region of the tuber and coincided with dormancy break and sprout emergence, but then sharply declined. Maltose contents were significantly higher in the rotundata cultivars relative to *D. alata* cultivar – CRI-*Ahoɔdenfoɔ* at all the storage points except after dormancy release and sprouting of the former cultivars, at which storage time point dormancy was yet to be released in CRI-*Ahoɔdenfoɔ*.

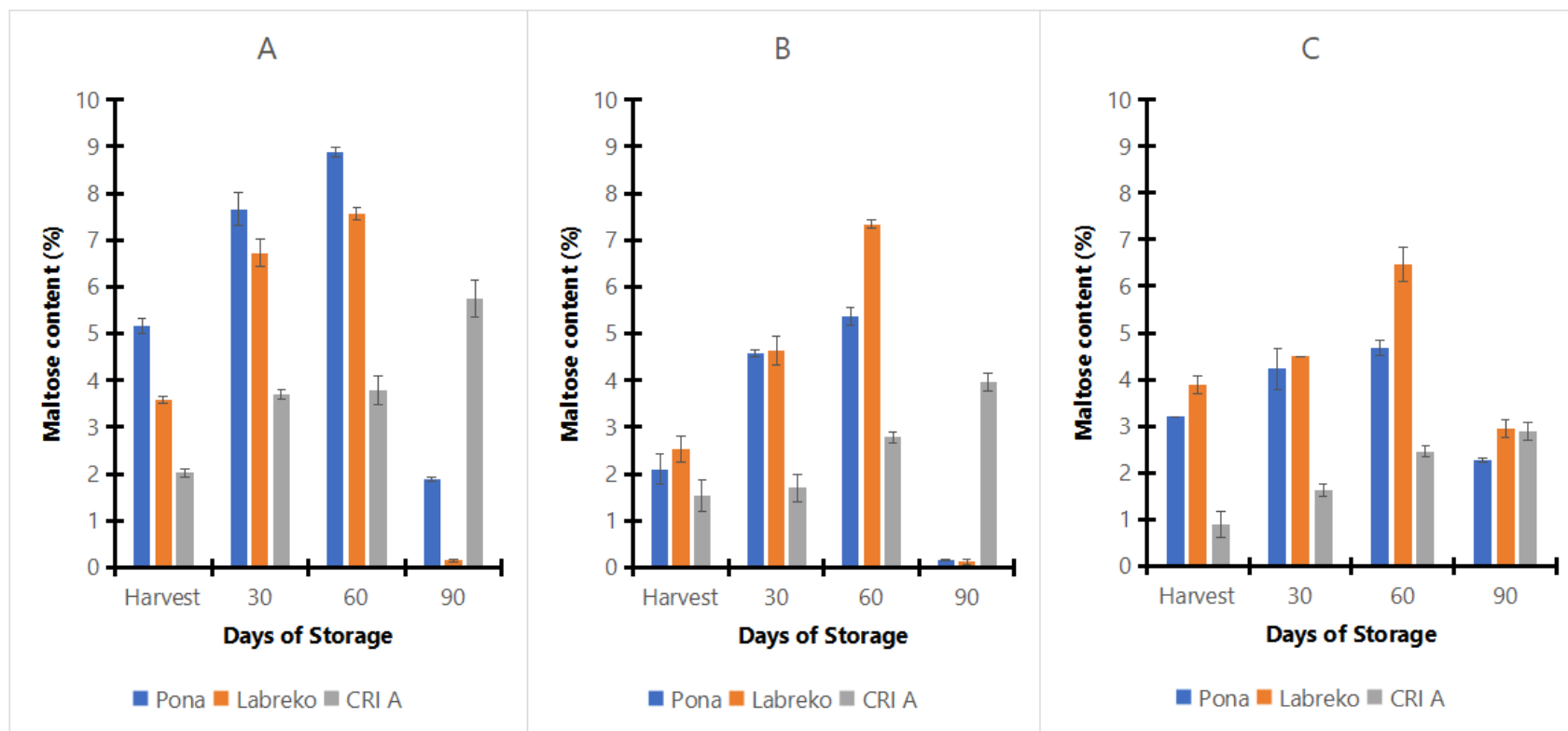


Figure 5: Maltose content (%) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and *CRI-Ahoɔdenfoɔ* (CRI A) yam cultivars during storage. Values are means ± SD of triplicate samples

Glucose

Glucose content progressively increased in a significant manner to its peak after storage for all the yam cultivars (Figure 6). At the various storage points, glucose level was significantly highest in the proximal region relative to the middle and distal regions. The highest contents recorded were 5.5%, 3.41% and 2.3%, respectively in *CRI-Ahoɔdenfoɔ*, *Pona* and *Labreko*, and this trend was consistent at all the storage points.

