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基于制样优化及极端梯度提升(XGBoost)特征提取的激光诱导击穿光谱(LIBS)技术鉴别猪肉品种

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摘　要　猪肉品种与其品质质量存在关联，然而当前肉类市场中商品猪肉与特色品种猪肉的品种混淆现象屡见不鲜。激光诱导击穿光谱(LIBS)具备猪肉品种鉴别能力，但其受生物样品复杂基体效应的影响，检测准确性与稳定性亟待提升。为探究猪肉品种LIBS鉴别效果，以滨湖黑猪、玉山黑猪两种江西特色品种猪与超市常售卖的商品白猪、商品黑猪共4类冷鲜猪肉为研究对象。分析其冷鲜制样、冷冻制样、熟化制样、干燥压片制样4种样品制备方式对猪肉样品MgⅡ(279. 46 nm)、C—N(388. 10 nm)、Ca(393. 17 nm)、NaⅠ(588. 98 nm)、NⅠ(746. 74 nm)、KⅠ(769. 68 nm)、OⅠ(777. 07 nm)等LIBS核心特征谱线的影响。结果表明，基于熟化处理的制样方法能够有效改善样品组织的均一性，使LIBS特征光谱信号增强且更稳定。采用极端梯度提升(XGBoost)算法进行LIBS光谱特征提取，将高维光谱数据进行精简化处理，并降至24维关键特征变量，有效剔除光谱冗余噪声。并基于此，构建随机森林(RF)与支持向量机(SVM)鉴别模型，熟化处理组的预测准确率分别达到99. 32%与99. 83%。表明猪肉样品基于熟化处理制样方法优化结合XGBoost特征降维，能够有效克服软组织样品的基体效应干扰，提升LIBS猪肉品种鉴别的准确率与鲁棒性，为肉类产品质量安全的快速、绿色鉴别提供了科学依据。

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关键词 激光诱导击穿光谱(LIBS);猪肉品种鉴别;制样;XGBoost特征提取;算法优化

要点

1) 对比了四种样品制备方法,熟化处理RSD较低、强度较高,证实其光谱质量更优。

2) 对全光谱数据进行XGBoost降至24维,预测准确率仍超90%。

3) 猪肉熟化组品种分类预测准确度分别为99.32%、99.83%,高于其他制样方法。

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猪肉是我国居民消费较多的肉类食品,其品质特性与品种密切相关[1]。随着居民消费水平的提升,市场对高品质肉类的需求增加,地方特色品种猪肉凭借独特肉质特性与营养价值,更受消费者的青睐[2]。然而,肉类市场中商品猪肉与特色品种猪肉的品种混淆现象屡见不鲜[3]。因此,对于商品猪、土猪等猪肉进行品质与品种鉴别,契合当前消费者对优质猪肉的需求[4-5]。猪肉品质及品种的常规检测主要依赖理化分析与感官评估,虽具一定参考价值,但在时效性、环保性和客观性等方面存在局限[6-7]。尽管近红外光谱[8]、电子鼻/电子舌[9]、拉曼光谱[10]、高光谱成像[11]及质谱法[12]等先进检测技术在猪肉品质与品种鉴别的精度方面提升显著,但其多数依赖有机物分子键信息,难以直接捕捉组织内部无机元素的变化特征,且易受样品处理方式与品质变化影响,导致信号稳定性不足。因此,探索一种简便、快速、精准的猪肉品种鉴别方法,符合现代食品安全领域高质量发展的实际需求。

激光诱导击穿光谱(Laser-induced Breakdown Spectroscopy,LIBS)通过高能激光束作用于样品表层形成等离子体,依据其特征光谱信号,可快速实现样品元素种类及含量分析[13]。该方法具备原位检测、前处理简单、高效和绿色无污染等优势,在食品安全检测领域展现出广阔的应用前景[14]。不同品种猪肉因遗传代谢差异,其组织内无机元素与有机基质元素呈现出独特的微观富集规律[15]。LIBS能够通过提取特征元素谱线信息,从元素组成上直接识别猪肉品种[16]。与其他检测方法相比,其无需繁琐的前处理方式,在微损条件下构建特征元素图谱,为猪肉品种的精准鉴别提供直观、可靠的数据支撑[17]。近年来,LIBS技术已成功应用于肉类产品的品质检测研究,Mo等[18]研究鸡、黑猪、牛等6种鲜肉样品经压平处理,结合Optuna算法对LightGBM模型进行超参数优化,结果显示该模型的分类准确率有效提高。Ren等[19]将LIBS与拉曼光谱技术结合,基于CNN模型对13种鱼类的双光谱分类检测大幅提升。孙浩然等[20]将LIBS与深度学习相结合,构建了以ResNet18为主干网络的模型,对猪肉、牛肉和羊肉的光谱数据进行了快速定性识别。前人的研究为猪肉品质及品种的LIBS分析提供了有价值的参考,但是对猪肉品种精准鉴别方面缺乏深入细致的研究。

