ESTELA CORRÊA DE AZEVEDO

CHARACTERIZATION OF SWEET POTATO GENOTYPES:

PHYSICOCHEMICAL AND BIOCHEMICAL ATTRIBUTES AND VOLATILE COMPOUND PROFILE

LAVRAS – MG
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Orientadora
Prof.ª Dsc Elisângela Elena Nunes Carvalho

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RESUMO

A batata-doce (*Ipomoea batatas* L. Lam.) apresenta ampla diversidade genética, refletida em variações na coloração da polpa, composição química e atributos funcionais. Neste estudo, foram conduzidos dois experimentos complementares com o objetivo de realizar uma caracterização integrada de cinco genótipos com diferentes colorações de polpa (roxa, alaranjada e branca), abordando parâmetros físico-químicos, propriedades funcionais, atividade enzimática e perfil de compostos voláteis. No primeiro experimento, os genótipos foram caracterizados quanto aos atributos físico-químicos, atividade enzimática, compostos bioativos e capacidade antioxidante. Genótipos de polpa roxa (SP1 e SP4) apresentaram maiores teores de fenólicos, flavonoides e antocianinas, correlacionados com elevada atividade antioxidante (ABTS e FRAP). Já o genótipo de polpa laranja (SP2) destacou-se pelo alto conteúdo de carotenoides e amido, indicando potencial para biofortificação e aplicações industriais, enquanto SP3 e SP4, com maior teor de amido resistente, demonstraram potencial funcional associado à saúde intestinal e ao controle glicêmico. O segundo experimento concentrou-se na avaliação do perfil de compostos orgânicos voláteis (COVs) por SPME/GC-MS, simulando cocção a vapor. Foram identificados 72 compostos distribuídos em oito grupos químicos, com predominância de aldeídos e terpenoides. β-ionona e β-ciclocitral destacaram-se como marcadores voláteis do genótipo de polpa laranja, derivados das vias de degradação de carotenoides, enquanto fenilacetaldeído e benzaldeído foram mais abundantes nos genótipos de polpa roxa, sugerindo predominância de reações de Strecker. A análise multivariada permitiu a discriminação entre os genótipos com base no perfil volátil. A combinação das análises composicionais e do perfil de voláteis demonstra o potencial dessa abordagem integrada como ferramenta para discriminação varietal, fornecendo subsídios relevantes para programas de melhoramento genético, avaliação da qualidade sensorial e desenvolvimento de produtos de maior valor agregado.

Palavras-chaves: *Ipomoea batatas,* Potencial nutricional, compostos bioativos, amido, melhoramento genético, industrialização, segurança alimentar.

ABSTRACT

Ipomoea batatas L. Lam. presents wide genetic diversity, reflected in variations in flesh color, chemical composition, and functional attributes. In this study, two complementary experiments were conducted with the aim of performing an integrated characterization of five genotypes with different flesh colors (purple, orange, and white), addressing physicochemical parameters, functional properties, enzymatic activity, and volatile compound profiles. In the first experiment, the genotypes were characterized regarding physicochemical attributes, enzymatic activity, bioactive compounds, and antioxidant capacity. Purple-fleshed genotypes (SP1 and SP4) exhibited higher levels of phenolics, flavonoids, and anthocyanins, correlated with elevated antioxidant activity as determined by ABTS and FRAP assays. The orange-fleshed genotype (SP2) stood out for its high carotenoid and starch content, indicating potential for biofortification and industrial applications, while SP3 and SP4, with higher resistant starch content, demonstrated functional potential associated with gut health and glycemic control. The second experiment focused on the evaluation of the volatile organic compound (VOC) profile by SPME/GC-MS, simulating steam cooking. A total of 72 compounds were identified, distributed across eight chemical groups, with aldehydes and terpenoids predominating. β-ionone and β-cyclocitral emerged as volatile markers of the orange-fleshed genotype, derived from carotenoid degradation pathways, while phenylacetaldehyde and benzaldehyde were more abundant in purple-fleshed genotypes, suggesting the predominance of Strecker degradation reactions. Multivariate analysis enabled discrimination among genotypes based on their volatile profiles. The combination of compositional analyses and volatile profiling demonstrates the potential of this integrated approach as a tool for varietal discrimination, providing relevant insights for breeding programs, sensory quality assessment, and the development of higher value-added products.

Keywords: *Ipomoea batatas,* Nutritional potential, bioactive compounds, starch, genetic improvement, industrialization, food safety.

INDICADORES DE IMPACTO

Os resultados obtidos neste estudo apresentam impactos de natureza científica, tecnológica, social e econômica, com efeitos diretos e potenciais sobre diferentes segmentos da sociedade, especialmente no contexto da segurança alimentar, da valorização da agricultura familiar e do desenvolvimento sustentável de cadeias produtivas agroalimentares. Do ponto de vista tecnológico e científico, a caracterização integrada dos genótipos de batata-doce, envolvendo atributos físico-químicos, funcionais, atividade enzimática e perfil de compostos orgânicos voláteis, gerou conhecimento sobre genótipos brasileiras ainda pouco exploradas. Esses resultados contribuem para a discriminação varietal, para a seleção de genótipos com maior valor nutricional, funcional e sensorial e para o direcionamento de aplicações específicas no processamento industrial de alimentos. Trata-se de um impacto potencial relevante para os setores de tecnologia e produção, ao subsidiar o desenvolvimento de produtos alimentícios de maior valor agregado, como ingredientes funcionais, alimentos biofortificados e produtos processados com melhor qualidade sensorial. A valorização de genótipos de batata-doce com características nutricionais e tecnológicas superiores pode favorecer a agricultura familiar, predominante no cultivo dessa cultura no Brasil, ampliando oportunidades de geração de renda e fortalecimento de cadeias produtivas locais. O impacto territorial concentra-se, principalmente, em regiões produtoras de batata-doce, com destaque para o estado de Minas Gerais e outras regiões agrícolas do Brasil, onde a cultura desempenha papel estratégico na alimentação e na economia rural. O público potencialmente beneficiado inclui produtores rurais, cooperativas agrícolas, agroindústrias, técnicos de extensão rural e consumidores finais. Embora o trabalho não tenha sido estruturado como uma ação de extensão formal, seus resultados apresentam elevado potencial de aplicação em atividades de transferência de tecnologia, capacitações técnicas, programas de melhoramento genético e ações futuras de extensão universitária, possibilitando a interação entre a universidade, produtores e o setor produtivo. O desenvolvimento da pesquisa envolveu diretamente docentes e estudantes de pós-graduação, contribuindo também para a formação de recursos humanos qualificados na área de Ciência dos Alimentos. Quanto às áreas temáticas da Política Nacional de Extensão, os impactos do trabalho enquadram-se predominantemente nas áreas de Tecnologia e Produção (7), Saúde (6) ao contribuir para a promoção de alimentos mais nutritivos e funcionais, e Educação (4), por meio da produção e disseminação de conhecimento científico. Os impactos desta pesquisa estão alinhados a diversos

Objetivos de Desenvolvimento Sustentável (ODS) da Organização das Nações Unidas, com destaque para o ODS 2 – Fome Zero e Agricultura Sustentável, ao promover o aproveitamento de culturas estratégicas para a segurança alimentar; o ODS 12 – Consumo e Produção Responsáveis; e o ODS 13 – Ação contra a Mudança Global do Clima, ao valorizar culturas adaptáveis e resilientes como a batata-doce.

IMPACT INDICATORS

The results obtained in this study present scientific, technological, social, and economic impacts, with direct and potential effects on different segments of society, particularly in the context of food security, the valorization of family farming, and the sustainable development of agri-food production chains. From a scientific and technological perspective, the integrated characterization of sweet potato genotypes—encompassing physicochemical and functional attributes, enzymatic activity, and the profile of volatile organic compounds—generated knowledge on Brazilian varieties that are still underexplored. These results contribute to varietal discrimination, the selection of genotypes with higher nutritional, functional, and sensory value, and the orientation of specific applications in food processing. This represents a relevant potential impact for the technology and production sectors, as it supports the development of higher value-added food products, such as functional ingredients, biofortified foods, and processed products with improved sensory quality. The valorization of sweet potato genotypes with superior nutritional and technological characteristics may also benefit family farming, which predominates in the cultivation of this crop in Brazil, by expanding income-generation opportunities and strengthening local production chains. The territorial impact is mainly concentrated in sweet potato–producing regions, particularly in the state of Minas Gerais and other agricultural regions of Brazil, where the crop plays a strategic role in food supply and the rural economy. Potential beneficiaries include rural producers, agricultural cooperatives, agro-industries, rural extension technicians, and end consumers. Although this study was not structured as a formal extension activity, its results show a high potential for application in technology transfer initiatives, technical training programs, plant breeding programs, and future university extension actions, enabling interaction between the university, producers, and the productive sector. The development of the research directly involved faculty members and graduate students, contributing to the training of qualified human resources in the field of Food Science. Regarding the thematic areas of the National Extension Policy, the impacts of this work are predominantly classified within Technology and Production (7), Health (6)—by contributing to the promotion of more nutritious and functional foods—and Education (4), through the generation and dissemination of scientific knowledge. The impacts of this research are aligned with several United Nations Sustainable Development Goals (SDGs), notably SDG 2 – Zero Hunger and Sustainable Agriculture, by promoting the use of strategic crops for food security;

SDG 12 – Responsible Consumption and Production; and SDG 13 – Climate Action, by valuing adaptable and resilient crops such as sweet potato.

SUMÁRIO

PRIMEIRA PARTE

1 INTRODUÇÃO

A batata-doce (*Ipomoea batatas* L. Lam.) é uma das hortaliças mais importantes do ponto de vista socioeconômico e apresenta ampla distribuição mundial, desempenhando papel relevante na segurança alimentar, especialmente em países em desenvolvimento. Sua elevada adaptabilidade a diferentes condições edafoclimáticas, o ciclo de cultivo relativamente curto e o alto potencial produtivo tornam essa cultura estratégica frente aos desafios impostos pelas mudanças climáticas. Segundo a FAO, em 2024, a produção mundial de batata-doce foi estimada em aproximadamente 90 milhões de toneladas, com a Ásia e a África concentrando a maior parte desse volume. No Brasil, a produção alcançou cerca de 970 mil toneladas, em uma área cultivada de 65,1 mil hectares, com produtividade média de 14,8 t ha^{-1}.

Além de sua importância agronômica, a batata-doce é amplamente reconhecida como um alimento de elevado valor nutricional e funcional. Trata-se de uma fonte energética de baixo índice glicêmico, rica em carboidratos complexos, fibras alimentares, vitaminas e minerais. A expressiva variabilidade genética da espécie resulta em ampla diversidade de cores da casca e da polpa, que podem variar do branco e creme ao amarelo, alaranjado e roxo intenso. Essas diferenças visuais refletem variações significativas na composição química e no conteúdo de compostos bioativos, os quais estão diretamente relacionados a potenciais benefícios à saúde.