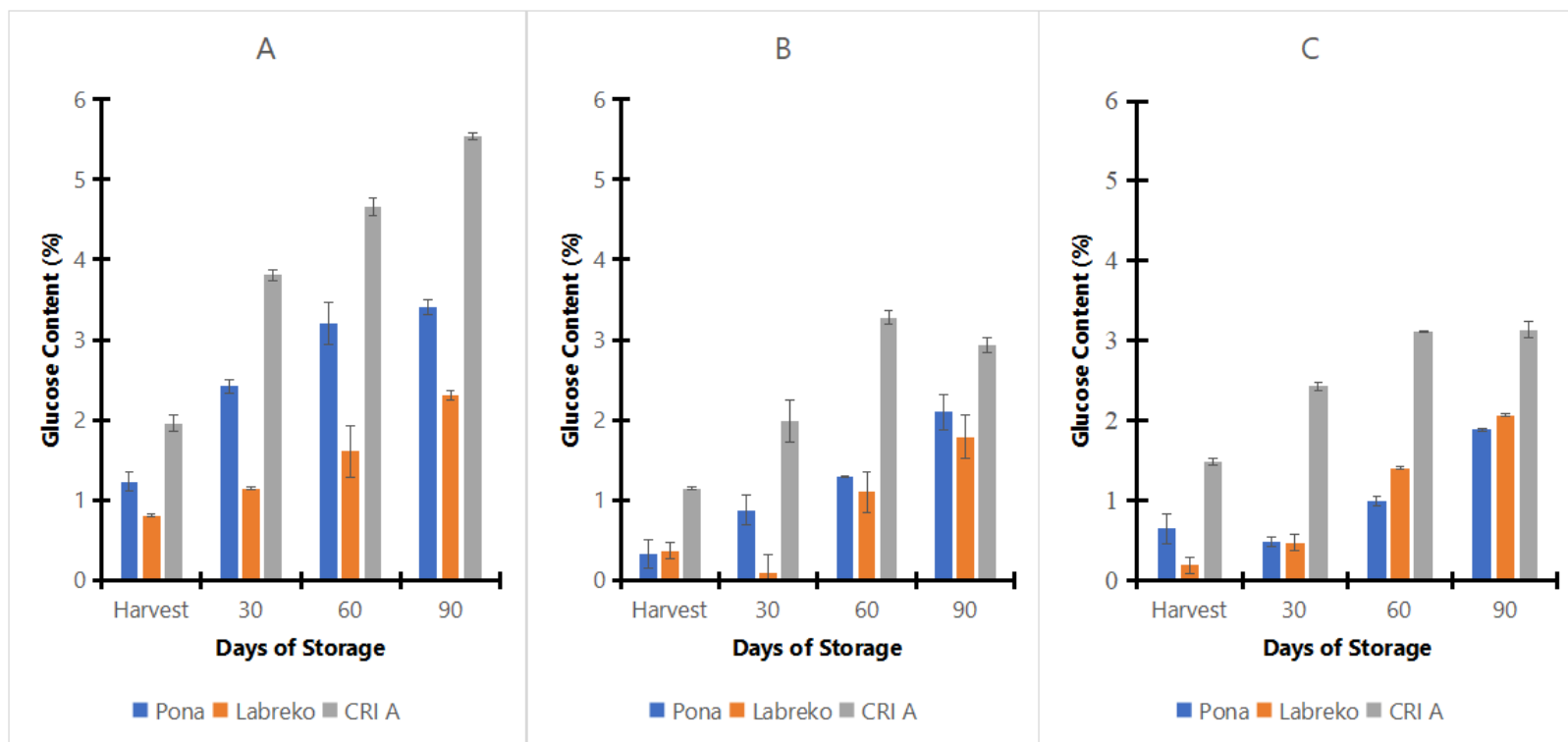


Figure 6: Glucose content (%) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and *CRI-Ahooḍenfoḍ* (CRI A) yam cultivars during storage. Values are means ± SD of triplicate samples

