

SWEET POTATO SKIN COLOR ANALYSIS ALGORITHM BASED ON IMAGE PREPROCESSING AND COLOR MODELS

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Abstract

Sweet potato breeding typically requires eight to ten years, during which phenotypic trait measurement and cultivar selection demand substantial labor and time. The Chiayi Agricultural Experiment Station in Taiwan, which hosts the nation's largest sweet potato germplasm collection, relies heavily on manual phenotypic trait evaluations throughout the breeding process. In particular, the assessment of skin color is highly susceptible to variations in lighting conditions and subjective judgment, resulting in reduced consistency and efficiency. With the continued advancement of breeding technologies, integrative analyses of genomic, transcriptomic, and epigenetic traits have become key strategies for accelerating the improvement of sweet potatoes. Consequently, the precise quantification of phenotypic traits—such as size, color, and count—has emerged as a critical enabling technology. In this study, a sweet potato skin color analysis algorithm was developed based on image preprocessing and color models. Gamma correction, white balance adjustment, edge contour extraction, and background removal were incorporated into the preprocessing pipeline. RGB, HSV, and CIELAB color spaces were adopted for classification and analysis. The dominant skin color was computed using an average color method, and three-dimensional scatter plots were generated to visualize the color distribution among different cultivars. The results showed that distinct clustering patterns among cultivars were observed in both the RGB and CIELAB color spaces. The proposed method demonstrates strong potential for digitization, standardization, and automation. It could be further enhanced with shape analysis modules to serve as a reliable tool for evaluating sweet potato phenotypic traits.

Keywords: Image Preprocessing, Color Space Analysis, Digital Breeding, Sweet Potato

INTRODUCTION

Traditional sweet potato breeding takes 8–10 years, with crossing and selection being labor-intensive and prone to inconsistent evaluation due to environmental and subjective factors. This study proposes a skin color analysis algorithm to support breeders with standardized and accurate phenotypic assessment.

MATERIALS AND METHODS

Sweet Potato Dataset

Images of Tainung No. 57 (TN_57), Tainung No. 66 (TN_66), and Tainung No. 73 (TN_73) sweet potatoes were captured using an iPhone with flash under dim indoor lighting. A Tiffen color calibration chart and black velvet background were used for standardization. Each tuber was photographed from four rotational angles to document surface color features.

Image Preprocessing

Before color analysis, gamma and white balance corrections were applied using grayscale patches from the color checker. Edge detection was then used to isolate the sweet potato region for background removal (Figure 1).

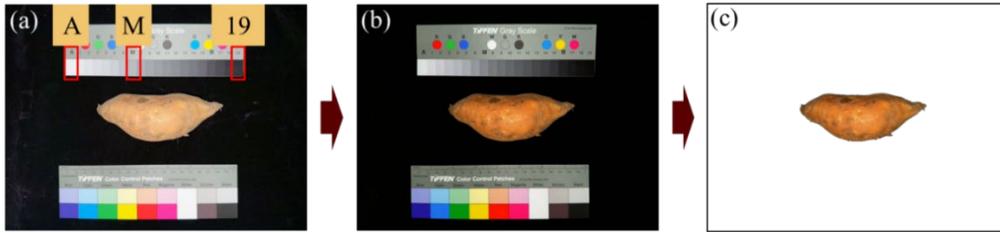


Fig. 1 Preprocessing workflow. (a)selection of grayscale patches. (b)gamma and white balance correction. (c)background removal.

Color Analysis

After background removal, sweet potato surface colors were analyzed using the average color method in RGB, HSV, and CIELAB color spaces. Each image's result was visualized in a 3D scatter plot. The average color was defined as:

$$Mean_R = \frac{1}{N} \sum_{i=1}^N R_i \quad Mean_G = \frac{1}{N} \sum_{i=1}^N G_i \quad Mean_B = \frac{1}{N} \sum_{i=1}^N B_i \quad (1)$$

RESULTS & DISCUSSION

Under consistent image size and lighting conditions, RGB, HSV, and CIELAB color spaces were analyzed for the distribution of sweet potato skin colors. HSV showed greater variation for TN_73, confirmed by higher standard deviation via Euclidean distance. CIELAB had the most stable values across cultivars.

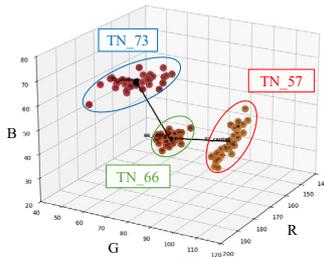


Fig. 2 RGB Distribution of TN_57, TN_66, and TN_73.

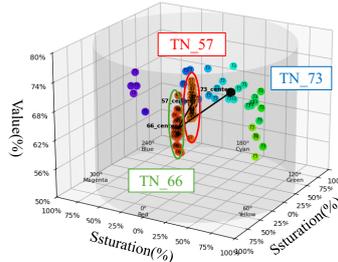


Fig. 3 HSV Distribution of TN_57, TN_66, and TN_73.

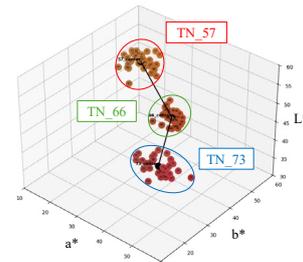


Fig. 4 CIELAB Distribution of TN_57, TN_66, and TN_73.

Table 1 Cluster centers and standard deviations of three cultivars under different color spaces.

Cultivar	TN 57	TN 66	TN 73
Samples (images)	35	30	33
RGB Cluster Centroid	(185,113,53)	(173,77,42)	(169,59,61)
RGB Cluster Std. Dev.	4.64	4.83	4.55
HSV Cluster Centroid	(14,181,185)	(8,193,173)	(88,173,169)
HSV Cluster Std. Dev.	4.62	4.38	14.54
CIELAB Cluster Centroid	(55,24,45)	(47,39,40)	(46,43,25)
CIELAB Cluster Std. Dev.	1.56	1.07	1.82

CONCLUSIONS

An image-based algorithm was developed to quantify the color of sweet potato skin. After color calibration and background removal, color features in RGB and CIELAB spaces were analyzed. CIELAB showed the smallest intra-group variation. This method offers strong potential for automated and standardized phenotypic assessment in breeding.

REFERENCES

- Neilson, J.A.D., Smith, A.M., Mesina, L., Vivian, R., Smienk, S. and De Koyer, D. 2021. Potato Tuber Shape Phenotyping Using RGB Imaging. *Agronomy*. 11(9): 1781.
- Youngha C. and Nobuhiko M. 2022. Color Feature Based Dominant Color Extraction. Access. 10: 93055-93061.