Os genótipos de polpa alaranjada destacam-se pelo elevado teor de carotenoides, especialmente o β-caroteno, reconhecido como precursor da vitamina A. O estímulo ao consumo desses genótipos é considerado uma estratégia sustentável de biofortificação, com potencial para reduzir a deficiência de vitamina A em populações vulneráveis. Por outro lado, genótipos de polpa roxa apresentam altos teores de compostos fenólicos, principalmente antocianinas, associadas à elevada atividade antioxidante e a efeitos anti-inflamatórios, contribuindo para a redução do estresse oxidativo e do risco de doenças crônicas não transmissíveis. Em contraste, raízes de polpa branca ou creme apresentam baixos teores de pigmentos e são compostas predominantemente por amido e açúcares.

A aptidão industrial da batata-doce vai além do consumo in natura e está fortemente relacionada às suas características físico-químicas, especialmente ao teor de matéria seca. Genótipos com maior conteúdo de sólidos totais são preferidos para a produção de farinhas,

amidos e chips, pois proporcionam maior rendimento industrial e menor absorção de óleo durante o processamento térmico. Além disso, a composição química de cada variedade, incluindo açúcares, aminoácidos e pigmentos, influencia diretamente o desenvolvimento das características sensoriais dos produtos processados.

Entre os atributos sensoriais, o aroma exerce papel fundamental na aceitação do produto pelo consumidor. Durante o processamento térmico, ocorrem reações químicas complexas, como a reação de Maillard, a degradação de Strecker, a oxidação de lipídios e a degradação térmica de carotenoides, que resultam na formação de compostos orgânicos voláteis (VOCs). Em variedades de polpa alaranjada, a degradação de carotenoides pode originar norisoprenoides, como a β-ionona, responsáveis por notas aromáticas frutais e florais. Já as reações de Maillard contribuem para aromas doces, caramelizados e tostados, geralmente associados a maior aceitação sensorial.

Apesar da ampla diversidade de genótipos brasileiros, ainda são escassos os estudos integrados que relacionem de forma multidimensional a qualidade nutricional, o potencial antioxidante e o perfil de compostos voláteis (VOCs). Muitas vezes, o foco reside apenas na produtividade ou em nutrientes isolados, ignorando-se o fato de que enzimas como a polifenoloxidase (PPO) e a peroxidase (POD) podem afetar a estabilidade da cor e a formação de odores, enquanto o perfil de carboidratos (amido total, amilose e amido resistente) dita as propriedades de textura e viscosidade. Assim, a caracterização detalhada dessas interações é essencial tanto para orientar o desenvolvimento de ingredientes funcionais quanto para subsidiar programas de melhoramento genético.

Dessa forma, o objetivo geral deste trabalho foi realizar uma caracterização de diferentes genótipos de batata-doce (SP1 a SP5), correlacionando seus parâmetros físico-químicos, nutricionais e funcionais com seu perfil aromático e de compostos voláteis. Buscou-se identificar marcadores químicos específicos que distinguem os genótipos de polpa roxa, alaranjada e creme, elucidando os mecanismos bioquímicos que regem sua funcionalidade e aceitabilidade.

Esta dissertação está estruturada no formato de artigos científicos, organizados em dois capítulos complementares. O primeiro artigo foca na caracterização físico-química, nutricional e funcional, abordando o potencial antioxidante dos genótipos. O segundo artigo

explora a composição de voláteis e as implicações aromáticas decorrentes do processamento térmico desses mesmos genótipos.

2. REFERENCIAL TEÓRICO

2.1 Batata-Doce

A batata doce (*Ipomoea batatas* L. Lam), hortaliça tuberosa da família Convolvulaceae, é a única espécie do gênero cultivada para consumo humano. Domesticada há cerca de 5.000 anos, apresenta uma grande diversidade genética, especialmente na América Central (ESCOBAR-PUENTES, 2022), região considerada o provável centro de origem da espécie, de onde se dispersou para outras partes do mundo (YAN, 2024). Por se adaptar facilmente, a batata-doce pode ser produzida em diversas regiões pelo mundo, sendo apreciada por consumidores de diferentes culturas, nacionalidades e realidades climáticas. Em todo o mundo, a batata-doce é a sexta cultura alimentar mais importante, após o arroz, o trigo, a batata, o milho e a mandioca (CIP, 2018; SAPAKHOVA, 2023).

Descrita inicialmente por Lineu como Convolvulus batatas em 1753, a batata-doce foi reclassificada por Lamarck em 1791 para o gênero *Ipomoea*, devido a características reprodutivas específicas, como a forma do estigma e a ornamentação do pólen. Essa reclassificação refletiu um avanço na compreensão das relações evolutivas entre as plantas. O caule da batata-doce é herbáceo e, na maioria das variedades, cresce de forma prostrada, expandindo-se horizontalmente pelo solo (HUAMÁN, 1999).

Em relação à morfologia, as folhas apresentam grande diversidade de formas, são simples e alternadas ao longo do caule, podendo ser arredondadas (orbiculares), em forma de rim (reniformes), cordiformes (em forma de coração), com lóbulos pontiagudos (hastadas) ou lobuladas. Além disso, as margens das folhas podem ser lisas, dentadas ou com recortes profundos. Algumas variedades apresentam mais de uma forma de folha na mesma planta (HUAMÁN, 1999).

A coloração das ramas da batata-doce pode variar do verde ao roxo, devido à presença de pigmentos como as antocianinas. A superfície das ramas pode ser lisa (glabra) ou coberta por pelos (pubescente), em diferentes densidades. O comprimento dos ramos é bastante variável e está relacionado à variedade, disponibilidade de água e ao hábito de crescimento da planta, sendo mais curtos em variedades eretas e mais longos em variedades prostradas (HUAMÁN, 1999).

O sistema radicular da batata-doce é composto por dois tipos de raízes: as absorventes, que se originam nos nós e entrenós do caule, responsáveis por captar nutrientes, água e fixação no solo, e as tuberosas, que se desenvolvem a partir de espessamentos de raízes laterais. As raízes tuberosas, também conhecidas como raízes de reserva, armazenam amido e outros nutrientes, constituindo a parte comestível da planta (HUAMÁN, 1999). As raízes de reserva da batata-doce apresentam um formato geralmente alongado, com uma região central mais espessa e extremidades afiladas. A parte externa, chamada periderme, pode ser lisa ou rugosa e apresenta diversas cores. A polpa, localizada abaixo da periderme, é composta principalmente por células parenquimáticas que armazenam amido e outros nutrientes. A cor da polpa pode variar significativamente, de branco, amarela, creme, laranja até o roxo intenso, e pode apresentar padrões variados. A cor externa não necessariamente determina a cor interna (HUAMÁN, 1999).

Além disso, a batata-doce apresenta uma grande variabilidade genética, o que leva à diversidade de formatos e cores da raiz, resultado de um longo processo evolutivo, moldado pela reprodução sexuada e assexuada, seleção natural e humana (FERNANDES, 2021). As variações na cor da polpa das diversas variedades de batata-doce são atribuídas à produção de pigmentos e a composição fitoquímica da raiz, como as de polpa alaranjada e roxa, que acumulam carotenoides e antocianinas, respectivamente. As outras cores têm pouco ou nenhum pigmento, resultando em cores mais claras. A composição nutricional, adaptabilidade da cultivar, compostos bioativos e características morfológicas também podem influenciar em suas diferentes características (AMOANIMAA-DEDE, 2020). Embora suas raízes sejam as partes mais consumidas, as suas folhas e caules também são comestíveis. Ressalta-se que o teor de nutrientes e fitoquímicos funcionais variam em função do genótipo, condições edafoclimáticas, tipos de cultivo, parte da planta e tipo de processamento (LAVERIANO-SANTOS, 2022).

As folhas da batata-doce, que podem ser consumidas normalmente como outros vegetais folhosos, são uma boa fonte de minerais (K, P, Ca, Mg, Fe, Mn, Cu), fibras alimentares e antioxidantes, como polifenóis, antocianinas além de carotenoides, incluindo luteína, neoxantina, β-caroteno e violaxantina (GAMA ET AL., 2023; KANG, 2017; NGUYEN, 2021). Nas folhas, os teores de glicídeos, fibras, proteínas, cinzas e lipídeos variam de, 42,0-61,3%; 5,9-14,3%; 3,7-31,1%; 1,5-14,7% e 0,3-5,3% da matéria seca,

respectivamente (Wang; Nie; Zhu, 2016). Os glicídeos predominam na matéria seca das raízes, variando de 42,4 % a 77,3%; seguido de fibras (1,9 a 6,4%) proteínas, de (1,3 a 9,5%); cinzas (1,1 a 4,9%) e lipídios (0,2 a 3,0%) (WANG; NIE; ZHU, 2016).

Curayag et al. (2019) avaliaram uma variedade batata-doce de polpa roxa e encontraram 90,63% glicídeos, 3,47% cinzas, 2,79% fibra, 1,82 proteína e 1,29% de lipídeos da matéria seca. Rodrigues et al. (2016) determinaram a composição nutricional de duas variedades, uma polpa laranja e uma de polpa roxa e os respectivos valores foram encontrados: 90,17 e 85,8% de glicídeos, 3,68 e 4,28% de fibra, 3,69 e 5,70% de proteína, 2,04 e 3,80% de cinzas e 0,42% de lipídeos.

A composição nutricional e a presença e quantidade de compostos bioativos da batata-doce variam de acordo com a variedade e as condições de cultivo. Com seu perfil nutricional completo, a batata-doce se destaca como um ingrediente promissor para a indústria de alimentos funcionais, além de ser uma excelente opção alimentar saudável para consumo diário.

2.2 Compostos bioativos em Batata-Doce

No reino vegetal, os compostos bioativos são essenciais para o metabolismo, atuando como reguladores do crescimento e protegendo as plantas contra diversos tipos de estresse, como a seca e a exposição a patógenos (SÁNCHEZ-CAPA ET AL., 2023; AMORIM ET AL., 2024). Além disso, eles desempenham um papel multifuncional na saúde humana. Sua ingestão, especialmente quando proveniente do consumo frequente de alimentos que são suas principais fontes, contribui para a redução do estresse oxidativo nas células e inibição do crescimento de tumores, contribuindo para o controle de processos inflamatórios e na prevenção de diversas doenças crônicas (BANOŽIĆ ET AL., 2020).

Os compostos bioativos das plantas podem ser classificados em três grupos principais: terpenos e terpenóides (unidades de isopreno formadas por cinco átomos de carbono), alcalóides (compostos orgânicos que contêm nitrogênio e têm efeitos fisiológicos em humanos) e compostos fenólicos (estruturas que incluem um anel aromático com um ou mais grupos hidroxila) (CROTEAU ET AL., 2000). No entanto, é importante mencionar que essa classificação pode ser inconsistente, pois alguns metabólitos primários, como carboidratos, proteínas e peptídeos, também podem apresentar atividades bioativas, incluindo propriedades

antioxidantes (AMORIM ET AL., 2024; TUŠEK ET AL., 2024). Um compilado de dados encontrados na literatura sobre o estudo de compostos bioativos em diferentes variedades de batata-doce é apresentado na Tabela 1.

