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Analysis Of Internal Abnormalities Of Tilapia Flesh Using Hyperspectral Imaging And Machine Learning Method

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ABSTRACT

Tilapia, the most produced aquaculture species in Taiwan, has experienced significant production loss due to internal abnormalities, notably streptococcosis, which remains undetectable until fillets are cut. The absence of visible external symptoms frequently leads to quality reduction and economic loss. To address this, hyperspectral imaging, capable of capturing subtle spatial and spectral differences, was employed. The objective of this study was divided into two phases: firstly, identification of normal fillets and streptococcosis fillets externally; secondly, classifying streptococcosis fillets into three different damage levels externally. A total of 63 Fillet samples were obtained from several fishery cooperation in Taiwan, including 30 normal and 33 streptococcosis fillets. For the first phase, down-sampling was conducted to generate training data efficiently. For the second phase, three levels of damage were labeled to every pixel from the inside image by referencing the visible symptoms on the fish meat. Next, flipping and mapping were executed to generate labels of the outside data. Three machine learning methods were implemented and compared. Among these methods, the one-dimensional convolutional neural network (1D-CNN) achieved the highest accuracy, reaching 0.92 for phase one and 0.78 for phase two. For the classification of normal and streptococcosis fillets, based on results from the validation and test sets, the minimum correct classification rate was 76.24% for every streptococcosis fillets and 71.21% for every normal fillets. By setting an appropriate threshold between these values, external identification is achievable. Visualization of the phase two model prediction result demonstrated the model's ability to detect affected areas externally. Results highlight hyperspectral imaging's capability of identifying streptococcosis fillets externally and its potential for locating affected area through external fish scales.

Keywords: Hyperspectral imaging, Aquaculture, Abnormalities identification

INTRODUCTION

In Taiwan, aquaculture constitutes a major economic sector, contributing substantially to the national fisheries industry. Among the cultured species, tilapia has the highest production. However, its yield has shown a declining trend in recent years, primarily resulted from the persistent occurrence of flesh abnormalities. Among these abnormalities, streptococcosis, represents the most prevalent condition. This disease can only be detected after the fish is sectioned, when visible symptoms within the flesh become apparent upon visual inspection. This issue may lead to conflicts between aquaculture farmers and fillet processors, ultimately

resulting in production losses. To address this problem, hyperspectral imaging (HSI) integrated with machine learning (ML) methods has been employed, as it enables the detection of subtle differences by capturing and analyzing both spatial and spectral information. In light of the above, the main objective of this study was divided into two phases. First, to develop an approach for externally identifying normal tilapia fillets and fillets affected by streptococcosis. Second, to externally classify the flesh area of infected fillets into three different damage levels.

MATERIALS AND METHODS

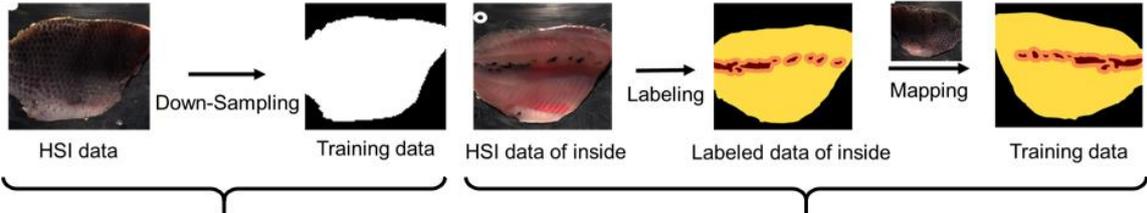
SAMPLE COLLECTION AND DATA ACQUISITION

During 2024 and 2025, frozen, vacuum-packed, sliced tilapia fillets were collected from multiple fishery cooperatives in Taiwan, which also assisted in assessing the condition of the flesh. In total, 88 fillets were collected, consisting of 30 normal and streptococcosis samples. A line-scan hyperspectral camera (MV.X; Headwall Photonics, Inc., Bolton, MA, USA) operating over a spectral range of 400–1000 nm with a spectral resolution of 2 nm was employed for data acquisition. HSI data of the fillets were acquired from both sides after completely thawed.

