



Detection of White Spot Syndrome Virus in Shrimp using Convolutional Neural Network

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ABSTRACT

Background: Shrimp rearing and wild-catch shrimp fisheries provide employment and income for millions worldwide. As the global population rises, shrimp plays a key role in addressing food security challenges. It is a nutritious and accessible food, widely consumed in diverse cuisines. Ecologically, it serves as scavengers and detritivores, maintaining stability in aquatic environments. This ecological role has driven the development of sustainable shrimp farming practices. Disease management, especially prevention and early detection, is a critical concern in shrimp farming. Automated image processing could speed up disease detection, ensuring timely intervention. This study focuses on detecting white spot syndrome virus (WSSV) in shrimp using convolutional neural networks (CNN) with promising accuracy.

Methods: The model uses a sequential convolutional neural network (CNN) to identify WSSV in shrimp. It is trained with images categorized into two groups: Healthy and diseased. Features like lesions and discoloration are used to detect infection. The dataset is preprocessed to reduce resolution variation through bilinear interpolation. The model's architecture consists of multiple layers that extract features and reduce spatial dimensions. Concatenation layers combine information from different network parts to enhance feature extraction. Performance is evaluated to determine the model's ability to make reliable predictions.

Result: The CNN model achieved a remarkable accuracy (93.75%) in detecting WSSV. It correctly identified all WSSV instances with minimal misclassification. The overall performance of the model demonstrates its robustness. The ROC curves further confirm its ability to classify both healthy and diseased shrimp effectively, highlighting its potential for early disease detection in shrimp farming systems.

Key words: Aquaculture, Convolutional neural network (CNN), Deep learning, Shrimp disease.

INTRODUCTION

The global shrimp industry has seen significant growth in both quantity and quality over the past 15 years, with farmed species, particularly Pacific white leg shrimp, dominating production. Farmed shrimp accounted for 63% of total production in 2022. The rising demand for shrimp is driven by health benefits and the introduction of shrimp-based products, particularly frozen shrimp, which offers extended shelf life. Despite challenges like oversupply and low prices, the industry has recovered post-COVID-19 and is expected to continue expanding. Future growth will depend on climate-smart aquaculture, sustainability certifications and efficient production practices (Mandal and Singh, 2025; Yang *et al.*, 2024).

The global demand for seafood has escalated, prompting countries to adopt better aquaculture practices to improve productivity, efficiency and sustainability. Advances in selective breeding and genetics have led to the development of improved shrimp, fish and other shell breeds with enhanced growth rates and nutritional value. Technologies like marker-assisted selection and genomic selection are accelerating breeding processes in marine species (Zenger *et al.*, 2019). Among various seafood products, shrimp holds a significant position. According to the Food and Agriculture Organization (FAO), shrimp is the most traded seafood commodity globally (FAO, 2022) and its consumption continues to rise, ranking alongside popular seafood items like fish, tuna and mollusks. Shrimp farming contributes billions of dollars annually to

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the global economy (Phong *et al.*, 2021). It is considered a sustainable method for meeting the growing food demand and bolstering social and economic stability worldwide.

Shrimp plays a vital role as a high-protein, nutrient-rich food source, contributing to global food security amidst a rapidly growing population. Its versatility in various cuisines has made it a favorite among consumers and chefs. Furthermore, shrimp helps maintain aquatic ecosystems by recycling organic matter and ensuring water quality (Depestele *et al.*, 2019; Hai and Duong, 2024; Maltare *et al.*, 2023; Bagga *et al.*, 2024). As scavengers and detritivores, shrimp populations support balanced food webs in aquatic environments. These roles have led to the innovation of shrimp farming models that prioritize environmental sustainability and commercial success. Additionally, shrimp farming holds cultural significance in coastal communities, where traditional practices are passed

down through generations, reinforcing local cultural identity.