Tabela 1. Compostos bioativos, capacidade antioxidante e pigmentos em polpa de batata-doce.

Coloração da Polpa	Componente		Referência
Compostos bioativos			
Amarela	Fenólicos Totais	17,8 GAE mg g^{-1} MS	Ji et al., 2015
Branca		9,6 GAE mg g^{-1} MS	
Alaranjada		0,211 CAE mg g^{-1}	Teow et al., 2007
Roxa		42,45 CAE mg g^{-1} MS	Ngcobo et al., 2024
		18.88 QUE mg kg^{-1}	
Roxa	Flavonoides	388.85 QUE µg g^{-1}	Park et al., 2016
Branca		19.83 QUE µg g^{-1}	
Alaranjada		59.96 QUE µg g^{-1}	
Capacidade Antioxidante			
Alaranjada	DPPH	4,64 mg Trolox g^{-1}	Gabilondo et al., 2022
Roxa		1,41 IC 50 TEAC mg g^{-1}	Ngcobo et al., 2024
Creme	FRAP	85% de redução	Costa et al., 2024
		2,0 mmol Fe^{2+} kg^{-1}	
Roxa		21,23 TEAC mM g^{-1}	Ngcobo et al., 2024
Pigmentos			
Roxa	Antocianinas	208,97 mg C3G/100 g^{-1}	Vizzotto et al., 2017
Alaranjada		0,16 mg C3G g^{-1}	Gabilondo et al., 2022
		712 µg.g^{-1}	
Alaranjada	Carotenoides	11,46 mg·100 g^{-1} MF	Setoguchi et al., 2024
Amarela		0,60 mg·g^{-1} MF	
Branca		4,66 mg·100 g^{-1} MF	Vizzotto et al., 2017
Creme		0,85 mg·100 g^{-1} MF	

2.2.1 Compostos fenólicos

Os compostos fenólicos, moléculas com ampla diversidade estrutural, desempenham papel significativo na atividade antioxidante de diversos vegetais. Essa diversidade permite classificá-los em fenólicos simples, como os ácidos fenólicos, que possuem apenas um anel aromático, e em compostos fenólicos mais complexos, como os flavonoides, caracterizados por dois anéis aromáticos e grupos funcionais variados, entre eles os grupos hidroxila (VUOLO ET AL., 2019).

Sintetizados pela via dos fenilpropanóides, a qual se inicia com a condensação de fosfoenolpiruvato e eritrose-4-fosfato, os compostos fenólicos passam por diversas etapas biosintéticas, incluindo a formação de ácido desidroquínico, ácido desidrochiquímico e ácido chiquímico. A via fenilpropanoides, também conhecida como a rota do ácido chiquímico, é assim denominada devido à estrutura básica dos compostos formados: o fenilpropano (C6-C3). Alguns compostos fenólicos importantes são gerados antes da formação do ácido chiquímico, como o ácido quínico, derivado diretamente do ácido desidroquínico, e o ácido gálico, que pode ser obtido tanto do ácido quínico quanto do ácido desidroquínico. Paralelamente a enzima fenilalanina amônia-liase desempenha um papel central nesse processo, catalisando a conversão da fenilalanina em ácido cinâmico. A partir do ácido cinâmico, ocorre a síntese sequencial dos ácidos cumárico, cafeico, ferúlico, sinápico e siríngico. O ácido clorogênico resulta da condensação do ácido cafeico com o ácido quínico. O ácido cumárico por sua vez pode formar cumaroil CoA, que, em conjunto com três moléculas de malonil CoA, leva à síntese de resveratrol e catequinas (COSTA ET AL., 2024; MACHADO ET AL., 2024).

Os compostos fenólicos possuem ações bioquímicas variadas e estão envolvidos na modulação de vias de sinalização relacionadas à inflamação, ao dano oxidativo, à autofagia, à apoptose, entre outros processos. Já foi comprovado que os compostos fenólicos podem aumentar a oxidação de gordura e melhorar a sensibilidade à insulina, especialmente em homens com sobrepeso ou obesos (MIR ET AL., 2019). No entanto, a exploração desses compostos, especialmente pelas indústrias alimentícia e de embalagens, bem como pelos setores cosmético e têxtil, constitui um campo de investigação relevante (NGCOBO ET AL., 2024). Na indústria alimentícia, os compostos fenólicos desempenham um papel fundamental, não apenas influenciando o valor nutricional dos alimentos, mas também conferindo atributos sensoriais como cor, textura, aroma e sabor (LIU ET AL., 2024).

A aceitação dos tubérculos pelos consumidores é influenciada por sua aparência externa e sabor, atributos diretamente relacionados à sua composição bioquímica. Nesse sentido, a composição nutricional e bioativa de diversas variedades de batata-doce tem sido extensivamente estudada, com destaque para as cultivares de polpa branca, polpa amarela, polpa laranja e polpa roxa. Os teores de fenólicos totais quantificados em *Ipomoea batatas* podem variar substancialmente em função da cultivar. A cultivar Purple-purple, de polpa roxa, apresentou o maior teor de fenólicos, com 42,45 mg de equivalente de ácido clorogênico por grama de matéria seca (mg CAE g^{-1} MS) (NGCOBO ET AL., 2024), demonstrando um potencial antioxidante consideravelmente superior quando comparada à cultivar Beauregar, de polpa laranja, que exibiu um teor de apenas 0,211 mg CAE g^{-1} MS (TEOW ET AL., 2007) .

Além da cultivar, o ácido padrão utilizado para quantificar os compostos fenólicos (ácido gálico ou clorogênico) pode influenciar significativamente nos resultados obtidos. A escolha do padrão pode levar a diferentes valores de absorbância e, consequentemente, a estimativas distintas do teor fenólico total, uma vez que esses ácidos possuem estruturas químicas e propriedades espectrais diferentes (FRANKOVÁ ET AL., 2022). Ao utilizar o ácido gálico como padrão para quantificar os compostos fenólicos totais das cultivares de batata doce de polpa branca e amarela, os autores encontraram valores de 9,6 e 17,8 GAE mg g^{-1} MS respectivamente (JI ET AL., 2015). Além disso, foi constatado que a coloração da polpa influencia a concentração de compostos fenólicos na batata-doce. Estudos relataram que o teor de compostos fenólicos totais (TPC) em batatas de polpa roxa é significativamente maior do que em variedades de polpa amarela e branca, o que indica um efeito significativo da coloração (FRANKOVÁ ET AL., 2022). O maior teor de polifenóis totais em variedades de polpa colorida está relacionado à alta proporção de antocianinas, que estão ausentes em variedades de polpa amarela ou branca.

A diversidade estrutural dos compostos fenólicos, decorrente de diferentes arranjos moleculares, os divide em duas grandes classes: flavonoides e não flavonoides. Os flavonoides constituem um grupo de compostos fenólicos amplamente distribuídos em plantas, especialmente em frutas e hortaliças (MACHADO ET AL., 2024). Eles incluem diversas variantes, como flavonas, flavonóis, flavanonas, antocianinas, catequinas, chalconas e isoflavonas. Por outro lado, os derivados dos ácidos hidroxicinâmicos, como os ésteres dos ácidos cafeico, cumárico (que, por ciclização, origina a cumarina) e ferúlico, e os ácidos hidroxibenzoicos, como os ácidos salicílico,

gálico, elágico, protocatequínico e vanílico, são classificados como compostos fenólicos não flavonoides (HARAHAP ET AL., 2024).

Nos últimos anos, os flavonoides têm sido objeto de pesquisas crescentes e apresentam inúmeras aplicações em grandes campos da pesquisa científica por apresentarem propriedades benéficas para a saúde humana. Entre os principais benefícios, destacam-se seus efeitos antioxidantes e antirradicais livres, bem como suas propriedades antibacterianas. Análises fitoquímicas revelaram a presença de diversos flavonoides em diferentes genótipos de batata-doce. Dentre os flavonoides identificados, a quercetina destacou-se por sua alta concentração, sendo encontrada em quantidades significativas tanto em cultivares de polpa branca (19.83 QUE $\mu g\ g^{-1}$) e laranja (59.96 QUE $\mu g\ g^{-1}$) quanto, de forma mais expressiva, nas cultivares de polpa roxa (388.85 QUE $\mu g\ g^{-1}$) (PARK ET AL., 2016). A miricetina também foi encontrada em quantidades significativas em cultivares de polpa branca. Kaempferol e luteolina foram relatados em menores quantidades, sendo a luteolina completamente ausente em raízes de polpa branca.

2.2.2 Pigmentos

As raízes tuberosas de batata-doce são uma fonte excepcional de carotenoides e antocianinas, pigmentos responsáveis pelas distintas colorações amarela, laranja e roxa presentes na casca e na polpa. No entanto, a concentração total desses pigmentos varia substancialmente conforme a cor e a variedade da raiz. As variedades de polpa amarela e alaranjada destacam-se pela alta concentração de carotenoides, enquanto as de polpa roxa são particularmente ricas em antocianinas (SETOGUCHI ET AL., 2024; GABILONDO ET AL., 2022). Além do papel na pigmentação, tanto os carotenoides quanto as antocianinas são considerados compostos bioativos, o que agrega apelo funcional à batata-doce.

2.2.3 Carotenoides

Os carotenoides são uma classe de compostos responsáveis pelas colorações amarelo, laranja e vermelho em diversos alimentos. São solúveis em água, lipídios e solventes orgânicos, atuando como agentes antioxidantes e antiangiogênicos, além de oferecerem proteção contra radicais livres. Estruturalmente, os carotenoides são tetraterpenos (C40), compostos por unidades de isopreno, pirofosfato de isopentenila (IPP) e seus isômeros, o dimetilalil difosfato (DMAPP), que contém cinco átomos de carbono (C5) em sua composição (PARK ET AL., 2016; SETOGUCHI ET AL., 2024). Os carotenoides são separados em carotenos e xantofilas, os últimos

derivados oxigenados dos primeiros. Licopeno e β-caroteno são exemplos de carotenos e caracterizados pela presença de cadeia linear ou cíclica em suas extremidades. Violaxantina, astaxantina e β-citraurina são exemplos de xantofilas (VIMALA ET AL., 2011).