需要提出的是,猪肉属于高水分、高蛋白的软组织样品,其复杂基体效应影响LIBS检测效果。制样过程是LIBS检测的关键前置环节,直接影响样品的均匀性和稳定性[21]。常用的样品处理方法包括冷鲜制样、冷冻制样、熟化处理及干燥压片等[22],每种制样方法均可针对性调控样品含水量与致密度,适配不同检测场景,有助于稳定蛋白质结构、保证元素分布均一性,提高等离子体激发效率。其中,冷鲜制样可最大程度保留样品原始理化状态,降低人为干扰[23]。冷冻制样可有效巩固易挥发元素,抑制样品组分降解,提升样品烧蚀一致性[24]。熟化处理通过温和加热方式,优化基质均一性,增强光谱信号可靠性[25]。干燥压片可精准去除样品水分,强化易挥发元素保留效果,提升等离子体信号的稳定性与LIBS检测精度[26]。

需要说明的是,LIBS检测过程中,样品形状、LIBS系统优化、光谱数据处理均对分析结果有重要影响。目前,研究主要集中在样品光谱数据分析与模型优化方面,且样品处理多采用单一制样方式,对光谱信息的干扰及对克服基体效应的作用有限,缺乏多种制样方式的对比优选。为提升猪肉品种LIBS鉴别效果,本工作系统对比四种制样方法对猪肉样品LIBS光谱信号的影响,并引入极端梯度提升(eXtreme Gradient Boosting,XGBoost)算法进行高维光谱数据的特征提取以剔除冗余信号干扰,并构建合适算法模型,以提升猪肉品种LIBS鉴别准确率与泛化能力,为肉类产品的快速、绿色鉴别提供科学依据。

1 材料与方法

1.1 猪肉样品制备

猪肉含水量、脂肪分布及元素组成等因素与其品种具有密切的关联度,这些基体因素在LIBS肉类分析检测中均能体现[27]。样品处理方法是降低

LIBS分析基体效应的有效途径[28]。本工作以江西地区超市常售卖的商品白猪(Commercial white pig)、商品黑猪(Commercial black pig)、滨湖黑猪(Binhu black pig)、玉山黑猪(Yushan black pig)四类品种猪的里脊肉作为实验样品。针对上述4种品种猪肉，分别采用冷鲜制样(Cold fresh sample)、冷冻制样(Frozen sample)、熟化制样(Cooked treatment)、干燥压片制样(Dry pressing sample) 4种方法进行样品处理，比较LIBS检测效果。

为保证样品处理的均一性，制备过程均遵循标准化操作，4种品种猪肉样品在每种制样条件下均设置4组平行对照，4类样品处理方法效果如图1所示。对于冷鲜制样，选取新鲜里脊肉样品，切割为1.5 cm×1.5 cm×2 mm规格的均匀切片，放入0～4 ℃，湿度85%左右的冷鲜环境中保存，并在24 h内进行光谱采集。对于冷冻制样，取与冷鲜组规格一致的片状猪肉，置于－20 ℃冰箱冷冻30 d保存，模拟长期低温冷藏条件，取出后在4 ℃冷藏室缓慢解冻，并去除表面凝结水珠，随后进行光谱采集。对于熟化处理，取与冷鲜组规格一致的片状猪肉，75 ℃持续加热15 min至中心温度达到65 ℃，自然冷却至室温后，用吸水纸轻轻吸干样品表面水分，平铺后进行光谱检测。对于干燥压片，选取新鲜里脊肉样品，针对每类品种猪肉的四种样品处理方法分别设置50 g样品，将其放入干燥箱，设置温度105 ℃，持续干燥48 h。再使用粉碎机将样品充分粉碎后，利用压片机在2 MPa的压力下将待测样品压制成直径约为25 mm、厚度约为3 mm的圆片，以供进行光谱采集。

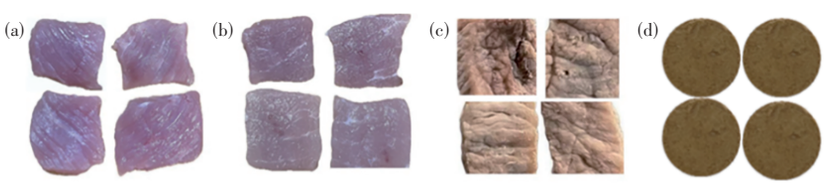


图1　4种样品处理方法效果图：(a)冷鲜制样；(b)冷冻制样；(c)熟化制样；(d)干燥压片

Figure 1　Sample processing effects of four preparation methods: (a) Chilled preparation; (b) Frozen preparation; (c) Curing treatment; (d) Drying and tableting.