However, the rapid expansion of the shrimp industry has highlighted environmental challenges such as habitat degradation, water pollution, overfishing and disease outbreaks. These issues have prompted the establishment of eco-certification programs and conservation initiatives aimed at minimizing environmental harm and improving resource management. Diseases such as White Spot Syndrome Virus (WSSV), Taura Syndrome Virus (TSV) and Early Mortality Syndrome (EMS) have significant economic and ecological impacts on shrimp farming. Molecular tools, such as polymerase chain reaction (PCR) assays and loop-mediated isothermal amplification (LAMP), have been developed for rapid and accurate disease detection in shrimp farming. However, these methods face limitations in terms of cost, complexity and time sensitivity (Islam *et al.*, 2023). Moreover, traditional disease detection methods rely heavily on farmer expertise, making them time-consuming, labor-intensive and expensive (Estevez *et al.*, 2023; Wang *et al.*, 2024).

To address these challenges, there is a growing need for affordable, user-friendly and field-deployable disease surveillance tools. Machine learning (ML) algorithms and artificial intelligence (AI) techniques offer promising solutions by enabling large datasets to be analyzed for early disease detection, health monitoring and environmental monitoring. Non-invasive, low-cost and user-friendly technologies, such as computer vision, are particularly promising for shrimp disease detection (Aung *et al.*, 2024). Using image acquisition equipment, data can be collected and used to train deep learning models that offer high accuracy and quick intervention opportunities (Abade *et al.*, 2021; Duong-Trung *et al.*, 2020; Min *et al.*, 2024; Zhang and Gui, 2023). Convolutional Neural Networks (CNNs) are emerging as a key technology for analyzing shrimp health. Deep CNN models can classify shrimp images based on disease symptoms, such as lesions, abnormalities and other visual signs. Object detection algorithms, including Faster R-CNN and YOLO (You Only Look Once), are designed to identify regions of interest in shrimp images, providing valuable inputs for disease diagnosis and monitoring. These CNN-based systems offer prompt disease detection with minimal human involvement, making them well-suited for large-scale aquaculture settings. An automated image-capture system, combined with CNN-powered disease recognition models, can significantly enhance disease surveillance, improving shrimp farm productivity and sustainability.

Several studies have addressed the need for efficient disease monitoring and classification in shrimp farming. Phong *et al.* (2021) discuss the market dynamics that drive farmers to optimize shrimp yields and productivity while maintaining environmental sustainability. Close supervision of shrimp farms is essential for adopting pro-environmental practices, such as avoiding excessive antibiotic use to prevent diseases. The shift from traditional manual disease detection to machine learning algorithms is gaining momentum

in aquaculture, with various ML models being applied for classification tasks.

The detection of shrimp diseases using CNN-based models is an evolving field with significant potential for improving aquaculture practices. The integration of machine learning techniques, such as CNNs, into disease monitoring systems enables more timely, accurate and scalable interventions. While many existing models have shown promising results, further research is needed to optimize these systems for large-scale deployment.

The current work proposes a CNN-based approach for classifying shrimp health states and emphasizes the importance of accuracy, efficiency and low-cost technologies in supporting sustainable shrimp farming operations. By enhancing disease detection and early intervention capabilities, this model contributes to the overall productivity and sustainability of shrimp aquaculture.

MATERIALS AND METHODS

The following parts outline the procedure employed to construct a sequential Convolutional Neural Network (CNN) model for the identification of shrimp infected with WSSV disease. The task is separated into multiple distinct parts, with the initial one including the collection of images for categorization using deep neural networks.

Dataset

The dataset is composed of images from two different groups: Healthy and WSSV (White Spot Syndrome Virus). WSSV is a serious viral infection affecting global shrimp aquaculture. Images of shrimp with normal physiological characteristics that is, without any obvious signs of disease or infection are included in the healthy class. On the other hand, images of shrimp in the WSSV class show signs of a WSSV infection, like discoloration, abnormal behavior, or visible lesions on the body surface. The dataset consists of 298 images, divided into three subsets. The training set has 238 images (80%). The validation and testing datasets each contain 30 images (10%). This 80-10-10 split helps ensure a balanced dataset for effective model training and evaluation. Fig 1 illustrates representative images of healthy shrimp and shrimp infected with White spot syndrome virus (WSSV).