O teor de carotenoides de batatas-doces de polpa creme, branca, amarela e alaranjada varia de 0,6 mg 100 g $^{-1}$ a 11,46 mg 100 g^{-1} de no material fresco. O β-caroteno é o carotenoide predominante nas batatas-doces de polpa alaranjada, contribuindo com mais de 99% do seu teor total. Nas variedades de polpa branca e roxa, o trans-β-caroteno é o principal carotenoide. Estudos demonstram que a concentração de β-caroteno nas batatas-doces alaranjadas pode variar significativamente, com valores entre 5,9 e 12,9 mg 100 g^{-1} (VIMALA ET AL., 2011) e 0,38 e 7,38 mg 100 g^{-1} (ALAM ET AL., 2016). Além do β-caroteno, a luteína e zeaxantina, embora em menores quantidades (0,1 - 0,4 mg 100 g^{-1} e 0,1 - 0,2 mg 100 g^{-1} de massa seca, respectivamente), também são encontradas nas batatas-doces (DONADO-PESTANA ET AL., 2012; PARK ET AL., 2016). As variedades de polpa roxa apresentam níveis mais elevados de luteína e zeaxantina em comparação com as cultivares de polpa branca (PARK ET AL., 2016). O estudo aprofundado dessa matéria-prima pode revelar novos compostos bioativos com potencial para diversas aplicações na indústria alimentícia, farmacêutica e cosmética.

2.2.4 Antocianinas

As antocianinas são pigmentos naturais encontrados em flores, frutos, folhas e raízes, solúveis em água e reconhecidos por sua ampla variedade de cores e efeitos antioxidantes benéficos à saúde. Esses pigmentos são sintetizados a partir da L-fenilalanina, um aminoácido derivado da via do ácido chiquímico (LAVERIANO-SANTOS ET AL., 2022). A via biossintética das antocianinas envolve uma série de reações enzimáticas, iniciando com a conversão da L-fenilalanina em ácido cinâmico, pela ação da fenilalanina amônia liase, seguida pela conversão dos derivados do ácido cinâmico em chalconas, pela chalcona sintase (CHS). Na sequência, a chalcona é convertida em di-hidroflavonóis, que por sua vez são transformados em leucoantocianidinas e, finalmente, em antocianidinas. A adição de açúcares às antocianidinas resulta na formação das antocianinas, pigmentos responsáveis pela coloração roxa da batata-doce (IM ET AL., 2021).

As concentrações totais de antocianinas são maiores nas variedades roxas do que naquelas com polpa branca ou alaranjada, com valores variando de 0,16 mg C3G g^{-1} a 208,97 mg C3G g^{-1} (GABILONDO ET AL., 2022; VIZZOTTO ET AL., 2017). As antocianinas predominantes em variedades de batatas roxas são, em sua maioria, 3-soforosídeos-5-glicosídeos das agliconas

peonidina, cianidina e pelargonidina. Além disso, as antocianinas são frequentemente modificadas pela adição de um ou dois grupos acil, como os ácidos p-hidroxibenzóico, ferúlico e cafeico, que se ligam aos açúcares da molécula. De acordo com Fossen e Andersen (2000), as antocianinas aciladas representam mais de 98% do teor total de antocianinas na batata-doce roxa. No entanto, a composição das antocianinas varia significativamente entre as variedades, como observado nos estudos de Im et al. (2021), que relataram que as variedades 'Sinjami', 'Danjami' e 'Yeonjami' contêm 72 - 77% de antocianinas diaciladas, enquanto 'Jami' e 'Borami' apresentam 90 - 95%. Além disso, 'Sinjami', 'Danjami' e 'Yeonjami' possuem uma maior proporção de antocianinas monoaciladas (21 - 24%), em comparação com 'Jami' e 'Borami'.

2.2.5 Capacidade Antioxidante

Os compostos antioxidantes podem ser extraídos das matérias-primas por meio de diferentes solventes e métodos de extração (ZHANG ET AL., 2024). São classificados como primários, que neutralizam radicais livres, e secundários, que inibem catalisadores pró-oxidantes. Com base no seu mecanismo de ação, são classificados como naturais ou sintéticos, como o hidroxianisol butilado (BHA), galato de propila (PG) e hidroxitolueno butilado (BHT), amplamente difundidos, apesar dos potenciais efeitos adversos à saúde que podem ser provocados com o uso prolongado desses compostos, como problemas no aparelho digestório e alergias na pele (PEIXOTO ET AL., 2022; USMAN ET AL., 2022). Assim, há um crescente interesse em substituí-los por antioxidantes naturais, como as vitaminas E e C, carotenoides e compostos fenólicos de origem vegetal, que não só possuem propriedades antioxidantes, mas também antifúngicas e antimicrobianas (GULCIN; ALWASEL, 2023).

Em sistemas alimentares, a utilização de antioxidantes contribui para a prevenção da peroxidação lipídica e a formação de produtos secundários desse processo, preservando assim o sabor, a cor e a textura dos produtos alimentícios durante o armazenamento. Além disso, demonstram potencial na redução da oxidação de aminoácidos e proteínas, assim como na interação entre carbonilas derivadas de lipídios e proteínas, resultando em alterações em suas funções (ZHANG ET AL., 2024).

A atividade antioxidante encontrada em batata-doce de diferentes cultivares está relacionada com a presença de compostos fenólicos, carotenoides e antocianinas. Estes compostos exibem atividade de eliminação de radicais livres e, consequentemente, o seu consumo está

associado a um menor risco de diabetes, doenças cardiovasculares, câncer e desempenho cognitivo. As antocianinas presentes na batata-doce roxa apresentaram maior eficiência na eliminação de radicais livres DPPH, quando comparadas aos outros genótipos. Nas batatas-doces amarelas ou laranja, o β-caroteno, principal pigmento responsável pela coloração, exerce uma potente atividade antioxidante devido ao seu sistema de ligações duplas conjugadas, atuando também como precursor da vitamina A (LAVERIANO-SANTOS ET AL., 2022).

2.3 Amido

O teor de amido nas raízes da batata-doce normalmente varia de 50 a 80%, de acordo com o tipo (ZHANG ET AL., 2018). Cerca de 20 - 30% do amido é composto por amilose linear e ligeiramente ramificada e 70 - 80% é amilopectina altamente ramificada (KRINGEL ET AL., 2020). A amilose é um polissacarídeo linear com unidades de glicose unidas por ligações α-1,4, enquanto a amilopectina é um polímero altamente ramificado e formada por unidades de glicose unidas por ligações α-1,4 e α-1,6 (YONG ET AL., 2018). A amilopectina inclui cadeias A, cadeias B (cadeias que conectam as cadeias A e C) e cadeias C com uma extremidade redutora (LI ET AL., 2020).

O amido pode ser usado como aditivo alimentar, aumentando a retenção de água para controlar a mobilidade da água e manter a qualidade dos alimentos durante o armazenamento (KOLARIC ET AL., 2020). Também é uma matéria-prima promissora para a produção de etanol por meio da fermentação (CARVALHO; TRIERWEILER; TRIERWEILER, 2024) e é usado na indústria farmacêutica como carreador de substâncias, como antioxidantes (GOU ET AL., 2019). Contudo, seu uso pode ser limitado por fatores indesejáveis, como instabilidade de temperatura, alta tendência a retrogradação durante o armazenamento, pior estabilidade de gelatinização durante aquecimento prolongado e alto comportamento de cisalhamento que interrompe a rede de gel de amido (SHAHZAD ET AL., 2019). Portanto, a concentração de amido e suas características, determinam se o amido da batata-doce pode ser usado para processamento industrial, alimento fresco ou para alimentação animal (YANG ET AL., 2018).

Em termos de valor nutricional, existem três tipos de amido: amido resistente (AR), amido de digestão lenta (ADL) amido de digestão rápida (ADR), que se baseia na rapidez com que a glicose é produzida e absorvida no intestino delgado (WANG ET AL., 2023). O ARD é facilmente encontrado em alimentos ricos em amido, como pão e batatas, que geralmente são cozidos úmidos e aquecidos e apresentam altos níveis de amido disperso ou amorfo (ÖZTÜRK; MUTLU, 2019). O ALD apresenta estrutura cristalina do tipo A e C, como a encontrada em cereais, e amido amorfo, que é fisicamente inacessível. Por outro lado, o amido do tipo B é resistente à digestão enzimática e é encontrado em tubérculos e raízes (ÖZTÜRK; KÖKSEL, 2014). O AR e seus produtos de decomposição não podem ser digeridos e absorvidos no intestino delgado, mas podem fermentar ou fermentar parcialmente no intestino grosso (SUN ET AL., 2022).

O amido resistente pode ser do tipo AR-1, que é o amido que está fisicamente indisponível e bloqueado dentro das paredes celulares; AR-2 é o amido granular que é resistente às enzimas digestivas e ambos serão destruídos durante o processamento dos alimentos; AR-3 é o amido de instância que pode suportar o calor de até 100°C antes de derreter a aproximadamente 155°C; e AR-4 é o amido que passou por modificação química (BABU; PARIMALAVALLI, 2015). Além desses, outro tipo de amido resistente, conhecido como AR-5, foi identificado como tendo um componente lipídico. Refere-se ao complexo amilose-lipídio (ALC), no qual a hélice da amilose é enrolada em torno do ligante lipídico para formar uma estrutura helicoidal com uma cauda de ácido graxo dentro da cavidade central (LI ET AL., 2021).

Em termos de qualidade, as propriedades do amido da batata-doce são influenciadas pela estrutura do amido, particularmente a distribuição da cadeia ramificada da amilopectina e o teor de amilose, que são responsáveis pelas aplicabilidades do amido (GUO ET AL., 2022). Para possíveis aplicações, estruturas granulares e finas de amido são tão importantes quanto a composição. Para a estrutura molecular do amido, a distribuição do comprimento da cadeia unitária é referida como o primeiro nível estrutural. Com base em classificações anteriores, ela é dividida em quatro grupos: fa (grau de polimerização (DP) = 6–12); fb1 (DP= 13–25); fb2 (DP = 25–36); fb3 (DP = > 36) (TONG ET AL., 2020). Normalmente, o amido de batata-doce tem 32–35%, 48–50%, ≈13% e ≈3% das cadeias fa, fb1, fb2 e fb3, respectivamente. Além disso, apresenta muitas cadeias curtas e a maior intensidade de pico (DP = 12) quando comparado a amidos de outras espécies (LEE; LEE, 2017).

Os agregados individuais de amido, conhecidos como grânulos, são mostrados na forma de anéis de crescimento e surgem de um ponto central, podendo apresentar diferentes formas microscópicas, incluindo oval, circular, semicircular, poligonal e em tamanhos pequenos e grandes (WANG ET AL., 2020A). Apesar do monômero de glicose ser o bloco de construção essencial do amido, a estrutura final desse polissacarídeo é bastante complexa, uma vez que as proporções de amilose e amilopectina influenciam diretamente em suas propriedades bioquímicas (LYU ET AL., 2021; AL-MAQTARI AT AL., 2023).

Por exemplo, uma maior proporção de cadeias curtas de amilopectina compromete a eficiência de empacotamento na cristalinidade do amido, resultando em menor estabilidade da dupla hélice, o que diminui a entalpia e a temperatura de gelatinização. Em contraste, a maior

proporção de longas e médias cadeias de amilopectina tornam simples a formação de uma estrutura de dupla hélice estável e de alta cristalinidade (WANG ET AL., 2020B). Além disso, a formação de estruturas supramoleculares de grânulos de amido de batata-doce é predominantemente formada por cadeias de amilopectina com DP = 10 - 24, enquanto defeitos nas estruturas supramoleculares e nas lamelas cristalinas são causados por cadeias curtas de amilopectina com DP < 10 (TONG ET AL., 2020).

