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COLOR IDENTIFICATION AND TEXTURE FEATURES OF PHALAEOPSIS USING DEEP LEARNING

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Abstract

As one of the most economically important and widely traded ornamental plants worldwide, *Phalaenopsis* hold a significant position in the global floriculture industry. The breeding process is traditionally labor-intensive, requiring careful visual assessment of numerous floral traits to select desirable varieties, which underscores the need for scalable, automated solutions. To enhance the efficiency of *Phalaenopsis* breeding and accelerate phenotypic comparison across varieties, this study presents an AI-based image analysis framework designed for large-scale, automated floral features detection and classification. The system integrates the Segment Anything Model (SAM) for high-precision flower segmentation and YOLOv11 for object detection within high-resolution *Phalaenopsis* images. To address the annotation bottleneck, a two-stage labeling strategy was used, starting with a small manually labeled dataset to train a base model that then assisted in labeling hundreds of additional images. The resulting model achieved high accuracy, as demonstrated by its strong mean Average Precision (mAP@0.5) and robust precision-recall characteristics. This approach provides a scalable solution for automatic floral trait profiling, facilitating early-stage visual phenotype screening and offering computational support for future integration with genetic data. Ultimately, the framework contributes to intelligent decision-making in *Phalaenopsis* variety selection and paves the way for AI-assisted breeding strategies in precision horticulture.

Keywords: *Phalaenopsis*, Deep Learning, Floral Trait Detection, Segment Anything Model, YOLOv11

INTRODUCTION

Large-scale phenotypic analysis of *Phalaenopsis* flowers remains predominantly manual, limiting the scalability of breeding programs. To address this, we propose a two-stage deep learning pipeline combining YOLOv11 for flower detection and the Segment Anything Model (SAM) for instance segmentation. The system is tailored for high-resolution orchid images and enables consistent, automated extraction of floral masks for downstream morphological analysis.

MATERIALS AND METHODS

A dataset of approximately 1,000 high-resolution *Phalaenopsis* flower images was collected from the 2025 Taiwan Orchid Exhibition. Among these, 90 images were manually annotated to establish a base set of bounding box labels. Annotation was performed using the X-AnyLabeling tool, and the remaining unlabeled images were processed using a pseudo-labeling strategy based on a trained object detector, followed by manual verification.

For object detection, the Ultralytics implementation of YOLOv11 was employed to localize individual flowers within each image. The bounding boxes produced by the detector were then used as prompts for the Segment Anything Model (SAM), specifically the vit_h variant, to generate high precision segmentation masks. The combination of bounding box guidance and SAM segmentation enabled the creation of both binary masks and cropped flower images, which served as inputs for downstream analysis.

The object detector was trained on 900 images using the Adam optimizer with a learning rate of 0.001 over 100 epochs. In the inference stage, each SAM predicted mask was post processed by combining all detected instances within an image into a single binary mask, and then used to generate background-free flower crops.

RESULTS & DISCUSSION

The proposed two-stage pipeline integrating YOLOv11 for object detection and SAM for segmentation achieved promising performance in *Phalaenopsis* flower analysis. Using a manually labeled subset of 90 images to bootstrap a pseudo-labeling process, the model was trained on approximately 900 images over 100 epochs. The resulting detector achieved a mean Average Precision (mAP@0.5) of 0.875, with a peak F1-score of 0.83 at a confidence threshold of 0.798. The system demonstrated strong precision across varying thresholds, reaching 1.00 precision at high confidence levels. While most flowers were correctly localized and segmented, minor failure cases occurred when bounding boxes clipped the petal edges, leading to incomplete masks. Despite this, the overall pipeline proved effective and scalable, offering a solid foundation for downstream phenotype profiling and supporting future integration with breeding analytics.

CONCLUSION

This study demonstrates the effectiveness of a two-stage deep learning pipeline for automated *Phalaenopsis* flower detection and segmentation. By combining YOLOv11 for object localization with the Segment Anything Model (SAM) for precise instance segmentation, the system successfully isolates floral regions with high accuracy and minimal human intervention. The approach proved scalable and robust, supporting consistent phenotypic data extraction across a diverse image set. These results highlight the potential of AI-assisted tools in accelerating orchid variety screening and morphological analysis. Moving forward, the extracted masks and cropped images can be integrated into downstream pipelines for trait-based clustering, color/texture analysis, and even parentage inference, paving the way toward data-driven breeding in precision horticulture.