Image preprocessing

Before training, preprocessing techniques are applied to every image to ensure uniformity and improve the quality of the dataset. Resizing the images was done to ensure that the dimensions were consistent across the collection. Bilinear interpolation was used to reduce images of varying resolutions to 128×128 pixels. The images were then transformed into grayscale. A significant number of training data is required at this pre-processing stage to explicitly learn the features of the training data. In the next step, the images of shrimp were categorized based on their type and then annotated with the corresponding acronym representing the specific disease. In this case, the test

collection and training dataset exhibited two distinct classes.

Data augmentation

An array of augmentation techniques is used in this study to add diversity to the original dataset. These methods were rotation, flipping, shifting, zooming and shearing. Rotation added random rotations to the images to simulate different views and orientations, which helped the model identify objects from a range of perspectives. Flipping created mirror images in the dataset by flipping images horizontally, which improved the model's ability to recognize objects in any orientation.

Training dataset

The technique includes the utilization of a Convolutional Neural Network (CNN) to create a model for assessing performance. The model was trained to utilize image data

as input. The flow chart illustrating the classification process of healthy and diseased shrimp using Convolutional Neural Network (CNN) is shown in Fig 2.

Architecture of convolutional neural network (CNN) model

The architecture of a neural network model includes various types of layers such as convolutional layers, max-pooling layers, flatten layers and dense layers (Fig 3). Table 1 represents the parameters used in the CNN algorithm. Starting with the input layer, labeled as "input_1," it takes input data with dimensions of 128x128x3, where 3 represents the number of color channels (typically red, green and blue in an image).

The subsequent layers include convolutional layers ("conv2d"), followed by max-pooling layers ("max_pooling2d"). These layers are responsible for extracting features from the input data while reducing spatial dimensions, thereby aiding in capturing important patterns efficiently. As the data

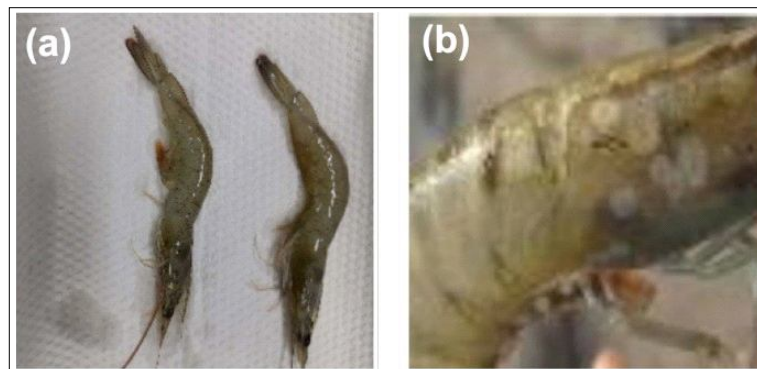


Fig 1: Healthy and WSSV-infected shrimp.

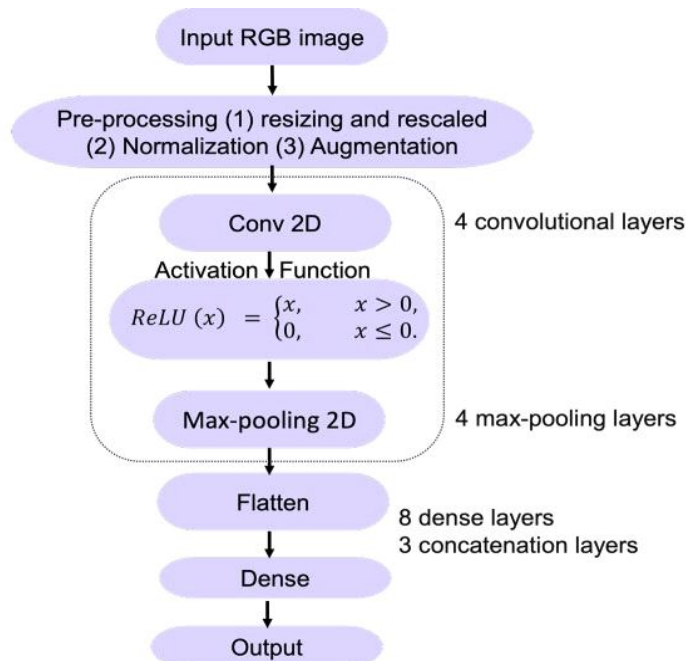


Fig 2: Flow Chart of the classification using CNN of healthy and diseased shrimp.

