Detection of moldy core in apples and its symptom types using transmittance spectroscopy

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Abstract: A detection method based on transmittance spectroscopy and support vector machine (SVM) was proposed to achieve rapid nondestructive detection of moldy core in apples. A visible to near-infrared (Vis/NIR) spectroradiometer was used for scanning transmittance spectra of 215 apple samples in the wavelength range of 200-1025 nm. Wavelet transform was used to reduce the dimensionality of the spectra and extract wavelet coefficients. Two classification algorithms including artificial neural network (ANN) and SVM were used to develop models whose parameters were optimized by genetic algorithms (GA) for determination of the presence and types of moldy core in apples. Comparisons results of the models showed that the GA-SVM model obtained the optimal result with an accuracy of 96.92% for detecting the presence of moldy core and 81.48% for distinguishing symptom types of the disease. These results indicate that it is feasible to detect moldy core in apples nondestructively and rapidly based on transmittance spectroscopy and that wavelet transform is an effective method for extraction of characteristics from spectra. Moreover, the GA-SVM algorithm in conjunction with Vis/NIR transmittance spectroscopy can accurately achieve fast and nondestructive detection of the presence and types of moldy core in apples.

Keywords: moldy core of apples, transmittance spectrum, wavelet transform, support vector machine, genetic algorithm, symptom types

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1 Introduction

Apple is a widely planted fruit in the world, and apple industry occupies a very important status in China's agriculture. It plays a pivotal role in exports, agricultural structure adjustment, famer's incomes and other aspects. Apple moldy core, also called mould core or core rot, is a major disease affecting the internal quality of apples. Fruits infected with moldy core gradually decay from inside to outside, but the fruit surface doesn't show obvious symptoms. Consequently, it is difficult to identify moldy core in apples. Once infected apples are mixed with good fruit and flowing into the market, the interests of consumers will be harmed and the reputation of fruit merchants and production locations, and even the country's reputation in the international market will be negatively affected. Based on the symptoms of the diseases, apple moldy core can be divided into three types: browning, moldy core, core rot (Figure 1), which account for 43.22%, 26.10%, and 30.68%, respectively[1], of all moldy core diseases in orchards. Due to the lack of effective and accurate

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means, detection of moldy core in apples has become a major problem to be solved in the apple industry.

a. Browning b. Moldy core c. Core rot

Figure 1 Types of symptoms of moldy core in apples

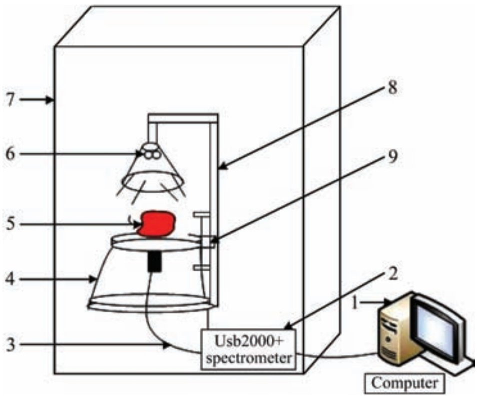
Many researchers have tried to detect moldy core in apples using different methods. Some researchers have used nondestructive testing (NDT) methods, including X-rays[2], nuclear magnetic resonance (NMR) and LF-NMR techniques[3] to detect internal defects in apples, but these methods are not suitable for practical applications due to the expensive equipment. Nondestructive detection of apple moldy core based on bio-impedance properties was proposed by Li et al.[4] In recent years, spectroscopic techniques have been used widely in the testing of agricultural products. Some researchers[5-7] used diffuse reflectance spectroscopy to detect moldy core in apples. However, the early-stage onset is located in the core of the fruit, which is difficult to be identified from the surface. The internal browning in apples was detected by Vis/NIR spectroscopy in the range of 650-900 nm. By analyzing the spectra, three wavelengths, 715 nm, 750 nm, and 810 nm, were selected and a classification accuracy of 95.65% was achieved[8]. Infrared spectroradiometer was used for scanning diffuse reflectance spectra of Braeburn apples in the wavelength range of 700-900 nm, and the optimal model had a R^2 value of 0.91[9,10]. The partial least squares regression (PLSR) models were established based on the transmittance spectroscopy data and the accuracy of the classification results was 90.1%[11]. Nevertheless, the detection accuracy and detection efficiency have yet to be improved. Multispectral imaging systems have been used widely in testing of agricultural products, and some researchers have used it to detect bruises on apples[12-14]. Moreover, there are no reports on the use of spectroscopic detection technology for distinguishing the types of moldy core in applies. There are two benefits to distinguish the types of moldy core in apples. Firstly, it helps preventing mistakenly eating moldy core apples. Secondly, this research has important significance for guiding the sterilization of the orchard and reducing the regeneration of the moldy core in apples.

