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Deep learning based identification of *Crocidolomia pavonana* larvae on mustard plants using Grad-CAM

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ABSTRACT

Mustard greens are an important vegetable commodity, but their production is often affected by pest attacks, especially the cabbage worm *Crocidolomia pavonana* (*C. pavonana*). The larvae damage leaf tissues and cause significant yield losses, while chemical control is often ineffective due to differences in insecticide sensitivity across larval instars. This study proposes a deep learning based classification approach combined with gradient weighted class activation mapping (Grad-CAM) to identify larval instars of *C. pavonana* on mustard plants. A dataset of 684 images covering instars 1 to 4 was collected from laboratory rearing and field observations, then processed using resizing and augmentation techniques and divided into training, validation, and testing sets with an 8 to 1 to 1 ratio. Two convolutional neural network (CNN) models, visual geometry group 19 (VGG19), and Xception, were implemented with additional fully connected layers. The VGG19 model achieved 94.20% accuracy and outperformed Xception. Grad-CAM successfully highlighted larval regions and supported visual interpretation. The results show that the proposed method can improve pest identification accuracy and support more effective pest management.

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1. INTRODUCTION

Vegetables are important agricultural commodities, including mustard plants. However, mustard production fluctuates annually. In 2021, Indonesia experienced a decline in mustard production compared to the period from 2020 to 2022 [1]. One of the main factors contributing to reduced productivity is pest infestation [2], which can cause severe economic losses for farmers, with crop failure reaching up to 90% [3]. A major pest affecting mustard crops is the cabbage worm, *Crocidolomia pavonana* (*C. pavonana*), particularly during its larval stage. These larvae damage plants by feeding on leaf tissues, including the veins, leading to significant crop deterioration [4].

To control pest attacks, farmers commonly rely on chemical insecticides [5]. However, the effectiveness of insecticides often varies depending on the developmental stages or instars of *C. pavonana* larvae. Early instars are generally more susceptible to insecticides, whereas later instars exhibit greater resistance [6]. Therefore, accurate identification of larval instar stages is essential for effective pest management and optimal insecticide application.

Traditionally, distinguishing between the four larval instars requires laboratory rearing and detailed morphological observations, including development duration, head capsule size, and larval coloration [7]. The developmental durations and average head capsule sizes for the first to fourth instars are approximately 2–3, 1–3, 1–3, and 3–6 days, with head capsule sizes of 0.3, 0.55, 0.97, and 1.5 mm, respectively. Larval color also changes from dark brown in the first instar to green with white stripes in the fourth instar. Although effective, this approach is time consuming, labor intensive, and highly dependent on expert observation, which limits its scalability in real agricultural environments. Furthermore, studies show that each instar responds differently to insecticide concentrations [8], emphasizing the need for precise classification to support effective and economical pest control strategies [9].

Recent advancements in artificial intelligence (AI), particularly deep learning, have shown significant potential in agricultural applications, including insect detection, classification, and identification [4]. Deep learning models, especially convolutional neural networks (CNNs), can automatically extract complex visual features from images, enabling more accurate classification of biological objects. Several studies have applied deep learning to larval image classification of other species [10], achieving moderate accuracy ranging from 70% to 81%, although challenges related to model loss and generalization remain [11]–[13]. The selection of appropriate CNN architectures is also critical, as factors such as network depth, pooling layers, and activation functions significantly influence classification performance [14].

For instance, previous research utilized a pre trained visual geometry group 19 (VGG19) model for pest recognition in natural image backgrounds and achieved an accuracy of 93.05% [15]. However, many previous studies did not comprehensively evaluate model performance in terms of both accuracy and loss, and some feature extraction approaches, such as principal component analysis, may result in information loss because they only capture linear relationships [16]. In addition, modifying pre trained CNN architectures by adding fully connected layers has been shown to improve classification performance for biological datasets [17]. To enhance model interpretability, visualization techniques such as gradient weighted class activation mapping (Grad-CAM) can highlight important regions in images and help explain model predictions, which is valuable for practical pest monitoring applications [18].

Previous studies have demonstrated the potential of deep learning methods for insect and larval classification tasks. However, most studies focused on general insect recognition or other larval species, often using controlled datasets or limited evaluation metrics [12], [13], [15]. In addition, several approaches primarily emphasized classification accuracy without incorporating interpretability techniques that can explain the model decision making process [16]–[18].