progresses through the network, the convolutional and max-pooling layers are stacked to deepen the network's configuration, gradually reducing the spatial dimensions of the data and increasing the number of channels. The architecture includes dense layers, also known as fully connected layers, which are responsible for learning complex patterns and making final predictions. These layers possess a large number of parameters because they are fully connected, which greatly enhances the model's ability to capture complex patterns in the data. The model employs concatenation layers ("concatenate") to combine features from different parts of the network, enhancing the model's ability to capture diverse and complementary information. Finally, the output layer, labeled as "dense_8," consists of two neurons, representing the classes that the model aims to classify. In this case, it's likely a binary classification task, as there are two output neurons. Overall, the presented architecture illustrates a deep neural network designed for processing image data, with convolutional layers for feature extraction, dense layers for pattern recognition and concatenation layers for integrating diverse information, culminating in a model capable of making accurate predictions based on the input data.

Performance evaluation parameters

The confusion matrix, which consists of the four essential components True Positive (TP), True Negative (TN), False Positive (FP) and False Negative (FN), is used to assess the model's performance.

Accuracy is a frequently used metric for assessing performance. It is a measure of the correctness of predictions, taking into account both true positives and true negatives, relative to the total number of predictions made. Usually, it provides insight into the accuracy of a trained model and offers an evaluation of its overall performance.

$$\text{Accuracy} = \frac{(TP+TN)}{(TP+TN+FP+FN)}$$

Precision is a metric that quantifies the frequency of accurate predictions generated by a model. The process involves dividing the total number of positive labels by the number of accurate positive predictions.

$$\text{Precision (P)} = \frac{TP}{(TP+FP)}$$

Recall measures the classifier's ability to correctly identify all relevant instances. This percentage is calculated by dividing the total number of positive reviews in the dataset by the number of correctly predicted positive observations. The objective of computing these metrics is to identify the most positive labels. The formula for calculating recall is as follows

$$\text{Recall (R)} = \frac{TP}{(TP+FN)}$$

Achieving an F1-score of 1 signifies complete performance, whereas a score of 0 signifies total failure. The F-measure is calculated using the following formula

$$\text{F1-Score} = \frac{2*(P)*(R)}{(P)+(R)}$$

RESULTS AND DISCUSSION

Intelligent aquaculture is essential for identifying shrimp diseases. Precise categorization of both healthy and WSSV is crucial for enhancing productivity and profitability. The main objective of this study was to achieve satisfactory outcomes in the area of disease detection. Fig 4 displays the training and validation loss along with the accuracy metrics.

A training loss of 0.0507 signifies an average difference of 0.0507 units between the model's predicted and actual target labels. Comparably, a validation loss of 0.0376 indicates that an average error of 0.0376 units is produced by the model's performance on unseen data (validation data). After 50 epochs, the model correctly classified every instance in the training and validation sets with an accuracy of 1.0000.

Fig 5 displays a collection of images that depict both the actual and the predicted labels. This presentation allows for an assessment of the efficacy and level of certainty of the trained model. The exhibited predicted outcomes are accurate and exhibit a high level of certainty.

The classification performance of the proposed model is summarized using a confusion matrix, as shown in Fig 6. The classification performance of the model for both classes is displayed in the confusion matrix. Two instances were mistakenly classified as WSSV (false negatives) out of the 17 cases in the Healthy class that were accurately identified as Healthy (true positives). On the other hand, none of the 13 WSSV class instances were incorrectly classified as Healthy (false positives), while all of the cases were accurately identified as WSSV (true positives). This matrix provides a clear visual representation of the model's ability to distinguish between the two classes, highlighting its potential to decrease misclassifications. This is particularly evident in the model's capacity to identify WSSV instances with accuracy. The performance of the classification model is summarized using key evaluation metrics, as presented in Table 2.