1.2　LIBS实验装置

LIBS实验装置如图2所示。本研究采用调Q的Nd：YAG激光器(Beamtech，Vlite200，中国)作为激发光源，其输出波长为1 064 nm，脉冲持续时间为8 ns，工作频率为2 Hz。为获取最佳光谱信噪比与激发的等离子体稳定性，在正式进行光谱采集前，本工作开展了LIBS系统参数预实验，对激光能量及采集延迟时间等关键参数进行了条件优化。基于预实验结果，出射激光能量经激光能量计(中国计量科学研究院，E-1000)校准后，最终设定为最佳激发能量170 mJ。在光谱采集过程中，为避免激光连续烧蚀同一点导致的等离子体累积效应并获取更具代表性的光谱信号，将猪肉样本固定于二维旋转平台(Zolix，SC300-1A，中国)上，确保激光脉冲能够均匀烧蚀样品表面的不同位置。激光诱导样品表面产生的等离子体发射光谱信号，经焦距为150 mm的石英透镜聚焦，由直径为600 μm的光纤探头收集，最终耦合进入波长范围为200～1 050 nm的光谱仪(Avantes，AvaSpec-2048FT-8R，荷兰)中完成光谱采集。整个系统的时序由数字延时发生器(Stanford Research Systems，DG645，美国)统一控制，以实现激光器脉冲输出与光谱仪采集的精确同步。实验针对四类品种猪肉在4种制样方法下进行光谱采集。每种处理条件下设置4个平行样本，每个样本随机采集150幅光谱，共计获得9 600幅原始光谱供后续分析。

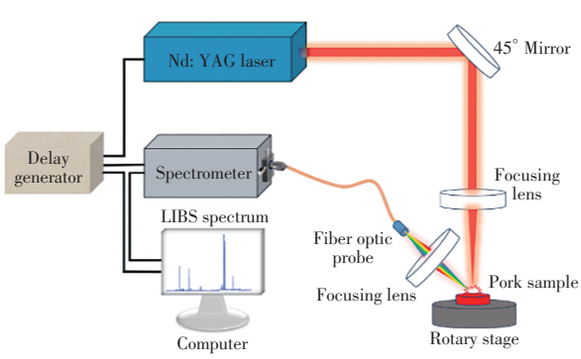


图2　LIBS实验装置示意图

Figure 2　Schematic diagram of LIBS experimental setup.

2　结果与分析

受猪肉品种和样品处理方法的双重影响，待测样品的元素组成及含量存在差异。在LIBS信号采集过程中，不仅制样造成的表面状态改变会引起信号

失真与信息损耗，原始光谱中还包含大量环境噪声与连续背景干扰[29]。为突出样品核心光谱特征、避免噪声主导后续模型，本研究选用碳(C)元素特征谱线进行归一化预处理。需要说明的是，C归一化能够精准抑制环境导致的加性基线偏移与乘性强度波动，经中心化处理后的数据更适配后续算法，是提升光谱分析精度的方法[30]。

2.1 样品处理方法对猪肉LIBS光谱强度的影响

猪肉样品经冷鲜制样、冷冻制样、熟化处理及干燥压片四种方法处理后的LIBS光谱特征如图3所示。可以看出，LIBS激发的特征谱线主要包含Mg Ⅱ(279.46 nm)、C—N(388.10 nm)、Ca(393.17 nm)、Na Ⅰ(588.98 nm)、N Ⅰ(746.74 nm)、K Ⅰ(769.68 nm)、O I(777.07 nm)等。研究表明，Na、K等金属元素主要分布于细胞内液与细胞外液，Mg、Ca则参与肌肉收缩相关蛋白的构成，而C、N、O主要来源于肌肉组织中的蛋白质与脂肪。制样过程中细胞组织被破坏，细胞外液中Na^+、K^+浓度显著增高，H、O广泛存在于肌肉组织的蛋白质、脂肪等有机物及水分中，使得其在LIBS光谱中强度凸显[31]。