Based on these studies, several research gaps can be identified. First, limited research specifically addresses the classification of *C. pavonana* larval instars using deep learning approaches. Second, many studies rely on controlled or laboratory datasets rather than images collected directly from real agricultural environments. Third, the integration of interpretability techniques, such as Grad-CAM, to visualize model attention in pest identification tasks remains limited.

Therefore, this study aims to address these gaps by developing a deep learning based classification system for *C. pavonana* larval instars using a dataset collected directly from cabbage plantations. The proposed approach employs modified pre trained CNN architectures, namely VGG19 and Xception, enhanced with additional fully connected layers [17]. Furthermore, Grad-CAM visualization is implemented to highlight larval positions on plant images, particularly for the fourth instar stage [18]. The novelty of this study lies in the integration of a field acquired dataset, optimized CNN architectures, and Grad-CAM based localization to support practical pest monitoring. The main contributions of this study are as follows. First, the development of a field acquired dataset of *C. pavonana* larval instars collected directly from cabbage plantations. Second, the comparative implementation of modified pre trained CNN architectures, namely VGG19 and Xception, for larval classification. Third, the integration of Grad-CAM visualization to enhance model interpretability by highlighting larval localization in plant images. This approach is expected to improve classification accuracy, support precision insecticide application, reduce operational costs, and minimize environmental contamination.

2. METHOD

This study develops a deep learning-based model to classify *C. pavonana* larval instars and detect their presence on mustard plants using VGG19 and Xception architectures. The method includes preprocessing, data splitting, model training, evaluation, and bounding area generation. Preprocessing involves resizing, augmentation, and normalization [19], followed by an 8:1:1 data split. Both models are trained for 25 epochs and evaluated using accuracy and loss to assess generalization performance [20]. Grad-CAM is applied to generate bounding areas for improving model interpretability.

2.1. Rearing stage of larva *Crocidolomia pavonana*

The study began with rearing *C. pavonana* larvae at the Gunadarma Technopark Laboratory in collaboration with local farmers to obtain complete instar stages (instar 1–4) [7]. Each instar lasts approximately two days, ensuring balanced dataset availability across developmental stages. The larvae originated from egg stages obtained from a research laboratory in Malang and were reared under controlled conditions using pesticide-free mustard leaves as feed. Standard rearing procedures were applied, including the use of containers, pupation media, and adult maintenance for continuous egg production [21]. This stage is essential to ensure complete instar representation, which directly affects classification performance [22].

2.2. Instar 1, 2, 3, and 4 larva *Crocidolomia pavonana* image acquisition

Instar 1, 2, 3, and 4 larvae of *C. pavonana* were acquired in the mustard plantations owned by farmers in the Depok area. The acquisition of images of *C. pavonana* larvae was done using a CANON EOS digital single lens reflex (DSLR) camera with a 55 mm lens and a resolution of 6000×4000 pixels. The acquired larvae instars were the result of cultivation and propagation of *C. pavonana* in the University Gunadarma Technopark Laboratory. The determination of instars 1, 2, 3, and 4 is carried out by the researcher for data acquisition based on visual observation. Larvae in instars 1, 2, 3, and 4 are placed in separate containers to prevent mixing, facilitating the acquisition, and labeling process for each instar. The larvae are observed every hour/day to understand the molting process and the development of each larval instar. Data acquisition for each larval instar is based on the age of the instar to obtain characteristics corresponding to the development duration of each instar. Instar stages one to three undergo instar changes more rapidly, as the larval development is influenced by temperature [23]. The temperature during data acquisition tends to be extreme. The highest daily temperature in the Depok region of Indonesia is around 32 °C, rarely below 30 °C or above 33 °C. The lowest average daily temperature is 32 °C during maintenance and acquisition in June and July of 2023. The duration of the larval instar stage in the study is also mentioned [7] the duration of the instar stages is longer, namely instar 1, 2, 3, and 4, each lasting for 2-3, 1-3, 1-3, and 3-6 days, respectively [24]. The maintenance of the larvae is in the temperature range of 25-28 °C.