The precision, recall, F1-score, support and overall performance measures are shown in the table for both classes. The prediction of all Healthy classes was correct, as evidenced by the precision score of 1.0000. Conversely, the recall score of 0.8947 means that 89.47% of actual occurrences of healthy were properly identified by the model. The F1-score of 0.9444, which strikes a balance between precision and recall, indicates an equitable distribution of true positives and false negatives. This demonstrates a slight limitation in recall but a high degree of accuracy in

classifying events as Healthy. However, the WSSV class displays a distinct set of performance indicators. The high recall score of 1.0000 signifies that the model accurately detected every instance of WSSV in the dataset, despite the precision of 0.8667 suggesting a comparatively small percentage of misclassifications within this category. An overall high performance for this class is indicated by the F1-score of 0.9286, which is slightly lower in accuracy than that of Healthy but perfect in recall, indicating robustness in capturing all occurrences of WSSV.

The provided ROC (Receiver Operating Characteristic) curves show the rate at which the model performed in distinguishing between the Healthy and WSSV classes (Fig 7). For different threshold levels, each curve illustrates the trade-off between the true positive rate (sensitivity) and the false positive rate (1-specificity). The ROC curves exhibiting identical AUC values of 0.9717 demonstrate robust classification performance for the Healthy and WSSV classes, confirming the approach's efficient ability to differentiate between the two groups.

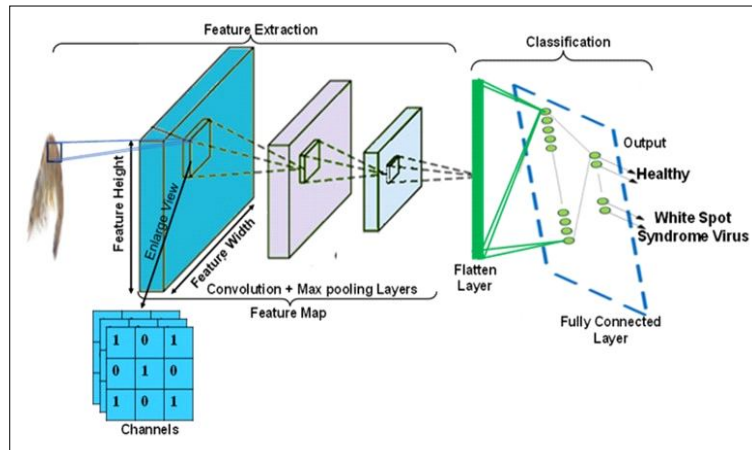


Fig 3: Architecture of Sequential CNN model.

Table 1: Parameters of CNN model.

Type =Layer	Output	Parameter
InputLayer (input_1)	(None, 128, 128, 3)	0
Conv2D (conv2d)	(None, 128, 128, 128)	3584
MaxPooling2D(max_pooling2d)	(None, 64, 64, 128)	0
Conv2D (conv2d_1)	(None, 62, 62, 64)	73792
MaxPooling2D (max_pooling2d_1)	(None, 31, 31, 64)	0
Conv2D(conv2d_2)	(None, 29, 29, 32)	18464
MaxPooling2D(max_pooling2d_2)	(None, 14, 14, 32)	0
Conv2D(conv2d_3)	(None, 12, 12, 128)	36992
MaxPooling2D(max_pooling2d_3)	(None, 6, 6, 128)	0
Flatten (flatten)	(None, 4608)	0
Dense(dense)	(None, 256)	1179904
Dense(dense_1)	(None, 128)	32896
Dense (dense_2)	(None, 64)	8256
Concatenate (Concatenate)	(None, 320)	0
Dense(dense_3)	(None, 32)	10272
Dense(dense_4)	(None, 64)	2112
Concatenate(concatenate_1)	(None, 96)	0
Dense (dense_5)	(None, 128)	12416
Concatenate(concatenate_2)	(None, 256)	0
Dense(dense_6)	(None, 64)	16448
Dense(dense_7)	(None, 32)	2080
Dense(dense_8)	(None, 2)	66
Total number of parameters: 1397282		
Trainable parameters: 1397282		
Non-trainable parameters: 0		

The model was trained for 50 epochs based on initial experiments, where we observed satisfactory convergence and performance within this timeframe. This number of epochs allowed the model to learn essential features from the dataset while reducing the risk of overfitting, as longer training durations can sometimes lead to memorization of the training data. Although increasing the number of epochs might improve accuracy, we considered the trade-off between training time and performance. Future experiments will involve training with more epochs to evaluate if further training leads to meaningful improvements or overfitting.