The objective of this study was to develop a nondestructive method for detection of presence and types of moldy core in apples using transmittance spectra, wavelet transform, and classification algorithms of back propagation neural network (BP-NN) and support vector machine (SVM) optimized with genetic algorithms.

2 Materials and methods

2.1 Composition of the testing platform

To study the relationship between moldy core in apples and transmittance spectra, a testing platform (Figure 2) was built, which including an illumination source, a detection chamber, a portable optical emission spectrometer, a computer, and so on.



Note: 1. Computer 2. Fiber-optic spectrometer (usb2000+) 3. Fiber-optic 4. Light-shading curtain 5. Apple 6. Illumination source 7. Opaque chamber 8. Holder 9. Height adjustable stage

Figure 2 Testing platform structure for moldy core in apples

A USB2000+XR1 portable spectrometer (Ocean Optics, Dunedin, Florida, USA) sensitive in the wavelength range of 200 nm to 1025 nm was used. The instrument was based on a Sony linear silicon CCD array with 2048 pixels and a 25 μm slit. The spectral sampling interval was 0.46 nm and the optical spectral resolution was 2 nm. Four 50 W tungsten halogen bulbs were installed in the dark testing room as illumination source. Apples samples were placed on a height adjustable stage with a hole. A fiber probe was located beneath the apple to detect the transmitted light which was transferred through the optical fiber to the spectrometer for processing. The apparatus was controlled by computer (4-core Intel (R) i5 CPU, clocked at 3.0 GHz, 4 GB memory) via a USB interface with software especially developed for transmittance data acquisition and storage. Data processing and modeling was performed using software Matlab R2014a.

2.2 Samples and spectrum collection

A total of 840 Red Fuji apples were collected in an orchard located in Haoyin Village, Fengxi Town, Luochuan County, Shaanxi Province, from which, 215 samples were carefully selected, cleaned, numbered and preserved for half a month in a laboratory (22°C, relative humidity 55%). After 10 days, apples naturally been infected, and three transmittance spectra were collected from each apple in three orientations by manual rotation through approximately 120° about its stem axis. After spectral scanning, the apple was cut through its equator and the cross sections were photographed with a digital camera (Canon-EOS6D) to determine the moldy degree of the apple. The image of the cross section was analyzed using the threshold method by means of the image processing toolbox of MATLAB. As shown in Figure 3, there were obvious differences in the transmittance spectra between the infected apple and the healthy one in the wavelength range of 680-750 nm.

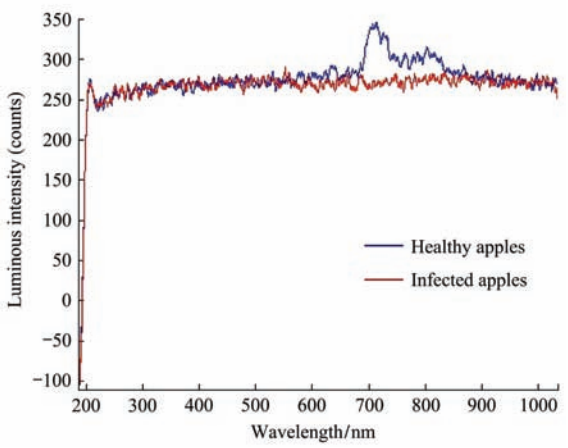


Figure 3 Transmission spectra of infected apples and healthy apples

For the development of model to determine the presence of moldy core in apples, 215 samples (Figure 4) were selected from the 840 samples, including a training set of 150 samples (20 infected apples and 120 healthy apples) and a test set of 65 samples (13 infected apples and 52 healthy apples). According to the suggestions of expert, 36 infected samples were selected from all samples for constructing models to identify the moldy core types, including a training set of 27 samples (13 with browning, 6 with moldy core, and 8 with core rot) and a test set of 9 samples (4 with browning, 2 with moldy core, and 2 with core rot).

Two classification models were established to detect the presence of moldy core and distinguish the types of moldy core, respectively. The models were evaluated based on the recognition correct rate (the ratio of the samples correctly distinguished in the test set to the total test samples).