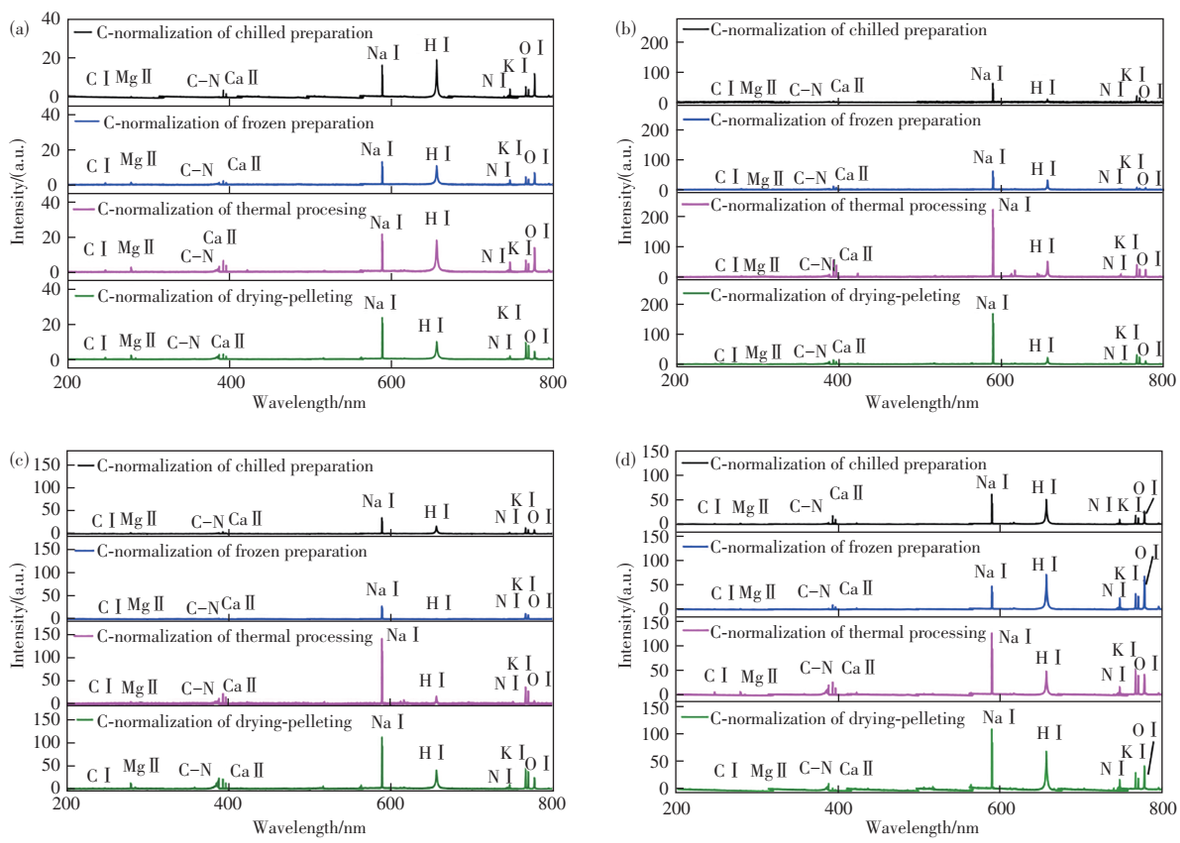


图3 四种样品处理方法对猪肉LIBS光谱强度影响：(a)冷鲜制样；(b)冷冻制样；(c)熟化处理；(d)干燥压片

Figure 3 Effects of four sample preparation methods on the LIBS spectral intensity of pork: (a)Chilled preparation; (b)Frozen preparation; (c)Curing treatment; (d)Drying and tableting.

图3表明，四种制样方法所激发的元素光谱强度呈现明显差异，整体表现为熟化处理组的光谱强度最高，干燥压片组次之，冷鲜制样组与冷冻制样组的光谱强度相对较低。其中，Na、K、O等元素谱线信号强度相对明显。这一现象与样品处理方法对猪肉水分含量及细胞结构的影响相关。熟化与干燥压片可有效去除水分、优化样品致密性，促进Na、K等特征元素的释放，提升激光烧蚀效率与等离子体激发稳定性。冷鲜与冷冻制样则因水分干扰、元素分布不均及烧蚀一致性不足，导致光谱强度偏低。而干燥压片虽实现完全脱水，但肌肉组织的纤维结构未像熟化处理那样通过高温收缩而致密化，单位体积内的元素富集程度低于熟化样品，最终导致光谱强度不及熟化处理组[32]。

2.2 样品处理方法对猪肉LIBS光谱稳定性的影响

为进一步评估光谱稳定性，本工作基于Mg Ⅱ(279.46 nm)、C—N(388.10 nm)、Ca(393.17 nm)、Na Ⅰ(588.98 nm)、N Ⅰ(746.74 nm)、K Ⅰ(769.68 nm)、

O Ⅰ(777.07 nm)等8条代表性的原子或离子特征谱线进行分析，将其进行1—8编号，计算其相对标准偏差(RSD)，如图4所示。对比4种处理方法可知，熟化处理组猪肉样品RSD最低，干燥压片组次之，且两组RSD均控制在10%以内；冷鲜与冷冻制样处理方法误差较高，其RSD超过20%。这一现象与样品处理方法对猪肉样品均匀性、元素分布相关。熟化处理通过高温实现水分去除与细胞结构瓦解，使特征元素均匀分布，保障激发稳定。干燥压片虽通过加热实现完全脱水，但其高温仅作用于水分蒸发，去除样品内部致密度，烧蚀一致性不及熟化处理，最终导致激光激发稳定性低于熟化组。冷鲜制样因细胞完整导致元素异质分布。冷冻制样受水分残留与结构松散影响，二者均降低烧蚀一致性，导致稳定性较差。