The proposed model is compared with the previously reported work based on a similar use of deep learning architecture. Satoto *et al.* (2023) employed the Inception

ResNetV2 deep learning model for coastal shrimp species classification, achieving an average accuracy of 99.4%. Despite promising results, larger datasets are needed for further validation. Hu *et al.* (2020) introduced ShrimpNet, a CNN-based system with two fully connected layers for shrimp identification. This model achieved an impressive 95.48% accuracy rate in distinguishing shrimp from other marine species. Lai *et al.* (2022) used the YOLOv4-tiny CNN model to estimate shrimp body length and classify shrimp into measurable and visible categories. The model showed a precision of 93.24%, though its infrastructure requirements and reliance on cloud computing make it less viable for some shrimp farmers.

Zhang *et al.* (2022) developed a lightweight YOLOv4-based model for automatic shrimp counting, achieving a

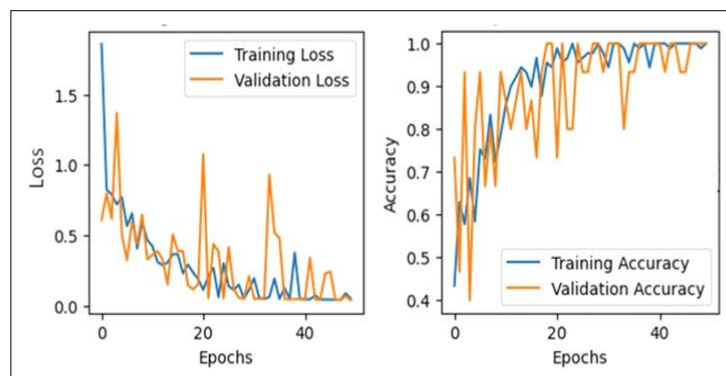


Fig 4: Loss and Accuracy measurements of training and validation datasets.

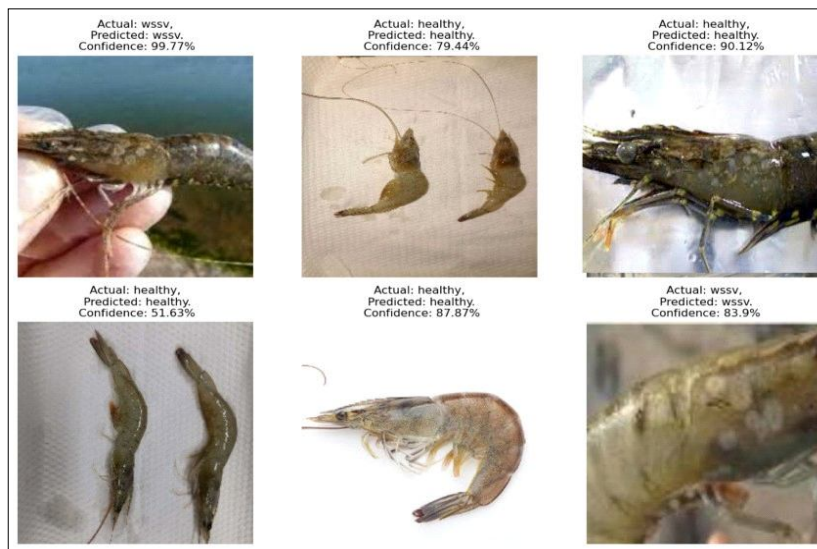


Fig 5: Actual and prediction of healthy and diseased shrimp.

Table 2: Classification matrix parameters.