DATA PRE-PROCESSING AND MODEL DEVELOPMENT

For the first phase, which aimed to identify normal and streptococcosis fillets, down-sampling was conducted by sliding 10 × 10-pixel windows across the fillet area and the spectrum for each window was obtained by averaging the pixel values in the spectral domain (Qin et al., 2020). Window classes were determined by the fillet condition, independent of visible lesions, yielding 376,155 windows for model development.

For the second phase of classifying different damage levels, the labels of each pixel in the image were first determined by inspecting the visible symptoms from the inside image. Three damage levels were defined, from severe to minor, as Level 1, Level 2, and Level 3, respectively. Level 1 for visible lesions, Level 2 for surrounding dilated regions, and Level 3 for the remaining pixels. These label definitions were based on the hypothesis that infection spreads outward from the initial symptoms. Labels were mapped onto the external surface by horizontally flipping the masks and applying coherent point drift (CPD) (Myronenko & Song, 1998) for alignment. Since most streptococcosis fillets exhibited only minor symptoms, the number of pixels of Level 1 and Level 2 was considerably lower than Level 3. Therefore, random sampling was performed on the Level 3 class to match the number of samples in the other classes, yielding a total of 2,419,350 pixels for model development. Three machine learning method were applied and compared in this study for both phases, including extreme gradient boosting (XGBoost), random forest (RF) and one-dimensional convolutional neural network (1D-CNN). The dataset was divided into training and testing subsets using an 80:20 ratio.



Phase 1: Identify normal and affected fillets Phase 2: Identify different damage levels
 Fig.1 HSI data pre-processing workflow for model development.

RESULTS & DISCUSSION

Among three evaluated machine learning models, the 1D-CNN achieved the highest accuracies of 0.92 and 0.78 for phase 1 and phase 2, respectively (Table 1). In phase 1, this superior performance highlights the model's capability to discriminate subtle spectral variations between normal and streptococcosis fillets, regardless of the presence of visible lesions. By establishing a propriate threshold for the proportion of windows classified as affected within a fillet, streptococcosis fillets could be accurately identified. For phase 2, visualization of the model result provided further insights, indicating the predicted results could be used to distinguish severity levels and localize different degrees of damage with the support of HSI data.

Table 1 Classification accuracies of all ML models using outside data.

Phase \ Model	RF	XGBoost	1D-CNN
Phase 1 (Identify fillets)	0.80	0.79	0.92
Phase 2 (Identify damage levels)	0.57	0.60	0.78

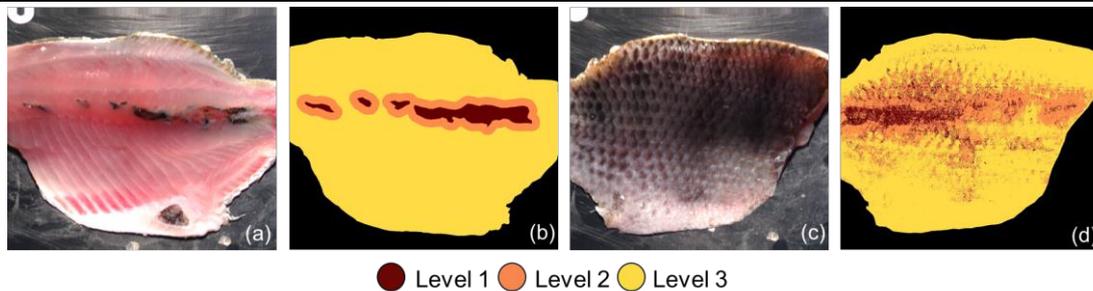


Fig.2 Classification result of 1D-CNN model in phase 2 for a streptococcosis fillet. (a) original image of inside fillet; (b) label result of inside fillet; (c) original image of outside fillet; (d) 1D-CNN classification visualization of outside fillet.

CONCLUSIONS

This study successfully applied hyperspectral imaging combined with machine learning methods to identify tilapia fillets affected by streptococcosis and to classify them into three severity levels. Key findings highlight the potential of integrating HSI with a 1D-CNN model for both abnormality detection and severity assessment as a rapid and non-destructive approach. Future work will focus on dataset expansion and feature wavelength selection to enhance model generalization and enable practical implementation.

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