Protein

Protein content varied throughout the storage period and the extent of change was cultivar dependent (Figure 7). At harvest, *Labreko* had the highest (8.0 – 9.5%) protein content, followed by *Pona* (7.0 – 7.9%) and *CRI-Ahooḍenfoḍ* (4.9 – 6.1%). Preceding and subsequent to the release of dormancy, an increase in protein content was observed in all the yam cultivars. While the increase was not significant in the rotundata cultivars – *Pona* and *Labreko* before sprout emergence, it was significant in *CRI-Ahooḍenfoḍ*. A significant increase was observed post-dormancy release in all the yam cultivars

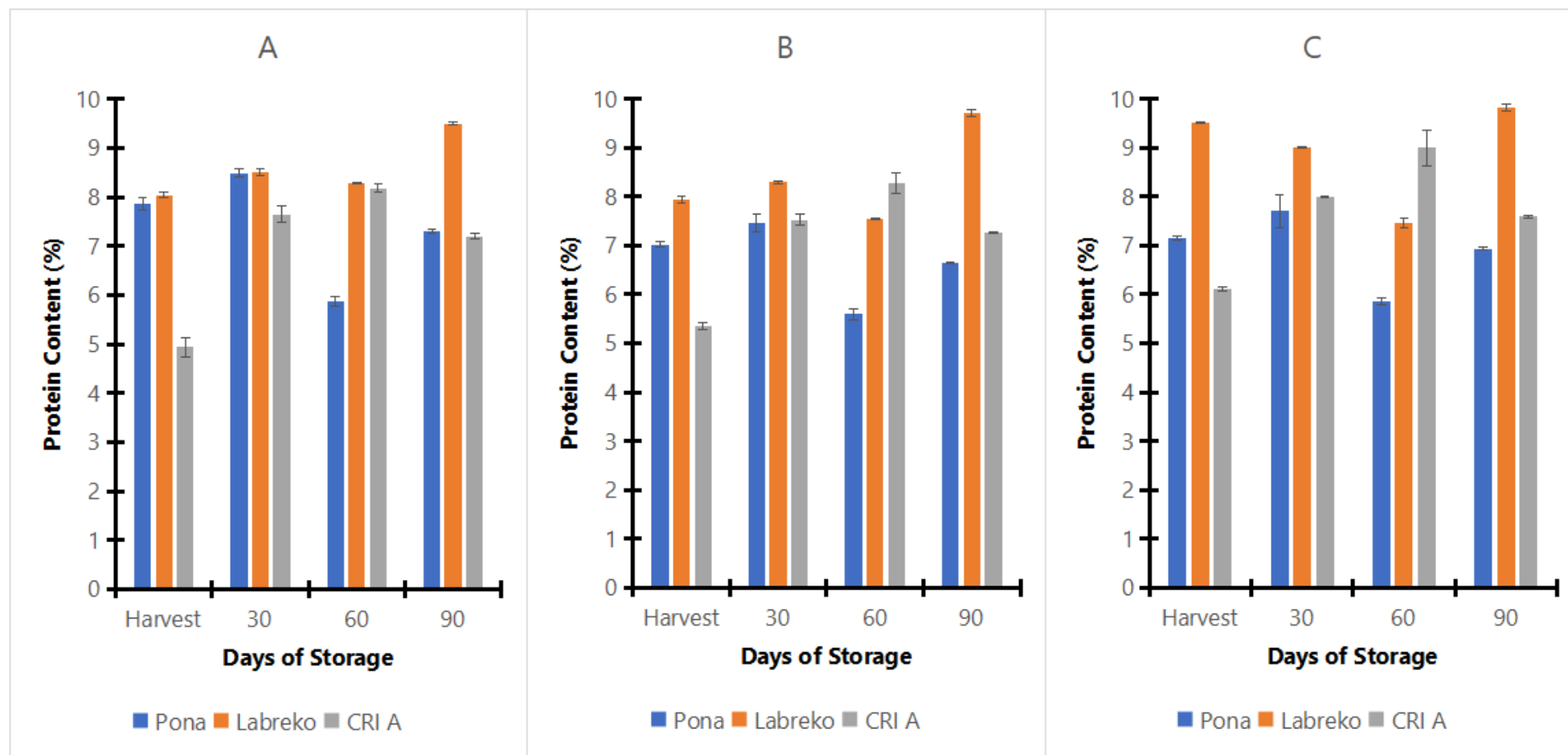


Figure 7: Protein content (%) in the meristematic layer of the proximal (A), middle (B) and distal (C) regions of *Pona*, *Labreko* and *CRI-Ahoadenfo* (CRI A) yam cultivars during storage. Values are means \pm SD of triplicate samples