	Precision	Recall	F1-Score	Support
Healthy	1.0000	0.8947	0.9444	19
WSSV	0.8667	1.0000	0.9286	13
Accuracy			0.9375	32
Macro avg	0.9333	0.9474	0.9365	32
Weighted avg	0.9458	0.9375	0.9380	32

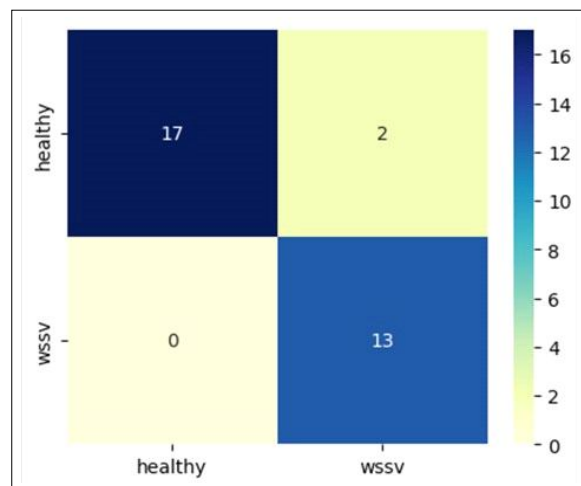


Fig 6: Confusion matrix of instances of healthy and WSSV disease.

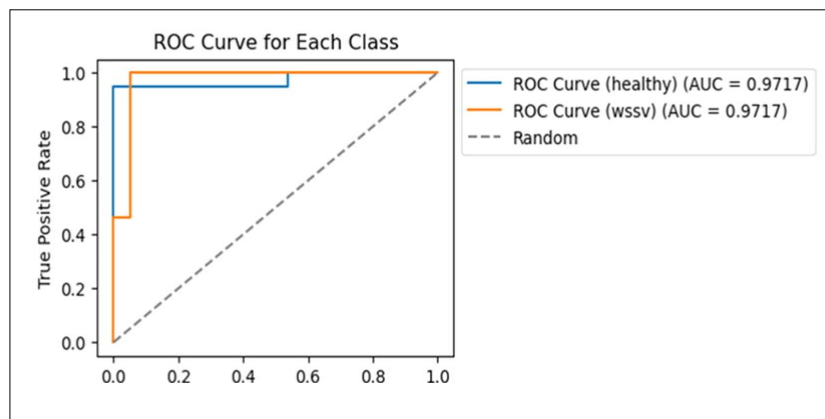


Fig 7: ROC Curve for both classes (healthy and WSSV).

well in counting shrimp, its application for disease detection remained limited. Prema *et al.* (2022) proposed a hybrid CNN-SVM model for shrimp freshness detection, focusing on quality control after harvest. However, their work did not address proactive disease prediction in live shrimp, which would be more beneficial for preventing health issues before harvest. Zhou *et al.* (2023) introduced an unsupervised learning approach for shrimp segmentation, providing a publicly available dataset for further research. This approach addresses the issue of limited resources for computer vision applications in aquaculture. The proposed model achieved a remarkable accuracy (93.75%).

These models heighten the need for more accurate models for disease detection to raise the yields in aquaculture farming. The model is an initiative with further upgrades for larger datasets. The overall performance of the proposed model is adequate and lays the foundation for more evolved CNN-based models with more layering.

CONCLUSION

In the domain of aquaculture, precise identification of shrimp diseases is essential for enhancing productivity

tory outcomes in disease detection. The provided table displays comprehensive performance measures, indicating the model's effectiveness in accurately classifying both healthy and diseased shrimp instances. The precision, recall and F1-score metrics highlight the model's ability to distinguish between healthy and WSSV instances, with notable robustness in WSSV detection. The provided ROC curves confirm the model's efficient classification performance for both classes, demonstrating its capability to differentiate between healthy and WSSV instances effectively. One limitation of this study is the small size of the dataset, particularly in terms of the number of images with two classifications. Future research should incorporate a larger number of images for better model performance. This study mainly focuses on the severe infection caused by the White Spot Syndrome Virus (WSSV) in shrimp. However, shrimp are also affected by other diseases, which should be considered in future studies. Additionally, this study uses a fully connected layer classifier for classification. Future research could compare machine learning techniques like support vector machines, random forests and decision trees for improved classification accuracy.

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Not applicable

Use of artificial intelligence

Not applicable

Declarations

Author declares that all works are original and this manuscript has not been published in any other journal.

Conflict of interest

Author declares that they have no conflict of interest.

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