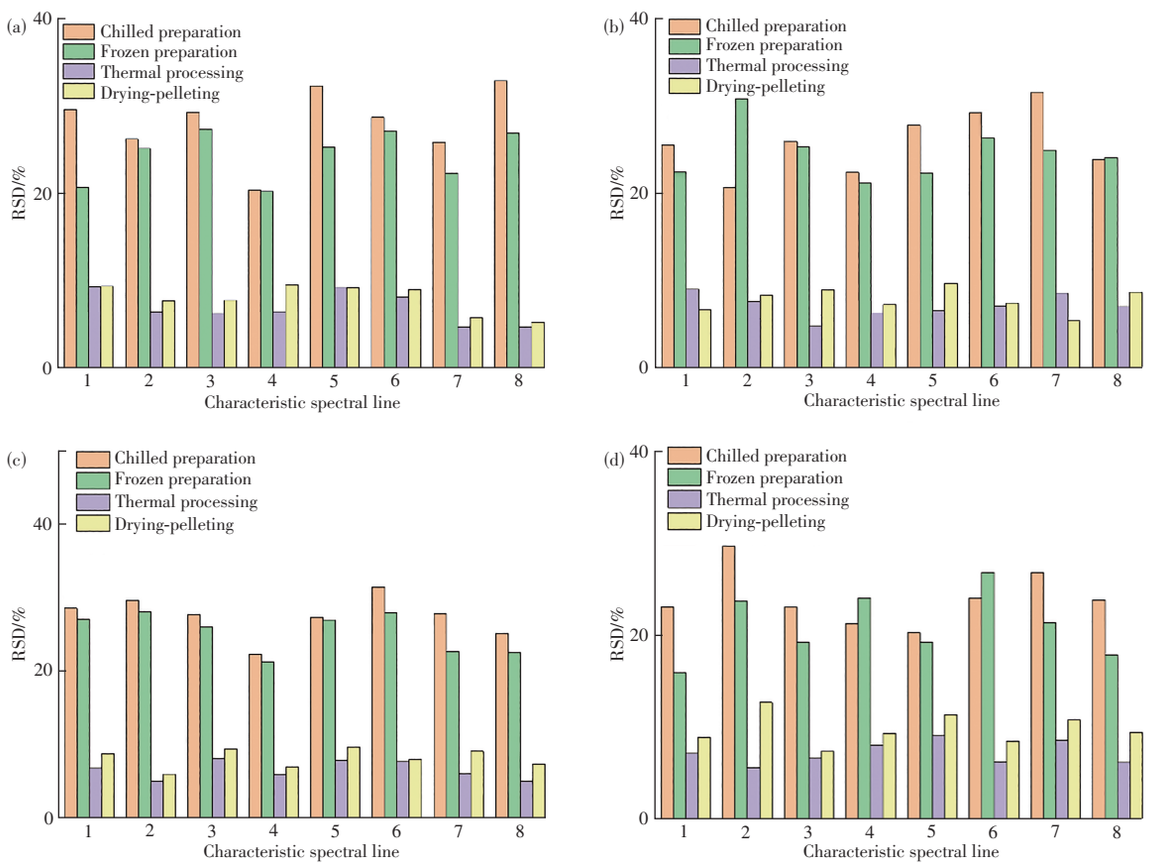


图4　4种样品处理方法对猪肉LIBS光谱RSD分析：(a)冷鲜制样；(b)冷冻制样；(c)熟化处理；(d)干燥压片

Figure 4　RSD analysis of pork LIBS spectra under four sample preparation methods: (a) Chilled preparation; (b) Frozen preparation; (c) Curing treatment; (d) Drying and tableting.

2.3　样品处理方法对LIBS特征光谱下猪肉品种鉴别模型的影响

以LIBS所采集猪肉样品200～1 050 nm光谱范围下的16 269维数据作为模型输入，模型在决策过程中涉及的特征过多，难以识别对鉴别真正重要的特征。因此针对各猪肉品种LIBS高维数据进行特征提取，减少噪声影响。极端梯度提升(eXtreme Gradient Boosting，XGBoost)支持并行计算，在大规模数据集处理方面具有一定优势。XGBoost算法已在医疗诊断[33]、环境监测[34]、农产品鉴别[35]等领域得到广泛且成熟的应用。该算法通过计算各特征在决策树构建过程中的增益值，实现特征重要性的定量评估，能够精准识别对分析结果贡献显著的关键特征，同时剔除对模型预测作用微弱的冗余变量。

基于XGBoost算法特征提取后的猪肉LIBS光谱数据，将数据维度由16 269维精简至24维，显著减少了数据的复杂性。并结合五折交叉验证方法，评估随机森林(RF)和支持向量机(SVM)模型输入的表现。在处理LIBS特征数据时，RF通过集成多棵决策树，在不同的光谱样本和特征子集上进行训练，能有效抵抗激光脉冲波动带来的噪声干扰，减少过拟合，提高模型对不同猪肉样品的泛化能力。SVM则