Discussion

Upon harvesting, cells of severed yam tubers undergo physiological and biochemical changes, utilizing the stored food reserves for general cellular maintenance and survival. Energy is needed for these essential metabolic activities, and starch – a primary carbohydrate reserve in yam (*Dioscorea spp.*) tubers, is mobilised for energy generation through respiration. These energy demands partly explain the consistent reduction in starch content in the tubers of all yam cultivars during storage. Starch hydrolysis requires the action of α - and β -amylase (Datir et al., 2024) and this was evidenced by a significant increase in catalytic activity of these hydrolytic enzymes, respectively, α -amylase within 30 DAH and until dormancy release and sprout emergence for β -amylase. α -Amylase randomly cleaves α -1,4-glycosidic linkages in starch and related polysaccharides to produce glucose, maltose, maltotriose and dextrans, whereas β -amylase activity primarily leads to maltose production (Das & Kayastha, 2023; Tomasik & Horton, 2012). The rise in hydrolytic activity of α - and β -amylase resulted in a significant increase in glucose and maltose levels, which reflected in the reduction in starch content until the release of dormancy leading to sprouting, particularly in the proximal (head) region of *Labreko* and *Pona* cultivars at 60 DAH and at 90 DAH for CRI-*Ahoɔdenfoɔ*. This was essential in generating energy for enhanced metabolic activities of meristematic cells in the proximal region of the tuber, where sprouting was pronounced. Whereas α -amylase catalytic activity at 30 DAH relative to harvest increased 1.7- to 2.5-fold depending on the yam cultivar, β -amylase activity increased between 2.7- and 3.9-fold. Notwithstanding, the units of catalytic activity per gram of sample for β -amylase were about ten times (10x) higher than that for α -amylase over the storage period, a similar observation having been made during sweetpotato root storage studies (Amankwaah, 2019; Nabubuya et al., 2012). Some studies have reported an increase in α -amylase activity to its peak during sprouting (Jaleel et al., 2007; Panneerselvam et al., 2007), but the activity of this enzyme rather increased from harvest, peaking at 30 DAH for all the yam cultivars that were used in the current study. However, thereafter, the activity decreased before sprouting was observed at 60 DAH in *Labreko* and *Pona* cultivars and at 90 DAH for CRI-*Ahoɔdenfoɔ*. The catalytic activity of β -amylase was also enhanced within this period – 30 DAH, but on the contrary, this increasing trend continued until dormancy was terminated to bring about sprouting, respectively at 60 DAH and 90 DAH in the *D. rotundata* and *D. alata* cultivars. The somewhat lesser fold increase in β -amylase activity (1.7 to 2.5-fold) in comparison with α -amylase (2.7 to 3.9-fold) suggests that the latter enzyme plays a more predominant role in starch hydrolysis for cellular maintenance in yam tubers at early stages of storage. Apparently, the initial significant increase in α -amylase activity over the first 30 DAH adapts cells in the meristematic layer to mobilising glucose for energy generation to drive vital metabolic processes within the dormancy duration.

Gibberellic acid was implicated to have induced the *de novo* synthesis of α -amylase and other hydrolases (Aubert et al., 2018; Salman et al., 2024; Yu et al., 2016). In this study, the catalytic activity of α -amylase correlated with enhanced accumulation of gibberellic acid, which significantly started post-harvest. Gibberellic acid did not induce β -amylase during the germination of sorghum and wheat seeds (Alybayev et al., 2024; Amisi et al., 2020; Zhang et al., 2005). Likewise, exogenous application of this growth hormone on rice seeds did not enhance β -amylase activity, but rather counteracted the inhibitory effect of abscisic acid on the expression of the enzyme (Wang et al., 1996). Additionally, the trends of gibberellic acid accumulation and α -amylase activity for the head and middle regions of the tubers for all the yam cultivars were similar in this study, thus confirming the influential effect of the plant hormone on the activity of α -amylase. A comparative metabolomics analysis by Nwogha et al. (2023) on two yam varieties revealed that phytohormones, amino acids, and their derivatives positively regulated dormancy, while sugars and other metabolites promoted the breaking of dormancy and sprouting.