Além disso, o genótipo da batata-doce e o ambiente de crescimento têm uma relação estreita com as propriedades estruturais, físico-químicas e funcionais do amido (ZHANG ET AL., 2018). Sajeev et al. (2012) estudaram três variedades de batata-doce branca, duas creme e duas laranja, e descobriram que suas propriedades texturais, reológicas e de gelatinização mostram diferenças significativas entre as diferentes variedades. Abegunde et al. (2013) usaram 11 variedades populares de batata-doce chinesa como materiais experimentais e descobriram que o teor de amilose tem uma correlação positiva significativa com o tamanho médio dos grânulos, e o poder de inchamento e a solubilidade dos amidos mostram correlação positiva entre si.

Portanto, conhecer sua estrutura e propriedades é fundamental para explorar seu uso e desenvolver novos produtos, visto que o amido da batata-doce é um biopolímero complexo com grande potencial para diversas aplicações.

2.4 Compostos Orgânicos Voláteis (COVs) em Batata-doce

Entre os atributos de qualidade, o sabor destaca-se como o principal fator de aceitação e preferência do consumidor. O sabor é uma percepção sensorial complexa que resulta da interação entre o gosto (detectado pela língua) e o aroma, derivado de compostos orgânicos voláteis (COVs) que estimulam os receptores olfativos (AL-KHALILI ET AL., 2025).

A matriz da batata-doce é quimicamente heterogênea, composta por carboidratos, principalmente amido, sacarose, glicose e frutose, proteínas, lipídios e pigmentos bioativos, como carotenoides, em cultivares de polpa alaranjada, e antocianinas, em cultivares de polpa roxa, (ZHAO ET AL., 2024; YAO ET AL., 2024). Esta complexidade bioquímica serve como reservatório de precursores que, sob condições de processamento térmico ou atividade enzimática, são convertidos em uma vasta gama de voláteis. Mais de 400 COVs únicos em batata-doce cozida foram identificados ao longo dos anos, dos quais pelo menos 76 são responsáveis pelo aroma característico. A composição e a concentração desses voláteis variam significativamente dependendo do genótipo, da cor da polpa e do método de cozimento empregado (ABUGU ET AL., 2025).

2.4.1 Principais Classes Químicas e Compostos Majoritários

O perfil volátil da batata-doce é composto por diversas classes funcionais, sendo as mais proeminentes os aldeídos, terpenos (monoterpenos e sesquiterpenos), álcoois, cetonas e furanos (YAO, ZHANG, JIA, DENG,E WANG, 2023; ZHANG, TANG, JIANG, MO, E WANG, 2021).

• Aldeídos: Esta classe é frequentemente citada como a mais numerosa e abundante em diversas cultivares. Compostos majoritários como o hexanal (odor de grama/gordura), benzaldeído (amêndoa/açúcar queimado) e benzenoacetaldeído (mel/floral) são onipresentes (ZHANG, TANG, JIANG, MO, E WANG, 2021; SHEN ET AL., 2024.) O benzenoacetaldeído, em particular, possui um alto valor de diluição de aroma (FD) e é crucial para o caráter doce do produto cozido (WANG AND KAYS, 2000).

• Terpenos: Responsáveis por notas florais, amadeiradas e doces, os terpenos representam uma fração significativa da complexidade aromática. O linalol, o geraniol, a β-ionona e a β-damascenone são os principais expoentes desta classe. A β-ionona e a β-

damascenone são extremamente potentes devido aos seus limiares de detecção excepcionalmente baixos (ZHANG, TANG, JIANG, MO, E WANG, 2021).

• Furanos e Compostos Heterocíclicos: Estes compostos tornam-se predominantes após o tratamento térmico, especialmente o assamento (ZHANG ET AL., 2023). O furfural, o 2-furanometanol, o 2-acetylfuran e o 5-methylfurfural conferem notas de caramelo, tostado e amêndoa, características da batata-doce assada (NAKAMURA, ONO, YAGI, E MIYAZAWA, 2013; YAO ET AL., 2023; J.-B. SUN ET AL., 1995).

• Cetonas: A cetona mais crítica para a batata-doce é o maltol (3-hydroxy-2-methyl-4-pyrone), que fornece um aroma doce e caramelizado indispensável para a identidade sensorial do produto assado. Outras cetonas comuns incluem a geranilacetona e a 6-metil-5-hepten-2-ona (WANG AND KAYS, 2000; ABUGU ET AL., 2025).

• Álcoois e Outros: O 1-octen-3-ol (odor de cogumelo), o álcool feniletílico e o guaiacol (aroma defumado/doce) também contribuem significativamente para o perfil final (AL-KHALILI ET AL., 2025; SHEN ET AL., 2024).

2.4.2 Mecanismos de Formação dos Voláteis

A origem dos COVs na batata-doce ocorre através de uma rede complexa de reações térmicas e enzimáticas que transformam precursores não voláteis em moléculas capazes de promover odor.

Reação de Maillard e Caramelização: Durante o cozimento, o amido é hidrolisado por enzimas (α e β-amilases) em maltose e outros açúcares redutores (SUN ET AL., 1995). Estes açúcares reagem com aminoácidos livres e peptídeos através da Reação de Maillard, gerando furanos, piróis e pirânicos. O maltol é um produto clássico desse mecanismo, derivado especificamente da degradação da maltose em presença de fontes de nitrogênio (WANG AND KAYS, 2000). A caramelização de açúcares a altas temperaturas também contribui para a formação de furfural e compostos com notas de açúcar queimado (TSAI ET AL., 2021).

Degradação de Strecker: Um subconjunto importante da Reação de Maillard é a Degradação de Strecker, onde α-dicarbonilas reagem com aminoácidos específicos. A fenilalanina é o precursor primordial do benzenoacetaldeído e do benzaldeído, compostos que elevam a percepção de doçura aromática e notas florais na polpa cozida. O metional, com odor de batata cozida, deriva da degradação da metionina (LIU ET AL., 2022).

Oxidação Lipídica: Embora o conteúdo lipídico da batata-doce seja baixo, a oxidação de ácidos graxos insaturados (linoleico, linolênico e oleico) é uma fonte vital de aldeídos e álcoois de cadeia linear. Através da via da lipoxigenase (LOX) ou autoxidação térmica, precursores como o ácido linoleico são convertidos em hexanal, 2-pentilfurano e 2,4-decadienal, que conferem notas gordurosas e verdes (SHAHIDI E HOSSAIN, 2022; YAO ET AL., 2024).

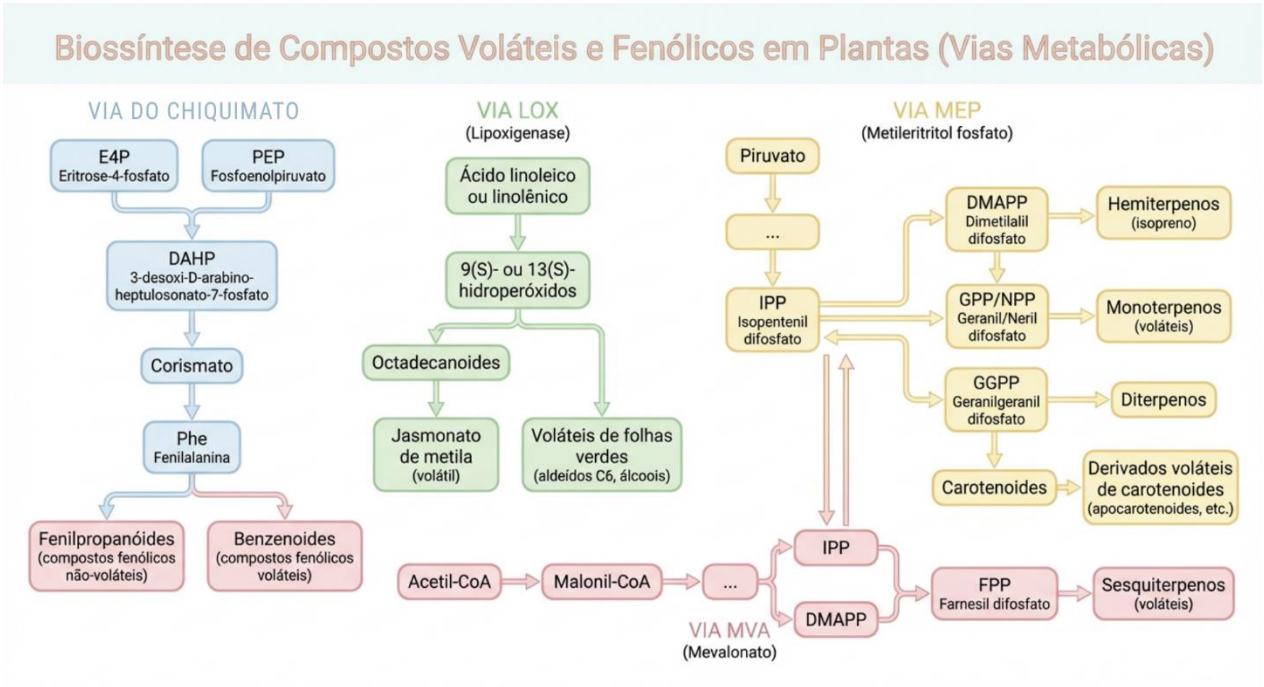
Degradação de Carotenoides: Em cultivares pigmentadas, a clivagem oxidativa térmica ou enzimática de carotenoides (como o β-caroteno) produz apocarotenoides voláteis. Este mecanismo é responsável pela formação de β-ionona, β-damascenone, di-hidroactinidiolida e geranilacetona, conferindo o aroma floral e frutado único das cultivares de polpa alaranjada (ZHANG, TANG, JIANG, MO, E WANG, 2021; WINTERHALTER E ROUSEFF, 2001).

Hidrólise de Glicosídeos: A batata-doce armazena terpenos na forma não volátil ligados a moléculas de açúcar (glicosídeos). O aquecimento promove a hidrólise térmica dessas ligações, liberando monoterpenos livres como linalool, geraniol e nerol, que aumentam substancialmente sua concentração após o cozimento, enriquecendo o buquê floral da matriz (ABUGU ET AL., 2025).

2.4.3. Vias Biossintéticas Gerais em Plantas

A biossíntese de VOCs depende da disponibilidade de carbono e energia provenientes do metabolismo primário. As principais estão apresentadas na Figura 1.

Figura 1: Representação esquemática das vias de formação envolvidas na síntese de Compostos Organicos Voláteis.