擅长处理光谱特征间的非线性关系，通过将提取后的LIBS特征映射至高维空间构建最优分隔超平面，有效克服了基体效应带来的信号偏移，显著提升了猪肉品种的分类鲁棒性与鉴别精度。同时为有效抑制脉冲间波动、提升光谱稳定性，将每采集的3个脉冲光谱均值作为一幅光谱，即每种样品处理方法累计获得250幅有效光谱数据，并按7∶3比例分配为训练集与测试集。随机森林(RF)及支持向量机(SVM)模型分析结果，鉴别结果如表1所示。

基于XGBoost特征提取结合RF和SVM模型的制样方式对猪肉品种的分类预测效果如图5和图6所示。可以看出，制样方法的选择对猪肉品种鉴别效果影响显著。在选择合适的前处理条件下，RF及SVM鉴别模型的提升效果明显。其中，熟化处理组预测效果最好，冷鲜制样效果最低。相比之下，全光谱数据输入的方式数据量繁杂、耗时长，可能出现过拟合现象。特征提取的策略使得制样与RF和SVM算法优化下猪肉品种LIBS鉴别效果显著提升，且耗时较短。

表1 基于XGBoost特征提取的RF及SVM模型对比

Table 1 Comparison of RF and SVM models based on XGBoost feature extraction

Sample preparation method	RF		SVM	
	Training accuracy/%	Prediction accuracy/%	Training accuracy/%	Prediction accuracy/%
Cold fresh sample	97.64	93.00	94.26	91.91
Frozen sample	97.23	97.01	97.41	96.54
Cooked treatment	99.86	99.32	99.97	99.83
Dry pressing sample	99.15	98.08	99.38	98.68