Apparently, the inducing influence of gibberellic acid on *de novo* synthesis of α -amylase and other hydrolases may explain the enhanced levels in protein content from harvest until 30 DAH. Hamadina et al. (2015) have reported an increase in yam tuber peel crude protein content between 30 DAH and 60 DAH for *D. rotundata* cultivars. This could have been for build-up of enzymes, particularly starch hydrolytic enzymes which are essential for energy metabolism, as well as lipases and proteases that are required for generating the building blocks of new macromolecules for the growing shoot bud. Interestingly, the trend of α -amylase activity coincided with that for protein content in this study. Preceding and subsequent to the release of dormancy, the enhancements in protein content explain an increasing requirement for enzyme proteins in the meristem as development and differentiation proceed (Chrungoo & Farooq, 1985; Joshi, 2018). This up-accumulation of proteins is related to enzymes in the pathways associated with energy production (glycolysis, TCA cycle and oxidative phosphorylation) and growth.

The catalytic activity of α -amylase was significantly higher in the head region of the tubers compared to the other regions, indicating heightened metabolic activity which explains the marked sprouting in this region of tubers of all the yam cultivars. β -Amylase activity consistently increased significantly post-harvest until dormancy was terminated to result in sprout emergence at 60 DAH for the *D. rotundata* cultivars, and at 90 DAH in the *D. alata* cultivar. Interestingly, after dormancy release and sprout emergence, the catalytic activity of β -amylase sharply

diminished. The outset of this decline which also coincided with a drastic depletion of accumulated maltose in the meristematic layer of the tuber signals dormancy termination and sprout initiation. This clearly shows that maltose build-up ensures the availability of a carbon source for energy generation to drive the surge in metabolic activities that lead to sprouting (Liu et al., 2022). Following sprouting, more maltose is further expended towards growth and maintenance of the growing bud into a shoot. A similar observation was also made in potato (*Solanum tuberosum*) tubers (Nabubuya et al., 2017) and saffron corms (Bagri et al., 2017). Obviously, the intense breakdown of maltose after sprouting also contributed to the increased levels in glucose, attributable to the enhanced catalytic activity of α -amylase. Clearly, the reduction in maltose content is an indication of it being consumed as a carbon source via glucose along with enhanced protein content to promote shoot development and growth (Muñoz-Llandes et al., 2023; Xu et al., 2010).

The significantly higher catalytic activity of α -amylase in *Labreko* relative to *Pona* after sprouting – 90 DAH (Figure 2A) ensured efficient generation and mobilisation of glucose for energy production that supported the observed vigorous bud growth into a shoot in *Labreko*. Efficient glucose mobilisation and consumption, prominently at the expense of maltose was evidenced at 90 DAH (Figure 5), which was associated with high protein content (Figure 7), implicating *de novo* enzyme synthesis. In contrast, the significantly high levels of maltose in the head region of *Pona* might have promoted sprout development in this cultivar, explaining the greater number of sprouts observed in *Pona* at 60 DAH.

The enhancement in maltose content to its peak until sprouting in all the yam cultivars clearly suggests that it is essential for dormancy termination. Additionally, it may be deduced that a continuous increase in the catalytic activity of β -amylase in the distal (tail) region of all the yam cultivars (Figure 3C) ensures maintenance of dormancy and may be responsible for the diminished propensity for sprouting in this region of yam tubers. Although the catalytic actions of α - and β -amylase led to consistent reduction in starch content, it was particularly intense at dormancy release and sprouts emergence; 60 DAH for the *D. rotundata* cultivars, and 90 DAH for the late-sprouting *D. alata* cultivar, as a result of the significantly enhanced β -amylase activity. Therefore, it can be suggested that the activity of β -amylase and gibberellic acid accumulation together play an important role in regulating dormancy and sprouting in yam tubers.

Conclusions

This study established the critical roles of carbohydrate metabolism and endogenous gibberellic acid (GA_3) in regulating yam tuber dormancy by assaying α - and β -amylase activity and quantifying GA_3 , starch, maltose, glucose, and protein in the tuber's meristematic layer. Specifically, enhanced β -amylase activity, which leads to substantial accumulation of maltose and GA_3 in the meristematic layer, was directly correlated with dormancy release. The identification of specific threshold values for maltose and GA_3 provides practical targets for manipulating tuber dormancy. These findings can be exploited for postharvest management. The study recommends applying an omics approach, combining proteomic and transcriptomic analyses, to validate these findings and identify specific metabolic pathways and regulatory candidate genes. From these candidates, specific molecular techniques could be developed to either extend dormancy for ware yam or shorten it for seed yam purposes.

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Conflicts of Interest

The authors declare no conflicts of interest.

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