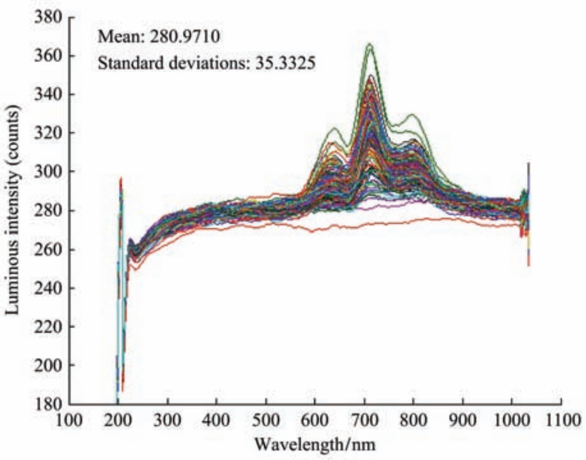


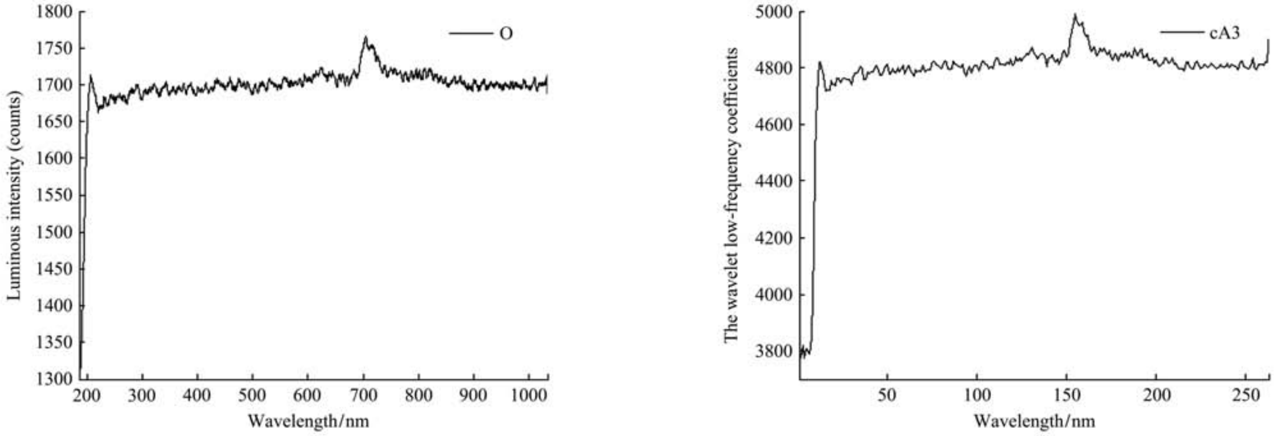
Figure 4 Transmittance spectra of 215 samples

3 Extraction of spectral characteristics

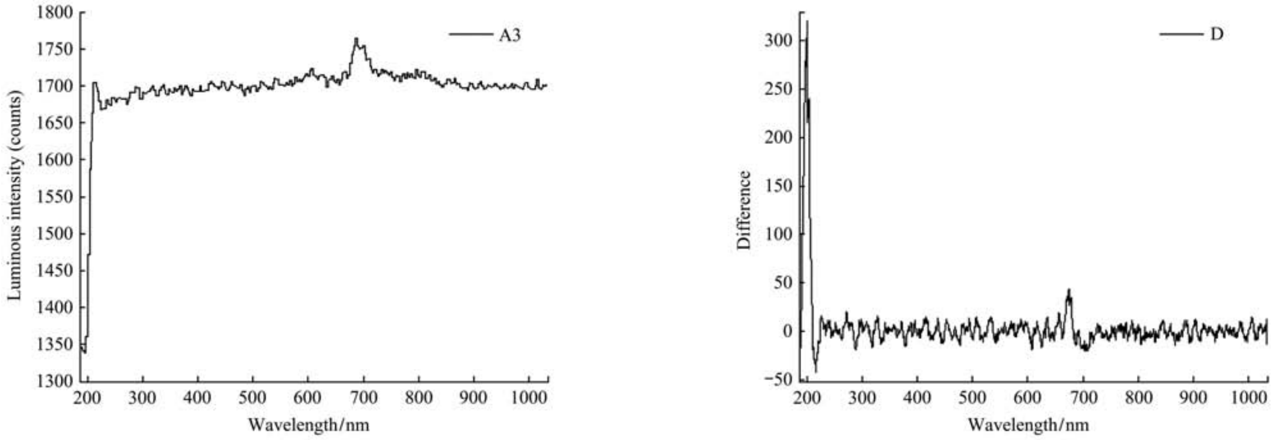
Since Vis/NIR spectra contain a large amount of information, noise disturbance, and overlapped spectra, direct analysis of original spectra may lead to low precision and poor stability. Therefore, it is necessary to eliminate the redundancy in the data without losing important information. As a powerful spectral analysis tool, wavelet transform can not only well capture frequency domain characteristics of local time domain process, but also well capture time domain characteristics of local frequency domain process[15]. Thus, Wavelet transform was used to reduce the dimensionality and extract wavelet coefficients in this research.