- Vias dos Terpenoides (MVA e MEP)

Os terpenoides representam a classe mais diversa de COVs e são biossintetizados a partir de de dois precursores comuns de cinco carbonos: o difosfato de isopentenila (IPP) e o seu isômero, o difosfato de dimetilalila (DMAPP). Em plantas, a síntese dessas unidades fundamentais ocorre por duas vias compartimentalizadas, a via do Ácido Mevalônico (MVA) que ocorre predominantemente no citosol, retículo endoplasmático e peroxissomos. Ela utiliza o Acetil-CoA como precursor para formar sesquiterpenos e terpenos irregulares. A via do Fosfato de Metileritritol (MEP), a qual é exclusivamente plastidial e utiliza piruvato e gliceraldeído-3-fosfato (GAP) derivados da glicólise. Esta via é responsável pela formação de hemiterpenos, monoterpenos e diterpenos (SIMKIN ET AL., 2011; PULIDO ET AL., 2012).

Existe um intercâmbio de metabólitos entre esses compartimentos, facilitado pelo transporte de isopentenyldiphosphate (IPP) e dimethylallyl diphosphate (DMAPP) através da membrana do plastídio, permitindo que uma via sustente a produção da outra dependendo da espécie ou do órgão da planta (ORLOVA ET AL., 2009). A diversidade final é gerada pelas Sintases de Terpenos (TPSs), enzimas capazes de converter um único substrato em múltiplos produtos voláteis (HUANG ET AL., 2012; GUTENSOHN ET AL., 2013).

- Via dos Fenilpropanoides e Benzenoides

Estes compostos originam-se do aminoácido aromático fenilalanina (Phe), que é sintetizado nos plastídios via rota do chiquimato (DUDAREVA ET AL., 2013).

A primeira etapa crítica é a desaminação da Phe em ácido trans-cinâmico pela enzima L-fenilalaninaamônialiase (PAL). A formação de benzenoides envolve o encurtamento da cadeia lateral, que pode ocorrer por uma via oxidativa (análoga ao catabolismo de ácidos graxos e localizada nos peroxissomos) ou por uma via não oxidativa. Outros derivados, como os fenilpropenes, compartilham etapas com a biossíntese da lignina até o estágio de monolignol (KOEDUKA ET AL., 2006).

- Via da Lipoxigenase (LOX) e Derivados de Ácidos Graxos

Os voláteis derivados de lipídios originam-se, principalmente, de ácidos graxos insaturados (ácidos linoleico e linolênico), com destaque para 2-hexanal, nonanal, heptanal, compostos prevalentes no perfil de batata-doce cozidas (SHEN et al., 2024; YAO et al., 2024). Esses COVs, responsáveis por atribuir aromas verdes e notas sebáceas a vegetais (SHAHIDI; HOSSAIN, 2022), originam-se via oxidação de ácidos graxos ou por meio da interação de compostos lipídicos com precursores reativos da Reação de Maillard (WHITFIELD; MOTTRAM, 1992)."

A biossíntese inicia-se por meio de auto-oxidação, foto-oxidação e/ou oxidação catalisada por enzimas (via da lipoxigenase). Na via da LOX os ácidos graxos insaturados sofrem uma oxigenação estereoespecífica formar intermediários 9-hidroperóxidos e 13-hidroperóxidos. Posteriomente são convertidos em em aldeídos e álcoois de cadeia curta, que conferem o aroma característico de "frescor verde" (ABUGU ET AL., 2025; YAO ET AL., 2024).

- Vias Derivadas de Aminoácidos de Cadeia Ramificada

Aminoácidos como alanina, valina, leucina, fenilalanina, cisteína e metionina, são capazes de participar da reação de Maillard (RM). Os COVs gerados nessa reação dependem do tipo de aminoacido que está participando, podendo formar numerosos voláteis, com aromas de flores, frutas, caramelo ou até mesmo odor sulfuroso (YAYLAYAN, 2003; LIU ET AL., 2022). O processo envolve a Degradação de Strecker, iniciada por uma transaminação para a formação de um α-cetoácido, seguida de etapas de descarboxilação e hidrólise que geram, predominantemente, aldeídos e cetonas. A transformação de aminoácidos em compostos orgânicos voláteis (COVs) é um processo dependente de muitos fatores e é favorecido pelo

tratamento térmico e pela complexidade da matriz química. O calor atua como o catalisador para a degradação de metabólitos, enquanto a interação entre aminoácidos específicos com açúcares redutores aumenta as reações de formação do COVs. Em síntese, essa transição envolve a quebra e o rearranjo estrutural de precursores sem aroma por meio de processamento témico e reações com grupos carbonila, resultando na formação de substâncias aromáticas sensorialmente ativas (ABUGU ET AL., 2025; DUDAREVA ET AL., 2013).

A compreensão dessas vias fundamenta estratégias de engenharia metabólica voltadas à biofortificação, ao aumento do vigor das culturas e ao refinamento do perfil sensorial de alimentos.

SEGUNDA PARTE

Artigo 3 - Elaborado conforme a norma NBR 6022	
Título do artigo:	Chemical, nutritional, and functional characterization of different sweet potato genotypes
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ARTIGO 1 - CHEMICAL, NUTRITIONAL, AND FUNCTIONAL CHARACTERIZATION OF DIFFERENT SWEET POTATO GENOTYPES[1]

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[1] Artigo científico apresentado à Universidade Federal de Lavras, como parte das exigências do Programa de Pós-Graduação em Ciência dos Alimentos, área de concentração em Ciência dos Alimentos.

Abstract: This study aimed to comprehensively characterize the chemical, nutritional, and functional composition of five sweet potato genotypes with different flesh colors (purple, cream, and orange) to identify their technological and functional potential. The storage roots were evaluated for physicochemical attributes, enzymatic activity (PPO and POD), bioactive compounds, and antioxidant capacity using different assays. Significant differences were observed among the genotypes. Purple-fleshed genotypes (SP1 and SP4) exhibited higher levels of phenolics, flavonoids, and anthocyanins, which were correlated with high antioxidant activity determined by ABTS and FRAP assays. The orange-fleshed genotype (SP2) stood out for its high carotenoid and starch content, indicating potential for biofortification and industrial applications. Conversely, genotypes with higher resistant starch content (SP3 and SP4) showed functional potential associated with gut health and glycemic control. The results demonstrate that flesh color reflects distinct metabolic profiles, reinforcing the importance of varietal selection for specific food and industrial applications.

Keywords: Ipomoea batatas L. Lam.; Bioactive compounds; Resistant starch; Antioxidant activity.

1 INTRODUCTION

Sweet potato (Ipomoea batatas L. Lam.) is a vegetable with wide global distribution and high socioeconomic relevance, especially in developing countries. Originating from Latin America, this crop stands out for its adaptability to different edaphoclimatic conditions and high productivity, playing a strategic role in global food security. According to data from the Food and Agriculture Organization (FAO), global sweet potato production in 2024 reached approximately 90 million tons, cultivated in an area of 7.2 million hectares, with the highest production concentration in Asia (over 63.87%), followed by Africa (31.4%). In Brazil, sweet potato cultivation occupies a relevant position, with a production of 970 thousand tons in 2024, distributed across nearly 65.1 thousand hectares, resulting in an average yield of 14.8 t ha^{-1}.

In addition to its agronomic importance, sweet potato is recognized for its nutritional and functional value. It is an energy source with a low glycemic index, rich in complex carbohydrates, fibers, vitamins, and minerals. The genetic diversity of the crop is directly reflected in the coloration of the skin and flesh, which can vary from white and cream to yellow-orange and deep purple (ALAM, 2021). This color variation is associated with the presence of different bioactive compounds, responsible not only for sensory characteristics but also for potential health benefits (ZHAO *et al.*, 2024; WANG; NIE; ZHU, 2016).

Orange-fleshed varieties stand out for their high carotenoid content, especially β-carotene, a vitamin A precursor, while purple-fleshed varieties present significant concentrations of phenolic compounds, particularly anthocyanins (ZHANG *et al.*, 2022; PARK *et al.*, 2016). These natural pigments are widely recognized for their high antioxidant capacity, acting in the scavenging of free radicals and contributing to the reduction of oxidative stress, a factor associated with the development of non-communicable chronic diseases. Studies indicate that anthocyanins present in purple sweet potato exhibit strong antioxidant activity, as well as anti-inflammatory properties and potential cardioprotective effects (GUCLU *et al.*, 2023; ESCOBAR-PUENTES *et al.*, 2022; IVANE *et al.*, 2024). In this context, orange-fleshed varieties can contribute to biofortification strategies aimed at combating “hidden hunger,” specifically vitamin A deficiency, which still affects vulnerable populations in various regions of the world. The replacement of white-fleshed varieties, which are low in provitamin A, with biofortified genotypes is a sustainable and cost-effective alternative (MULWA *et al.*, 2023).

Although sweet potato is widely consumed boiled and utilized in animal feed, its potential for industrial applications remains underexplored, especially in the Brazilian context. However, the industrial suitability of this root is not only related to the presence of functional compounds but fundamentally depends on its physicochemical characteristics, particularly the dry matter content. Genotypes with high solid contents are more suitable for the production of flour, chips, and starches, as they provide higher industrial yield and lower oil absorption during frying, while varieties with lower dry matter content are generally directed towards domestic consumption or the production of sweet pastes (HISTIFARINA; PURNAMASARI; RAHMAT, 2023). Nevertheless, integrated studies relating physicochemical quality, antioxidant potential, and varietal characteristics of Brazilian genotypes, particularly those with different flesh colors, are still scarce. Furthermore, national cultivation is predominantly carried out by smallholders, often with a low level of technology adoption, contributing to yields below the crop's potential (VIEIRA *et al.*, 2023). Conversely, the growing consumer interest in healthier and functional foods has driven breeding programs aimed at developing new cultivars with higher agronomic yield and an improved nutritional profile (TANAKA *et al.*, 2017).

Despite the vast biodiversity of sweet potatoes in Brazil, many local varieties and promising genotypes from breeding programs still lack detailed chemical characterization. The selection of new varies has historically prioritized agronomic traits, such as yield and pest resistance, often at the expense of nutritional quality and industrial suitability. Consequently, mapping the physicochemical and functional profile becomes an indispensable step for identifying genotypes that combine high field performance with superior quality attributes, both for the consumer and the processing industry.

Given these gaps, this study aimed to characterize, in an integrated manner, the physicochemical quality and antioxidant potential of sweet potato genotypes with purple, cream, and orange flesh developed in Brazil. Understanding these characteristics is fundamental not only to guide consumption and nutritional valorization strategies but also to support the development of functional ingredients. Thus, the comparative analysis between genotypes of different flesh colors contributes to expanding scientific knowledge about the crop, strengthening its insertion into higher value-added production chains.

2 MATERIALS AND METHODS

2.1 Plant Material and Sample Processing

The plant material was obtained from a field experiment established at the Center for Development and Technology Transfer of the Federal University of Lavras (CDTT/ESAL/UFLA). The crop was planted in December 2024 and harvested 150 days after planting at Palmital Farm, located in the municipality of Ijaci, Minas Gerais, Brazil (altitude: 918 m; latitude:21°14′16″ S; longitude: 45°08′00″ W). For each genotype (Figure 1), five intact, medium sized sweet potato tuberous roots (100–150 g) were selected, washed, sliced, frozen and stored at −80 °C until further analyses. The roots were coded as follows: SP1 – UFLA R1440 (purple-fleshed); SP2 – UFLA 286 (white-fleshed); SP3 – UFLA B556 (white-fleshed); SP4 – UFLA 1192 (purple-fleshed); and SP5 – BRS Cotinga (purple-fleshed).