In this study, the first instar is recognized on one side at the age of one day. The second and third instar larvae are acquired at the ages of one day and two days. At the age of one day, two types of characters are observed in the larvae, namely, newly molted larvae, indicating that the larvae have undergone further instar changes. Newly molted larvae show a paler body and head. In particular, for the first-day instar larvae that have fed on cabbage, there are changes in character, such as the body color and the appearance of the head capsule no longer being pale [24], the size also experiences a slight increase both in terms of width and length of the larva's body. The fourth instar is acquired at the age of one, two, three, and four days. Instars one to three have a stage lasting for two days, as on the third day, the larva undergoes molting to become the next instar [25]. The fourth instar has the longest developmental stage, lasting for four days, and on the fourth day, there is a pre-pupa stage. Pre-pupa refers to the final fourth instar larva that will transform into a pupa, characterized by a paler color and the release of fluid to adhere to the cocoon medium [19]. The characteristics of each larval instar can be described based on their morphological differences and image acquisition conditions. The acquisition of larval images was conducted by carefully taking a single larva using a small brush and placing it on a mustard green leaf. The dataset of *C. pavonana* larvae was obtained through direct acquisition in mustard plantations in the Depok area. Image acquisition was performed using a camera with a distance of 10 to 12 cm between the camera and the object. The capture position followed the movement of the larvae to obtain clear images, including views from the top, right side, and left side. The image acquisition process was conducted between 10:00 AM and 3:00 PM western Indonesian time.

The acquisition of instar 1, 2, 3, and 4 larvae is closely related to differences in sensitivity to insecticides at each developmental stage [8]. Later instars tend to show reduced sensitivity to active substances [26]. Insecticides containing active ingredients such as emamectin benzoate, lufenuron, and profenofos exhibit different LC50 values for larval mortality in *Spodoptera litura* and *Plutella xylostella* across instars [27]. Therefore, monitoring larval instars is essential to improve the accuracy of insecticide application, reduce control costs, and minimize environmental contamination caused by chemical substances [9].

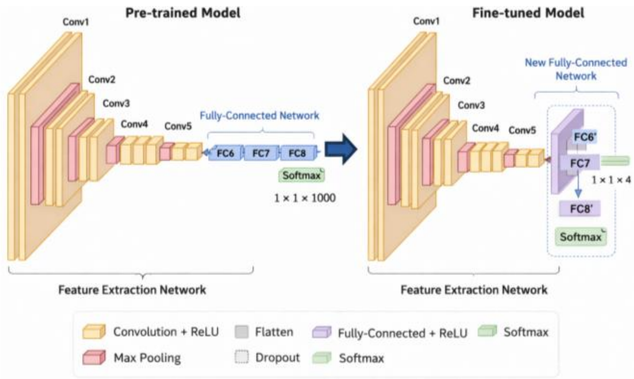
2.3. Preprocessing dataset of larva *Crocidolomia pavonana*

In the data preprocessing stage, the collected images of *C. pavonana* larvae are prepared for deep learning model training through several steps. The images are first resized to 256×256 pixels to meet the input specifications of the pre-trained VGG19 and Xception architectures, both of which require red green blue (RGB) images. Data augmentation is then applied using horizontal flipping, zooming, rotation, shearing, and normalization techniques [28]. Finally, the dataset is divided into training, validation, and testing subsets with an 8:1:1 ratio, while maintaining class balance through stratified sampling to ensure proportional distribution across subsets [29].

2.4. Larva *Crocidolomia pavonana* classification model shaping

The modeling stage is the core of this research, where deep learning models are initialized, trained, and evaluated using pre-trained architectures combined with fully connected layers to improve efficiency and accuracy [30]–[32]. Two CNN models, VGG19, and Xception, accessed via *tf.keras.applications*, are fine-tuned by allowing weight and bias adjustments during training to capture detailed features of *C. pavonana* larvae [33]. As the default output layers classify 1000 categories, they are replaced with a new fully connected network for four classes, consisting of one flatten layer, three dropout layers, three dense layers (256, 128, and 64 nodes), and one output layer. This structure integrates feature extraction from pre-trained models [34] with additional fully connected layers that refine features for final classification [35], as illustrated in Figure 1.

Figure 1 illustrates the architectural modification applied in this study. Figure 1(a) presents the original pre-trained CNN architecture, while Figure 1(b) shows the fine-tuned model with modified fully connected layers designed to classify four instar classes of C. *pavonana* larvae.