As shown in Figure 5a, the original spectrum has 2048 wavelengths. After one dimensional discrete wavelet transform was applied to the original spectrum, high-frequency coefficients and low-frequency coefficients were obtained based on binary decomposition structure. The same decomposition structure was used to decompose low-frequency coefficients into high- and low-frequency parts. With three levels of decomposition of the original spectrum using Daubechies 5 (db5), 263 dimensional wavelet coefficients—cA_3 were obtained. The projection of the wavelet low frequency space is shown in Figure 5b. A comparison of Figures 5a and 5b showed that the two curves were very similar although the dimension of cA_3 was far lower than the dimension of the original spectrum, indicating that the change trend of the original spectrum can be observed by the wavelet low-frequency approximation coefficients. Figure 5c shows the spectrum A_3 reconstructed from the wavelet coefficients cA_3. Comparing Figure 5a with Figure 5c, the curve of A_3 based on cA_3 and original spectrum were very similar. Figure 5d shows the difference between the original and reconstructed spectra. The difference or noise was obviously high at the low wavelengths or high frequencies due to the effect of the sensitivity of the instrument[16]. Thus, the wavelength range of 350-900 nm was selected to exclude the noisy signal at the lower wavelengths.

In addition, A_3 was the signal after the high-frequency noise was subtracted from the original signal, and reconstructed from cA_3. The low-frequency coefficients cA_3 were the characteristic features extracted from the original spectrum. Wavelet multi-scale decomposition could effectively distinguish the feature information and noise. Thus, with three levels of decomposition of the original spectrum (in the wavelength range of 350-900 nm) using db5, 172 dimensional wavelet coefficients—cA_3 were obtained, and cA_3 accounting for 13.03% (172/1320) of the original data was used as characteristic feature information for quantitative analysis.



a. Original spectrum b. Low frequency wavelet coefficients



c. Reconstructed spectrum based on low frequency wavelet coefficients d. Difference spectrum between original and reconstructed spectra

Figure 5 Original spectrum and reconstructed spectrum by Wavelet transform

4 Classification model for moldy core in apples

Several methods such as curve fitting, multiple linear regression, partial least and squares regression are usually used for spectral quantitative analysis. However, these methods are suitable for quantitative descriptions and fitting of linear problems. For nonlinear problems, traditional artificial neural network has been used[17], but randomly-generated initial values and over-fitting and other issues limit its application. SVM[18], as a high-dimensional information processing tool, is a fast and efficient method for multivariate modeling and analysis, but the selection of the kernel parameters and penalty coefficients has an significant influence on the performance of SVM. In this study, the initial weights and threshold value matrix of BP-NN and the parameters of SVM were optimized using GA[19] to effectively improve training efficiency and accuracy. To detect the presence of moldy core in apples and distinguish the symptom types, two classification models, GA-BP-NN and GA-SVM, were established.

4.1 BP-NN based classification model with GA-optimized initial weights and threshold

Table 1 shows the network structure and parameters of the BP-NN and GA optimized BP-NN models with a single hidden layer. The number of nodes in the hidden layer was obtained by adjusting various parameters by trial-and-error, and the transfer functions of the hidden layer and the output layer were the S-type tangent function and linear function, respectively. Through simulation, the optimal parameters of GA were determined with the population size of 40, the maximal number of hereditary iterations of 500, the crossover probability of 0.7, and the mutation probability of 0.01.