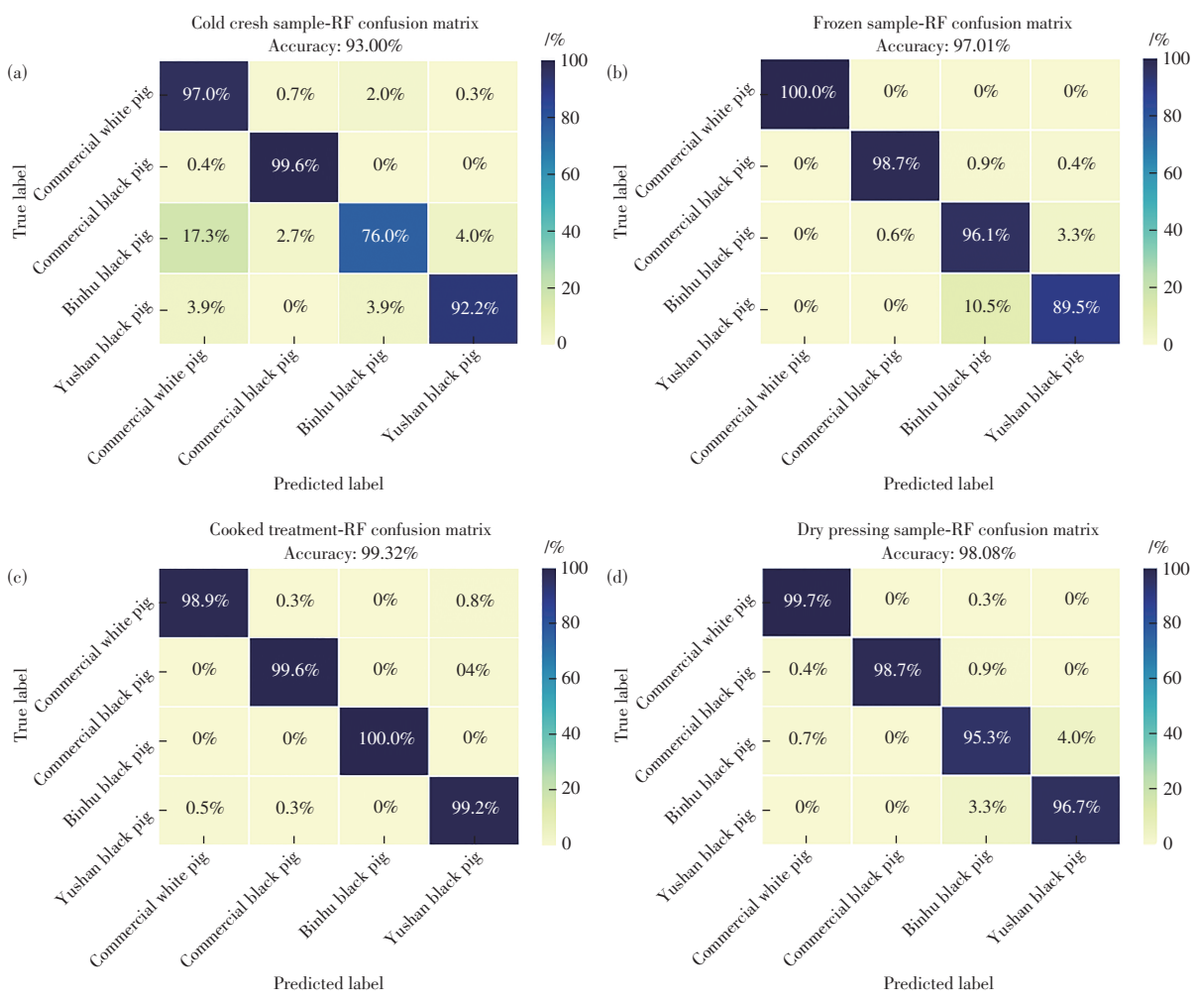


图5 4种样品处理方法下猪肉品种XGBoost-RF分类预测结果：(a)冷鲜制样；(b)冷冻制样；(c)熟化处理；(d)干燥压片

Figure 5 Prediction results of XGBoost-RF classification for pork breeds under four sample preparation methods: (a) Chilled preparation; (b) Frozen preparation; (c) Curing treatment; (d) Drying and tableting.

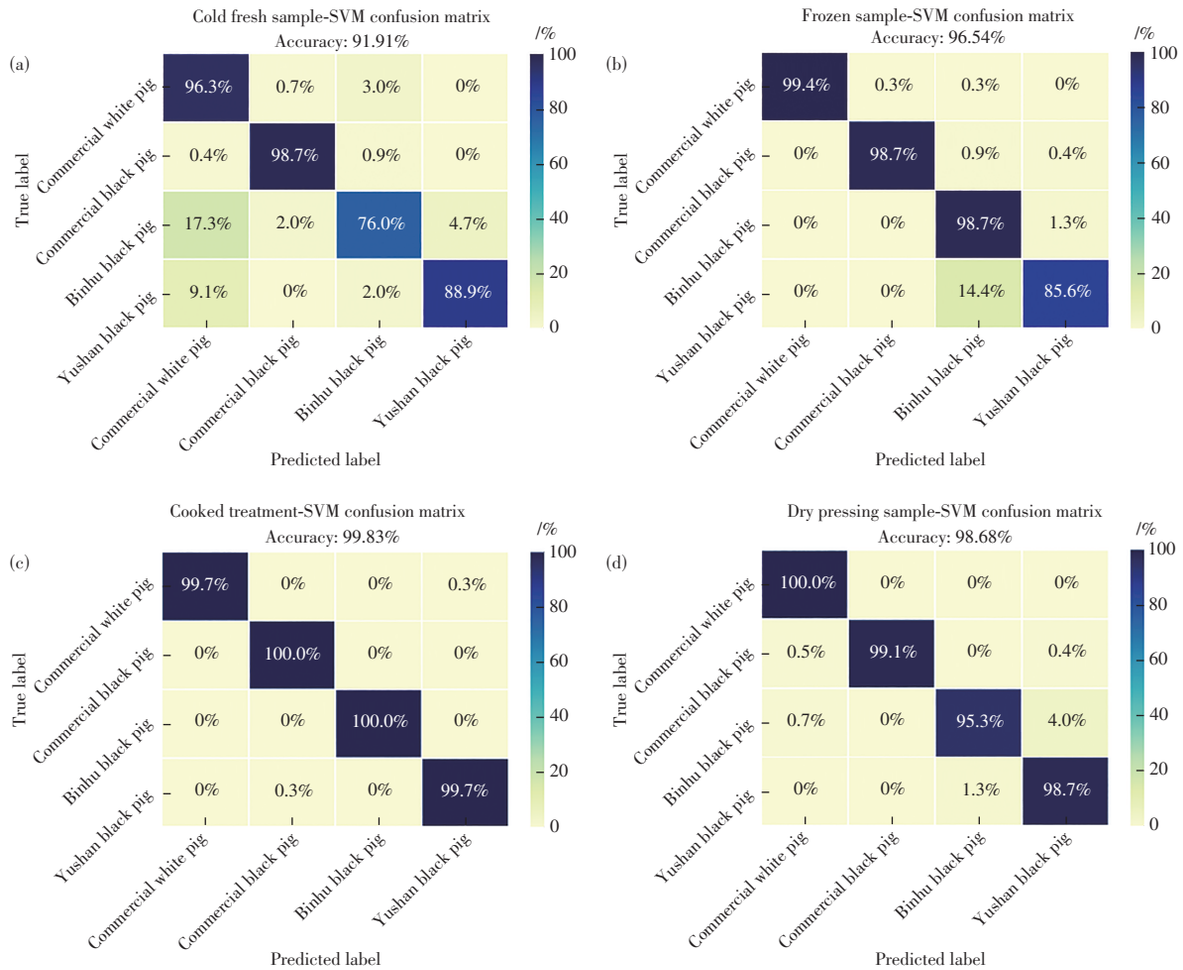


图6　4种样品处理方法下猪肉品种XGBoost-SVM分类预测结果：(a)冷鲜制样；(b)冷冻制样；(c)熟化处理；(d)干燥压片

Figure 6　Prediction results of XGBoost-SVM classification for pork breeds under four sample preparation methods: (a) Chilled preparation; (b) Frozen preparation; (c) Curing treatment; (d) Drying and tableting.