Figure 1- Visual appearance of roots from five sweet potato genotypes.

2.2 Analyses

2.2.1 Proximate composition

Proximate composition was determined according to the official methods (AOAC, 2023). Moisture and ash were determined gravimetrically, while crude fiber was analyzed by acid digestion, the resulting residue was washed with hot water, dried in the oven, and weighed. Protein content was calculated from total nitrogen using the semi-micro Kjeldahl method with a conversion factor of 6.25. The lipid content was quantified using the cold extraction method (BLIGH; DYER, 1959).

2.2.2 Color parameters

The color parameters were determined using a Minolta CR-400 colorimeter (Minolta Corp., Ramsey, NY, USA). The CIELab coordinates were recorded, and chroma (C*) and hue angle (°h).

The surface of each sweet potato cylinder was randomly measured fifteen times per treatment (ABREU *et al.*, 2022).

2.2.3 pH, Titratable Acidity, and Soluble Solids

Samples were homogenized in distilled water at a 1:3 (w/v) ratio, filtered through organza cloth, and the resulting filtrate was used for the determination of pH, titratable acidity (TA), and soluble solids (SS). The pH was measured using a TECNAL® pHmeter, previously calibrated with standard buffer solutions (pH 4.0 and 7.0). Titratable acidity was determined by titration with 0.01 N sodium hydroxide (NaOH), using phenolphthalein as an indicator, according to AOAC methods (2023), and the results were expressed as mg citric acid per 100 g of sample. Soluble solids were measured using a digital refractometer (ATAGO PR-100, Tokyo, Japan) with automatic temperature compensation, and the results were expressed as percentage (%) (AOAC, 2023).

2.2.4 Extraction of phenolics, flavonoids, and antioxidants

The extract was prepared with minor modifications (BARROS *et al.*, 2021). Approximately 2 g of sample were placed in a centrifuge tube and homogenized with 25 mL of 50% (v/v) methanol. The mixture was then shaken for 1 h in the dark at room temperature and subsequently centrifuged (Hettich ROTINA 380R centrifuge). The supernatant was collected, and a second extraction was performed under the same conditions using 25 mL of 70% (v/v) acetone. The two supernatants were then combined, filtered into amber flasks, and stored at $-18\,^{\circ}\mathrm{C}$ until analysis. The resulting extract was used for the determination of total phenolic content, flavonoids, and antioxidant activity.

2.2.5 Total Phenolic Content and Flavonoids

Total phenolic content (TPC) was determined using the Folin–Ciocalteu method with adaptations (PARADISO *et al.*, 2018). In a 96-well microplate (Biochrom, Bio EZ Read 2000), the extract was reacted with 10% (v/v) Folin–Ciocalteu reagent and 4% (w/v) sodium carbonate. After incubation for 2 h at room temperature in the dark, absorbance was measured at 720 nm. Results were expressed as milligrams of gallic acid equivalents per 100 g of fresh matter (mg GAE $\cdot$ 100 g^{-1} FM).

Flavonoid content was determined with adaptations (SAVI *et al.*, 2017). Aliquots of 150 μL of the extract were mixed with 150 μL of 2% (w/v) aluminum chloride solution. After incubation for 60 min at room temperature, absorbance was measured at 425 nm. Results were expressed as milligrams of catechin equivalents per 100 g of fresh matter (mg CE · 100 g^{-1} FM).

2.2.6 Antioxidant Activity

Antioxidant activity was evaluated using the $ABTS^{\bullet+}$ radical scavenging assay (2,2azino-bis(3ethylbenzothiazoline6sulfonic acid)), the ferric reducing antioxidant power (FRAP) assay, and the phosphomolybdenum complex assay (PRIETO; PINEDA; AGUILAR, 1999). Aliquots of the extracts were transferred to 96-well microplates, and after the respective reaction times, absorbance readings were obtained using a microplate reader (EZ Read 2000, Biochrom®) at 734 nm, 595 nm, and 695 nm, respectively. $ABTS^{\bullet+}$ and FRAP results were expressed as micromoles of Trolox equivalents per 100 g of fresh matter (μmol TE · 100 g^{-1} FM), while the phosphomolybdenum assay results were expressed as milligrams of ascorbic acid equivalents per 100 g of fresh matter (mg AAE · 100 g^{-1} FM).

2.2.7 Carotenoids

Carotenoid analysis was performed using the spectrophotometric method (RODRIGUEZ-AMAYA, 2001), and the results were expressed as mg $100g^{-1}$ of fresh matter. Absorbance readings were obtained using a spectrophotometer at 444, 450, 456, 462, and 470 nm, corresponding to the characteristic wavelengths of α-carotene, β-carotene, σ-carotene, λ-carotene, and lycopene, respectively.

Total carotenoid content was calculated according to the following equation:

$$\text{Total carotenoids } (m\text{g } 100\text{g}^{-1}) = \frac{A \times V \times 10^6}{\alpha \times M \times 100} \times 100$$

where A is the absorbance of the solution at the specific wavelength, V is the final volume of the extract, α is the specific extinction coefficient of the pigment in the solvent (petroleum ether), and M is the sample mass (g) used for the analysis.

2.2.8 Anthocyanins

Total anthocyanin content was determined using the single-pH method (BARCIA *et al.*, 2012). Absorbance was measured at 535 nm using a spectrophotometer. The results were expressed as milligrams of cyanidin-3-glucoside per 100 g of fresh matter and calculated according to the following equation:

$$\text{Total anthocyanins (mg } 100\text{g}^{-1}) = \frac{A \times MW \times DF}{\varepsilon \times 1} \times 100$$

where A is the absorbance of the sample, MW is the molar mass of cyanidin3glucoside (449.2 g mol^{-1}), and DF is the dilution factor. The parameter ε is the molar extinction coefficient of cyanidin3glucoside (26,900 L mol^{-1} cm^{-1}).

2.2.9 Total Sugars

Total sugars were extracted using 95% ethanol and quantified by the anthrone method (DISCHE, 1962). Glucose was used as the standard for calibration curve preparation, and absorbance was measured at 620 nm. Results were expressed as mg of total sugars per 100 g of sample (mg 100 g^{-1}).

2.2.10 Polyphenol Oxidase (PPO) and Peroxidase (POD) Activity

Enzymatic activity was determined with adaptations (CAMPOS; SILVEIRA, 2003). Approximately 10 g of sample were homogenized with 50 mL of 0.05 mol L^{-1} phosphate buffer (pH 7.0) until complete homogenization. The homogenate was filtered through organza cloth and subsequently centrifuged at $9{,}083 \times g$ for 10 min at 4 °C. The supernatant was collected in amber flasks. Both the enzyme extracts and reagents were stored under refrigeration at 4 °C until analysis for PPO and POD activity.

For PPO activity determination, 1.0 mL of enzyme extract was mixed with 1.8 mL of 0.1 mol L^{-1} phosphate buffer (pH 7.0) and three drops of 10 mol L^{-1} catechol. The reaction mixture was incubated in a water bath at 30 °C for 30 min. The reaction was stopped by adding 1.6 mL of 2 mol L^{-1} perchloric acid. Absorbance was measured at 395 nm using a Micronal spectrophotometer (model AJX-1000).

For POD activity, 3 mL of enzyme extract were added to 5 mL of 0.02 mol L^{-1} phosphate–citrate buffer (pH 5.0) and 0.5 mL of guaiacol. The reaction mixture was incubated in a water bath at 30 °C for 5 min and subsequently stopped by the addition of 1.0 mL of 30% (m/v) sodium bisulfite. Absorbance was measured at 470 nm, and the results were expressed as enzyme units (EU).

2.2.11 Total starch

Sweet potato starch was extracted and enzymatically hydrolyzed to glucose (AREAS; LAJOLO, 1980) and subsequently quantified by the anthrone method (DISCHE, 1962), using a spectrophotometer. Absorbance was measured at 620 nm, and results were expressed as g 100 g^{-1} of fresh sample.

2.2.12 Amylose

Amylose and amylopectin contents were determined using the K-AMYL assay kit (Neogen/Megazyme), based on the specific precipitation of amylopectin by the lectin concanavalin A (Con A). Initially, sweet potato flour samples (20–25 mg) were dispersed in dimethyl sulfoxide (DMSO) in a boiling water bath and pretreated with 95% ethanol to remove interfering lipids and soluble sugars. The recovered starch sediment was dissolved in acetate buffer (Solution A). An aliquot of this solution was mixed with Con A solution to precipitate amylopectin for 1 h at room temperature, followed by centrifugation. The amylose present in the supernatant, as well as total starch from a separate aliquot of Solution A, was enzymatically hydrolyzed to D-glucose using a mixture of amyloglucosidase and α-amylase. Glucose quantification was performed by a colorimetric assay using the GOPOD (glucose oxidase/peroxidase) reagent, with absorbance read at 510 nm. Amylose content was calculated as the ratio between the absorbance of the supernatant from the Con A-precipitated sample and the absorbance of the total starch sample.

2.2.13 Resistant Starch

Resistant starch (RS) content was determined using the K-RSTAR assay kit (Neogen/Megazyme), following the official AOAC Method 2002.02. Approximately 100 mg of sample were incubated with 4.0 mL of a solution containing pancreatic α-amylase (10 mg mL^{-1}) and amyloglucosidase (AMG; 3 U mL^{-1}) in sodium maleate buffer (pH 6.0). Hydrolysis of non-

resistant starch was carried out at 37 °C for exactly 16 h under continuous agitation (200 strokes min^{-1}). The reaction was stopped by the addition of 99% ethanol, followed by centrifugation at $1{,}500 \times g$ for 10 min to recover the resistant starch sediment. The pellet was washed twice with 50% ethanol and then dissolved in 2 M KOH under vigorous stirring in an ice bath. After solubilization, the solution was neutralized with sodium acetate buffer (1.2 M; pH 3.8), and the remaining starch was quantitatively hydrolyzed to D-glucose by the addition of AMG (3,300 U mL^{-1}) at 50 °C for 30 min. Glucose was quantified by a colorimetric assay using the GOPOD reagent, with absorbance measured at 510 nm against a reagent blank. Resistant starch content was calculated based on absorbance values, considering sample dry weight and the appropriate conversion factors from free glucose to anhydrous starch.

2.2.14 Statistical analysis

The data obtained for the different sweet potato genotypes were subjected to statistical analysis using Statistica software (version 14.1.0.8, TIBCO Software Inc., USA). All analyses were performed with five replicates, and results were expressed as mean ± standard deviation. Analysis of variance (ANOVA) was applied, and mean values were compared using Tukey's test ($p < 0.05$) to identify significant differences among the evaluated varieties. In addition to univariate analysis, multivariate techniques were applied to achieve a more comprehensive understanding of similarity patterns among genotypes. Principal Component Analysis (PCA) was employed to explore the overall variability of the physicochemical variables and to identify the main axes of data dispersion. Furthermore, a Pearson correlation matrix was constructed, and its visualization as a heatmap enabled the identification of positive and negative linear relationships among the analyzed variables.