(a) (b)

Figure 1. Pre-trained and fine-tuned CNN architectures; (a) pre-trained model and (b) fine-tuned model with modified fully-connected layers

2.5. Detection of *Crocidolomia pavonana* larvae in mustard greens

The stages of creating a bounding area in this research involve delineating the region of *C. pavonana* in an image that is most significant in influencing the classification. The pest area of *C. pavonana* on mustard plants can be identified with the help of bounding area. Mapping the pest area of *C. pavonana* can facilitate farmers in identifying pests on mustard plants. The bounding area creation algorithm involves the following steps:

a. Larval images of *C. pavonana* are fed into a deep learning model. These images are processed through CNN layers and the feature maps from the final convolutional layer are extracted to generate a heatmap.
b. The model maps input images to the activations of the last convolutional layer and computes the gradient of the predicted class with respect to these activations [36]. The gradients are averaged across channels to obtain weights, which are then combined with the feature maps to produce a normalized class activation heatmap, where higher values indicate stronger influence.
c. The heatmap is combined with the original image to generate Grad-CAM visualization, where regions with high influence are highlighted in red and less significant regions appear in blue [37]. The Grad-CAM process includes; i) loading the image as a matrix, ii) expanding dimensions to form a batch input, iii) generating a class activation heatmap [38], iv) scaling the heatmap, v) applying a colormap, and vi) overlaying the heatmap onto the original image to produce the final visualization.
d. The bounding area is generated by selecting regions with high activation values from the Grad-CAM output. This process involves; i) reading and resizing the Grad-CAM image, ii) converting the image from RGB to hue saturation value (HSV) color space, iii) applying thresholding using predefined tolerance values to segment larval regions [39], iv) filtering pixels outside the threshold range, and v) converting the image back to RGB format for visualization [40]. The segmentation is based on color similarity using a tolerance threshold, which determines the similarity between larval and background pixels. This approach addresses challenges such as small object size and similarity between larval and leaf colors.

The overall steps of creating a bounding area to detect *C. pavonana* larvae are illustrated in Figure 2.