Table 1 Network structure and parameters of BP-NN and GA-BP-NN

Parameters	Classification model for disease presence		Classification model for types of disease symptoms	
	BP-NN	GA-BP-NN	BP-NN	GA-BP-NN
Number of nodes in input layers	172	172	172	172
Number of nodes in hidden layers	345	345	345	345
Number of nodes in output layers	2	2	3	3
Training time/s	500	500	500	500
Target error	0.01	0.01	0.01	0.01
Learning rate	0.1	0.1	0.1	0.1
Mean square root error	0.08	0.06	0.09	0.07

4.2 SVM-based classification model with GA-optimized parameters

4.2.1 Classification algorithm based on SVM

The two-class SVM-based classification model was used to determine the presence of moldy core in apples and the SVM-based decision tree was used to distinguish the types of moldy core in apples. Since the SVM-based classification model with one versus rest (OVR) is simple, effective and needs shorter training time, three two-class classification models were established to separate each of the three types of symptoms from the other two.

4.2.2 Parameters optimization for SVM using GA

The selection of the function type and parameters is the main task for constructing a SVM model. It has little effect on performance of SVM[20], so the radial basis function (RBF) is commonly used. Nevertheless, the kernel parameter σ^2 and the penalty coefficient C are the key factors influencing the performance of SVM. Therefore, the parameters σ^2 and C were optimized with GA. To overcome the shortcomings of binary encoding which requires repeated coding and decoding during genetic manipulations, float encoding was used in this study. Moreover, the float encoding can overcome the effect of the length limit of binary strings, thus improving the performance and accuracy of GA.

Research by Keerthi et al.[21] showed that for a given large enough C, when σ^2 approached to zero, serious overfitting appeared. Although training samples could be correctly classified using the RBF-based SVM, the generalization of the samples became poor. When σ^2 approached to infinity, there existed serious under-fitting. Consequently, the RBF-based SVM tended to classify the training samples into the class with a relatively large number of samples. Therefore, it is important to determine the appropriate search region for σ^2 and then optimize the range of σ^2. Through analysis of the expression of the kernel function and validation of experiments, the search region of σ^2 was determined to be $[\min(\|x_i - x_j\|^2\times10^{-2}), \max(\|x_i - x_j\|^2\times10^{2})]$ in which satisfactory results were achieved when the search range was gradually reduced according to the classification results.

The penalty coefficient C is an assigned constant, and it can control the degree of punishment for wrongly classified samples and achieve a good tradeoff between the proportion of wrongly classified samples and the algorithm complexity. The larger C value is, the better the simulation degree of the train samples is, but the generalization ability of models will be weakened, so it is important to optimize the range of C. For the search region of C, a large enough C value (such as 3000) should be first selected, and then one group solution a_i ($i = 1, 2, \ldots, n$), where n is the total number of training samples, and can be obtained by training SVM with the given C. Suppose that $C_1 = \max(a_i)$. If $C_1<C$, C_1 can be used as the upper bound of the search region of C; and if $C_1 \geq C$, Lagrange coefficient α_t will be constrained by C and it is necessary to choose a larger C for training SVM until C_1 is far smaller than C. Thus it can be determined that (0, C_1) is the search region of C. The fitness function for GA is as following:

$$F(\sigma^2, C) = \frac{1}{Error} \tag{1}$$

where, *Error* is the SVM classification error of the training set. After repeated testing and verification, the optimized parameters of SVM are shown in Table 2.

Table 2 Optimized parameters of SVM and GA-SVM

Parameters	Classification model for disease presence		Classification model for types of disease symptoms					
	SVM	GA-SVM	SVM			GA-SVM		
			Type I-rest	Type II-rest	Type III-rest	Type I-rest	Type II-rest	Type III-rest
Penalty coefficient (C)	0.5	7.7924	1	32	1	5.0764	7.8213	8.6301
Kernel function parameter	0.0136	0.0288	0.0026	0.0059	0.0412	0.1272	7.5669	0.0658

5 Results and discussion

5.1 Test results and analysis of classification models for presence of apple moldy core

The classification results of the optimized GA-BP and GA-SVM models are shown in Table 3. The classification accuracy of BP-NN and SVM for the test set was 83.08% and 95.38%, respectively, indicating that SVM was more superior than BP-NN. The classification accuracy was 89.23% for GA-BP-NN and 96.92% for GA-SVM, indicating that the optimized models obviously improved classification results and that GA-SVM performed better than GA-BP-NN. The main reason for the poorer prediction performance of GA-BP-NN was that the structure and the number of nodes in the hidden layer of artificial neural network were determined by experience. Moreover, possible premature convergence to the local optima and overfitting to the samples in the training set also affected the performance. Even though there were fewer samples, the classification accuracy of GA-SVM for the test set was the highest (96.92%) by applying GA to the global optimization for SVM.