3　结论

本工作针对制样方法与RF和SVM算法优化下的猪肉品种LIBS鉴别效果进行分析。结果表明，制样方法对猪肉LIBS光谱强度与稳定性影响显著。其中，熟化处理为猪肉LIBS检测的最优前处理方式，光谱强度及稳定性明显优于其他3种样品前处理方法。通过XGBoost算法对猪肉LIBS高维光谱数据的特征提取与降维，有效降低了数据分析的复杂性。经特征提取后，RF与SVM模型均展现出良好的猪肉品种鉴别能力，且模型鉴别效果受样品处理方法的影响，其中熟化处理组鉴别效果最优，预测准确率分别达到99.32%和99.83%，冷鲜制样鉴别效果最差，冷冻制样与干燥压片效果次之。因此，采用熟化处理结合XGBoost特征优选与RF或SVM算法优化，能够有效克服肉类样品的基体效应干扰，显著提升LIBS技术在猪肉品种鉴别中的准确率与泛化能力，为肉类产品质量安全的快速、绿色检测提供坚实的方法参考。

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Identification of Pork Breeds by Using Laser-induced Breakdown Spectroscopy (LIBS) Based on Sample Preparation Optimization and XGBoost Feature Extraction

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Abstract The intrinsic quality characteristics of pork are closely associated with its specific breed; however, breed mislabeling between common commercial pork and indigenous specialty pork is frequently observed in the contemporary meat market. Although laser-induced breakdown spectroscopy (LIBS) can achieve pork breed discrimination, its detection accuracy and signal stability are significantly compromised by the complex matrix effects inherent in biological soft tissue samples, necessitating methodological improvements. To investigate the efficacy of LIBS for precise pork breed discrimination, chilled pork samples from four breeds-two Jiangxi indigenous breeds (Binhu black pig and Yushan black pig) and two commercial breeds (commercial white pig and commercial black pig)-were selected as the primary research subjects. This research systematically analyzed the effects of four distinct sample preparation methods, chilled, frozen, thermal processing, and drying-pelleting, on the emission characteristics of LIBS spectral features. Specifically, the spectral variations of key elemental lines and molecular bands, including Mg Ⅱ (279.46 nm), C—N (388.10 nm), Ca Ⅱ (393.17 nm), Na Ⅰ (588.98 nm), N Ⅰ (746.74 nm), K Ⅰ (769.68 nm), and O Ⅰ (777.07 nm), were comprehensively evaluated. Results showed that the thermal processing-based sample preparation method effectively improved the structural homogeneity of the sample tissues, yielding enhanced and more stable LIBS spectral signals. During the subsequent data processing stage, the eXtreme Gradient Boosting (XGBoost) algorithm was implemented to perform LIBS spectral feature extraction. This approach streamlined the high-dimensional raw spectral data, reducing it to 24 critical feature variables while eliminating redundant spectral noise. Using these optimized feature subsets, Random Forest (RF) and Support Vector Machine (SVM) classification models were subsequently constructed. Classification performance strongly depended on the preparation methods, with RF and SVM models achieving predictive accuracies of 99.32% and 99.83%, respectively, in the thermal processing group. These findings demonstrate that optimizing pork sample preparation via thermal processing, combined with XGBoost-based feature dimensionality reduction, can overcome matrix effect interferences typically associated with soft tissue samples. This integrated approach substantially enhances the accuracy and robustness of LIBS for pork breed discrimination, providing a reliable scientific foundation for the rapid, non-destructive, and green evaluation of meat product quality and safety.

Keywords laser-induced breakdown spectroscopy (LIBS); pork breed discrimination; sample preparation; XGBoost feature extraction; algorithmic optimization

HIGHLIGHTS

1) Lower relative standard deviations and higher signal intensities were exhibited by the thermal processing method in comparison with the other three preparation methods, and its superior spectral quality was confirmed.
2) The full-spectrum data were reduced to 24 dimensions via the XGBoost algorithm, and prediction accuracies above 90% were retained.
3) Prediction accuracies of 99.32% and 99.83% were achieved by the models of the thermal processing group, which were proven to be higher than the values acquired by other preparation methods.