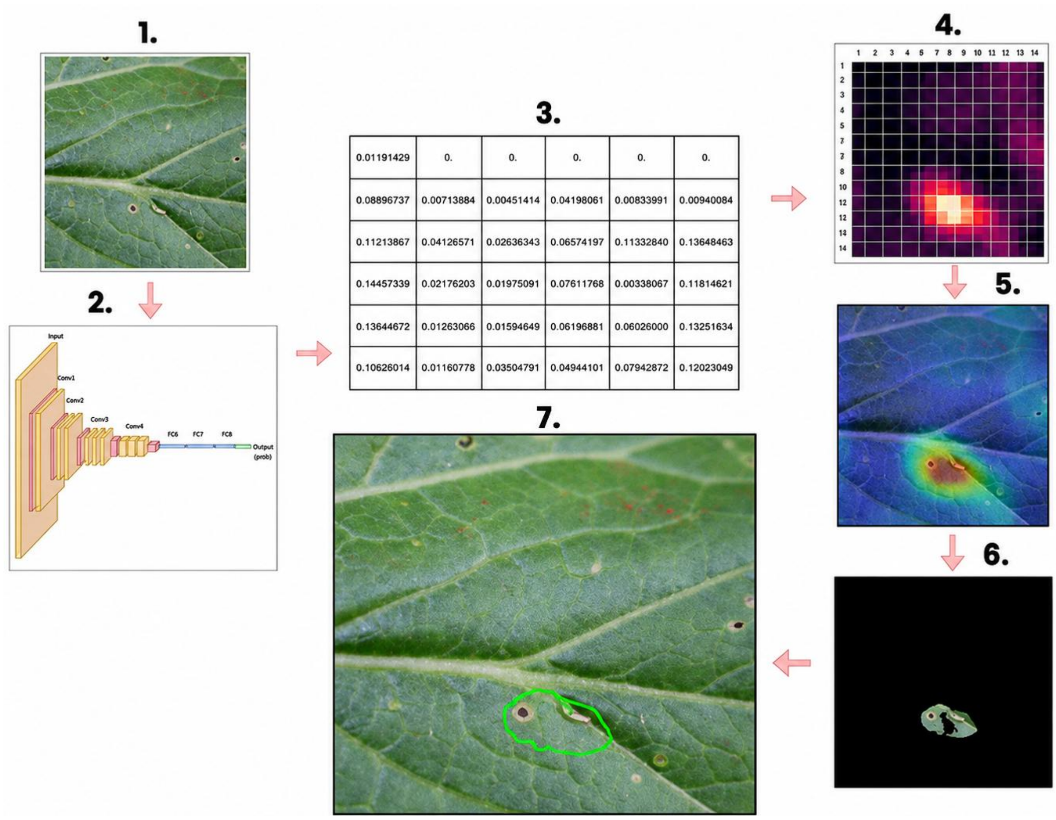


Figure 2. Step-by-step Grad-CAM visualization and bounding area generation

3. RESULTS AND DISCUSSION

This section presents the main findings of the study, including dataset generation through larval rearing, evaluation of deep learning classification models, and Grad-CAM visualization results. Both pretrained architectures demonstrate high accuracy in classifying *C. pavonana* larval instars, with VGG19 showing more stable training performance and Xception achieving slightly higher validation accuracy, indicating their effectiveness for automated pest monitoring. Additionally, experiments on testing data were conducted to evaluate classification outputs and corresponding bounding areas, providing insight into model performance and interpretability.

3.1. Rearing result of larva *Crocidolomia pavonana*

The larva of *C. pavonana* in each instar has variations in characteristic size, texture, and color, but the shape is almost similar in the growth and development phases. The first instar has a relatively small body size, visually difficult to spot individually on plants except when clustered together [41]. Each instar has differences with the addition of size in the head and abdomen capsules. Research [10], [24] stated that the size of the head capsule of instar 1, 2, 3, and 4 larvae of *C. pavonana* is 0.27, 0.46, 0.84, and 1.40 mm, respectively. The acquired dataset comprises 684 images of *C. pavonana* larvae, consisting of 131 images for instar 1, 132 images for instar 2, 154 images for instar 3, and 267 images for instar 4. This dataset, formed during this research, is a new compilation. This dataset, formed during this research, represents a newly compiled field-based dataset that can support future studies on automated pest detection and classification.

3.2. Results of the formation of the classification model for *Crocidolomia pavonana*

In this study, the classification model for *C. pavonana* is developed by fine-tuning pre-trained models combined with fully connected layers. The pre-trained architectures are obtained from the *tf.keras.applications* module [42], while the TensorFlow functional API is used to construct and visualize the model. Training is conducted over 5×5 epochs with callback functions to monitor performance metrics, including loss, accuracy, learning rate, and training time [43]. The results show that the VGG19-based model achieved 97.25% training accuracy and 94.18% validation accuracy in 24 minutes and 34.71 seconds, while the Xception model reached 94.88% training accuracy and 97.05% validation accuracy in 46 minutes and 49.36 seconds. Compared to

Xception, VGG19 requires shorter training time with competitive accuracy, indicating better computational efficiency, whereas Xception provides slightly higher validation accuracy, suggesting stronger feature representation capability.

3.3. Evaluation result of training model

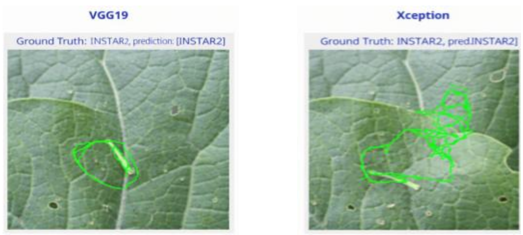
The accuracy and loss metrics are used to evaluate model performance on training and validation datasets. Figure 3(a) presents the training and validation loss curves of the VGG19 model, while Figure 3(b) shows the training and validation accuracy curves over 25 epochs. The VGG19 model demonstrates decreasing training loss from 0.4 to near zero and increasing training accuracy from 85% to 100% over 25 epochs, although validation metrics fluctuate, with the best loss at epoch 17 (0.15629) and the highest accuracy at epoch 12 (95.588%). The model achieved accuracies of 93.75% (loss 0.1233), 96.78% (loss 0.0968), and 94.20% (loss 0.1374) on training, validation, and testing datasets, respectively. The Xception model obtained 93.75% (loss 0.1546), 93.75% (loss 0.1130), and 94.20% (loss 0.1957). Compared to Xception, VGG19 shows slightly lower validation accuracy but lower testing loss, indicating more stable generalization. The high testing accuracy demonstrates strong performance on unseen data. These results are consistent with previous studies reporting accuracy ranges of 70% to 93% for larval classification tasks [12]–[15], indicating that the proposed approach is competitive and reliable for field-acquired datasets.