Table 3 Classification accuracy of infected and healthy apples by different classification models

Classification model	Training set			Test set		
	Number of misclassified apples		Classification accuracy/%	Number of misclassified apples		Classification accuracy/%
	Infected apples (total: 30)	Healthy apples (total: 120)		Infected apples (total: 13)	Healthy apples (total: 52)	
BP-NN	2	6	94.67	3	8	83.08
GA-BP-NN	2	4	96	2	5	89.23
SVM	0	0	100	1	2	95.38
GA-SVM	0	0	100	1	1	96.92

5.2 Test results and analysis of classification models for symptom types of moldy core in apples

The classifications results of the two models BP-NN and SVN and the two optimized models GA-BP-NN and GA-SVM are shown in Table 4.

By comparing the prediction results between BP-NN and SVM, it was found the classification accuracies of BP-NN and SVM for the test set were 55.56% and 77.78%, respectively, i.e., SVM performed better than BP-NN. The classification accuracies for GA-BP-NN and GA-SVM were 77.78% and 81.48%, respectively, indicating that the optimized models improved classification results. Although the optimized model GA-SVM can be used to distinguish the types of the symptoms of moldy core in apples, the classification accuracy has yet to be improved.

Table 4 Classification accuracy of three types of symptoms of apple moldy core

Classification model	Training set				Test set			
	Number of misclassified apples (classification accuracy/%)			Average classification accuracy/%	Number of misclassified apples(classification accuracy/%)			Average classification accuracy/%
	Browning Type I (total: 13)	Moldy core Type II (total: 6)	Core rot Type III (total: 8)		Browning Type I (total: 4)	Moldy core Type II (total: 2)	Core rot Type III (total: 3)	
BP-NN	3 (76.92%)	1 (83.33%)	2 (75%)	77.78	2 (50%)	1 (50%)	1 (66.67%)	55.56
GA-BP-NN	2 (84.62%)	1 (83.33%)	1 (87.5%)	85.18	1 (75%)	1 (50%)	0 (100%)	77.78
SVM	2 (92.59%)	0 (100%)	0 (100%)	97.53	2 (77.78%)	3 (66.67%)	1 (88.89%)	77.78
GA-SVM	1 (96.55%)	0 (100%)	0 (100%)	98.85	2 (77.78%)	2 (77.78%)	1 (88.89%)	81.48

5.3 Discussion

Results acquired indicate that it is feasible to detect moldy core in apples nondestructively and rapidly based on transmittance spectroscopy and wavelet transform is an effective method for extraction of characteristics from spectra. The main reason for the poorer prediction performance of GA-BP-NN was that possible premature convergence to the local optima and overfitting to the samples in the training set. Moreover, the simulation results show that the GA-SVM algorithm has the best generalization ability and precision, and the model has a worth of practical use. The research may offer a necessary theory base for fast, real-time, online and nondestructive detection of the presence and types of moldy core in apples. Due to the fast scanning speed, production lines in the online and real-time detection need to adjust the movement speed to the spectrometer to ensure adequate time for scanning the samples. It is also necessary to establish a stable model that covers a wide range of samples. Following researches are to establish the extensively representative and significant spectral measurement models based on in-depth analysis for spectral characteristics of moldy core in apples of different varieties and different producing areas.

Collecting transmittance spectra from intact apples have been proved to be difficult and unstable, since apple skin and tissues are high scattering materials. Transmittance spectra through apples would be weak and noisy, and are often affected by the size and shape of fruits. So, it is suggested that illumination source should reach a certain light intensity and it is necessary for noise removal to perform the spectral data preprocessing.

6 Conclusions

(1) Discrete wavelet transform can accurately distinguish feature information and noise to realize the feature extraction and noise elimination. Hence, wavelet transform can simplify modeling structure and shorten modeling time, thus improving the overall modeling performance.

(2) Through analyzing spectral response characteristics of infected and healthy apples, it was found that there were obvious differences in the spectral curves between the infected and healthy apples in the wavelength range of 680-750 nm. This result provides a theoretical basis for detection of moldy core types in apples using transmittance spectroscopy.

(3) The GA-optimized model GA-SVM achieved a classification accuracy of 96.92% for detecting the presence of moldy core in apples, and an accuracy of 81.48% for distinguishing the three symptom types of moldy core in apples. These results indicate that it is feasible to detect moldy core in apples and its symptom types nondestructively and rapidly based on transmittance spectroscopy.

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