(a) (b)

Figure 3. Training performance of the VGG19 model; (a) training and validation loss and (b) training and validation accuracy

3.4. Bounding area result

The bounding area generated in this study serves to identify the regions where *C. pavonana* larvae are the primary focus of the classification model, with results presented as annotated images showing ground truth labels and green bounding outlines. Figure 4(a) illustrates the Grad-CAM localization results generated using the VGG19 model, while Figure 4(b) presents the localization results obtained using the Xception model. Both models successfully highlight larval regions for test samples, including the Instar 2 class. However, differences are observed in activation patterns, with VGG19 producing more focused regions around the larval body, while Xception tends to highlight broader surrounding leaf areas, indicating variations in feature representation. Despite these differences, both models achieve correct classification, and the use of Grad-CAM enhances model interpretability by clearly indicating regions influencing predictions, which is valuable for practical pest monitoring and supports prior findings on improving transparency in deep learning-based image analysis [18].



(a) (b)

Figure 4. Grad-CAM localization of *C. pavonana* larvae; (a) VGG19 prediction result and (b) Xception prediction result

4. CONCLUSION

This study developed a deep learning framework for the classification and localization of the four instar stages of *C. pavonana* larvae. A real-field dataset was constructed through controlled rearing and image acquisition under natural plantation conditions, ensuring representative instar characteristics. Fine-tuned VGG19 and Xception models demonstrated high classification accuracy and reliable generalization performance. Grad-CAM visualization combined with color-based segmentation enabled precise localization of larval regions, improving model interpretability and supporting practical pest monitoring. The main contributions include the creation of a field-acquired dataset, optimization of pre-trained CNN architectures, and the implementation of an interpretable detection mechanism for precision pest management. However, several limitations remain. The dataset size is relatively limited (684 images), which may restrict the model's ability to capture broader variations in larval appearance and environmental conditions. In addition, the dataset was collected from a single plantation environment, which may not fully represent variations in lighting conditions, leaf textures, and background complexity across different agricultural locations. Furthermore, the models were evaluated under offline experimental settings, and their computational requirements may limit direct deployment on low-power devices used in field monitoring systems. Future work will focus on expanding the dataset with images collected from multiple plantation environments to improve model generalization. Further research will also explore lightweight deep learning architectures, such as MobileNet or EfficientNet, to enable real-time pest detection on edge devices, as well as investigate more advanced explainable AI techniques to enhance the transparency and reliability of automated pest monitoring systems.

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AUTHOR CONTRIBUTIONS STATEMENT

This journal uses the Contributor Roles Taxonomy (CRediT) to recognize individual author contributions, reduce authorship disputes, and facilitate collaboration.

Name of Author	C	M	So	Va	Fo	I	R	D	O	E	Vi	Su	P	Fu
Diana Tri Susetianingtias	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓
Sarifuddin Madenda	✓	✓		✓	✓		✓			✓	✓	✓		
Risnawati		✓	✓			✓		✓		✓				
Maukar	✓			✓	✓					✓	✓		✓	
Eka Patriya		✓			✓	✓	✓			✓				
Rodiah	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓	✓

C : **C**onceptualization	I : **I**nvestigation	Vi : **Vi**sualization
M : **M**ethodology	R : **R**esources	Su : **Su**pervision
So : **So**ftware	D : **D**ata Curation	P : **P**roject administration
Va : **Va**lidation	O : Writing - **O**riginal Draft	Fu : **Fu**nding acquisition
Fo : **Fo**rmal analysis	E : Writing - Review & **E**diting	

CONFLICT OF INTEREST STATEMENT

Authors state no conflict of interest

INFORMED CONSENT

This study did not involve human participants; therefore, informed consent was not required

ETHICAL APPROVAL

This study utilized pest dataset and did not involve human or vertebrate animal subjects; therefore, ethical approval was not required.

DATA AVAILABILITY

The data collected for this study are part of ongoing research with potential commercial applications. Therefore, we are unable to make the data publicly available at this time due to intellectual property restrictions and the ongoing commercialization process. However, researchers interested in accessing the dataset are welcome to contact the corresponding author at rodiah@staff.gunadarma.ac.id for further information and to discuss potential data sharing under appropriate conditions.

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