3 RESULTS AND DISCUSSION

The moisture content of the samples ranged from 66.46% (SP5) to 77.48% (SP2), with SP2 being significantly moister than the other genotypes (Table 1). The high-water content observed in SP2 may compromise postharvest stability; however, it may favor applications requiring greater softness, such as purée production.

Table 1: Mean values of moisture, ash, protein, lipids, fiber, pH, TTA, and TSS for five sweet potato genotypes.

Sample	Moisture (%)	Ash (%)	Protein (%)	Lipids (%)	Fiber (%)	pH	TTA (%)	TSS (%)
SP1	66.58 ± 1.48^{b}	0.32 ± 0.02^{a}	1.26 ± 0.23^{b}	0.18 ± 0.06^{a}	1.58 ± 0.34^{a}	5.74 ± 0.09^{ab}	0.33 ± 0.02^{b}	6.36 ± 0.62^{ab}
SP2	77.48 ± 1.50^{a}	0.22 ± 0.01^{b}	1.22 ± 0.46^{b}	0.17 ± 0.05^{a}	1.92 ± 0.46^{a}	4.40 ± 0.37^{c}	0.65 ± 0.11^{a}	6.09 ± 0.69^{ab}
SP3	67.31 ± 1.47^{b}	0.32 ± 0.01^{a}	1.79 ± 0.62^{ab}	0.25 ± 0.08^{a}	2.18 ± 0.75^{a}	5.40 ± 0.21^{b}	0.58 ± 0.03^{a}	5.58 ± 0.88^{b}
SP4	68.41 ± 2.27^{b}	0.30 ± 0.02^{a}	1.44 ± 0.15^{b}	0.22 ± 0.05^{a}	2.46 ± 0.22^{a}	5.68 ± 0.04^{ab}	0.43 ± 0.13^{b}	6.99 ± 0.50^{a}
SP5	66.46 ± 4.51^{b}	0.34 ± 0.06^{a}	3.27 ± 1.99^{a}	0.20 ± 0.09^{a}	2.11 ± 0.54^{a}	5.96 ± 0.06^{a}	0.35 ± 0.03^{b}	5.82 ± 0.92^{ab}

Note: Values are described as mean ± standard deviation ($n = 5$). Means followed by different letters in the same column differ significantly by Tukey's test ($p < 0.05$). TTA: Total Titratable Acidity; TSS: Total Soluble Solids. Codes: SP1 – UFLA R1440 (purple-fleshed); SP2 – UFLA 286 (white-fleshed); SP3 – UFLA B556 (white-fleshed); SP4 – UFLA 1192 (purple-fleshed); and SP5 – BRS Cotinga (purple-fleshed).

Ash contents, which reflect the mineral fraction, ranged from 0.22% (SP2) to 0.34% (SP5). Genotype SP2 exhibited a significantly lower ash content, suggesting a reduced mineral concentration, whereas SP1, SP3, SP4, and SP5 showed similar values. Protein was the component displaying the greatest variability among the samples. Genotype SP5 stood out by presenting the highest protein content (3.27%), approximately two to three times higher than the other genotypes, conferring enhanced nutritional value and potential for protein-enriched products. SP1, SP2, and SP4 exhibited the lowest protein levels, while SP3 showed intermediate values.

All evaluated genotypes exhibited low lipid contents (Table 1), with no statistically significant differences among them. This finding confirms that sweet potato is inherently low in fat and reinforces its suitability for low-lipid diets. Regarding dietary fiber, no significant differences were observed among the genotypes. Nevertheless, SP4 presented the highest mean fiber content, which may contribute to functional benefits such as improved intestinal health and glycemic control. Genotype SP2 was characterized by the lowest pH (4.40) and the highest total titratable acidity (TTA, 0.65%), indicating a more acidic profile. Such characteristics may enhance microbiological stability but could negatively affect sensory acceptance. In contrast, SP5 exhibited the highest pH value (5.96) and low acidity, suggesting a milder flavor profile. Soluble solids (SS) content varied significantly among the samples. SP4 showed the highest SS levels, indicating greater sweetness, whereas SP3 presented the lowest SS content, which may result in reduced sensory acceptance in applications where sweetness is a desirable attribute.

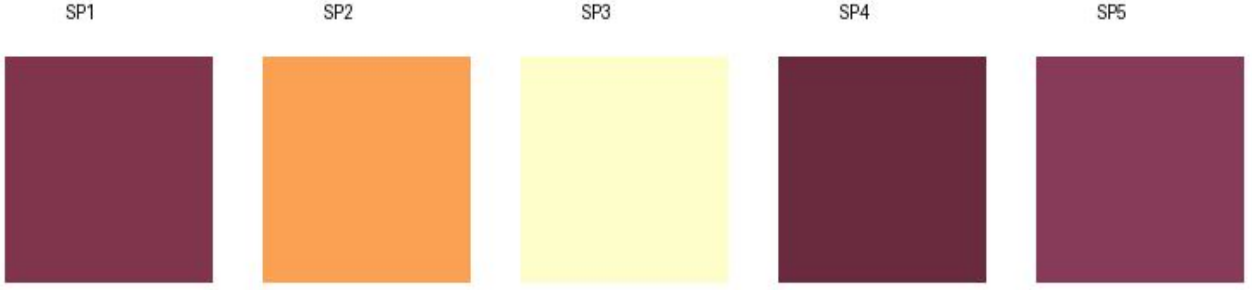
Significant differences were observed in the color parameters L*, C*, and h° among the evaluated genotypes (Table 2), indicating a wide variability in flesh coloration (Figure 2). Genotype SP3 exhibited the highest L* value and was therefore characterized as the lightest-fleshed sample. In contrast, SP4 showed the lowest L* value, indicating a darker flesh color. Reduced lightness values are generally associated with the presence of dark pigments, such as anthocyanins, which decrease surface reflectance[25].

Table 2: Mean values of color parameters (L^*, C^*, and h°) of five sweet potato genotypes.

Sample	L^*	C^*	h°
SP1	33.53 ±2.42^c	35.02 ±1.18^b	3.08 ±1.27^d
SP2	73.97 ±0.68^b	59.91 ±2.41^a	62.43 ±2.95^c
SP3	98.77 ±0.81^a	27.99 ±2.44^c	100.26 ±0.46^b
SP4	27.52 ±1.59^d	30.67 ±2.31^c	2.70 ±0.78^d
SP5	36.07 ±2.72^c	36.86 ±1.80^b	356.13 ±1.26^a

Note: Values are described as mean ± standard deviation ($n = 5$). Means followed by different letters in the same column differ significantly by Tukey's test ($p < 0.05$). Codes: SP1 – UFLA R1440 (purple-fleshed); SP2 – UFLA 286 (white-fleshed); SP3 – UFLA B556 (white-fleshed); SP4 – UFLA 1192 (purple-fleshed); and SP5 – BRS Cotinga (purple-fleshed).

Figure 2- Colorimetric reconstruction of sweet potato flesh. Colors were derived from instrumental parameters (L*, C*, and °h) and converted from CIELab to RGB space using standard illuminant D65.



The highest chroma (C*) value was recorded for genotype SP2, indicating a more vivid and saturated flesh color. The hue angle of this genotype fell within the yellow–orange region, a characteristic typical of carotenoid-rich cultivars (RODRIGUEZ-AMAYA, 2019). In contrast, genotypes SP1 and SP4 exhibited very low hue angle values, close to the red–purple axis, suggesting a predominance of anthocyanins pigments responsible for darker and less saturated hues. The instrumental color differences observed among the genotypes are directly related to their bioactive compound profiles and antioxidant activity (Table 3). Genotype SP2 showed a high total carotenoid content, which is consistent with its elevated C* value and yellow–orange hue. Carotenoids are widely recognized for their provitamin A activity and associated health benefits; however, their contribution to antioxidant activity in assays such as ABTS and FRAP may be limited due to their lipophilic nature and lower reactivity in electron transfer based methods (RIBEIRO *et al.*, 2018; QUEIROZ *et al.*, 2020). This characteristic explains the moderate antioxidant activity observed for SP2, despite its high carotenoid content.

Table 3: Mean values of carotenoids, total phenolic compounds, flavonoids, anthocyanins, and antioxidant potential (ABTS, FRAP, and Phosphomolybdenum) of five sweet potato genotypes.

Sample	**Carotenoids** *(mg/100g)*	**Phenolics** *(mg GAE/100g)*	**Flavonoids** *(mg CE/100g)*	**ABTS** *(*µmol *TE/100g)*	**FRAP** *(*µmol *TE/100g)*	**Phosphomolybdenum** *(mg AAE/100g)*	**Anthocyanins** *(mg C3G/100g)*
SP1	1.34 ± 0.44^{b}	193.27 ± 13.68^{ab}	397.10 ± 20.20^{a}	165.82 ± 13.73^{a}	1481.97 ± 42.46^{ab}	524.02 ± 37.57^{b}	32.08 ± 6.63^{b}
SP2	45.26 ± 4.13^{a}	51.03 ± 12.90^{c}	185.32 ± 14.36^{b}	87.72 ± 10.57^{b}	1312.16 ± 102.37^{bc}	610.94 ± 50.70^{ab}	9.11 ± 1.07^{c}
SP3	0.23 ± 0.21^{b}	57.44 ± 24.30^{c}	187.04 ± 17.68^{b}	98.29 ± 7.02^{b}	1226.12 ± 59.10^{c}	598.78 ± 27.75^{ab}	2.23 ± 0.24^{d}
SP4	0.58 ± 0.60^{b}	213.36 ± 23.93^{a}	402.52 ± 5.67^{a}	180.53 ± 16.82^{a}	1633.68 ± 246.64^{a}	734.85 ± 141.60^{ab}	42.77 ± 2.11^{a}
SP5	0.90 ± 0.32^{b}	149.13 ± 6.72^{b}	375.89 ± 10.02^{a}	191.62 ± 12.90^{a}	1528.14 ± 47.21^{ab}	785.03 ± 210.38^{a}	14.44 ± 2.77^{c}

Note: Values are described as mean ± standard deviation ($n = 5$). Means followed by different letters in the same column differ significantly by Tukey's test ($p < 0.05$). TE: Trolox Equivalents; GAE: Gallic Acid Equivalents; CE: Catechin Equivalents; AAE: Ascorbic Acid Equivalents; C3G: Cyanidin-3-glucoside. Codes: SP1 – UFLA R1440 (purple-fleshed); SP2 – UFLA 286 (white-fleshed); SP3 – UFLA B556 (white-fleshed); SP4 – UFLA 1192 (purple-fleshed); and SP5 – BRS Cotinga (purple-fleshed).

Conversely, genotypes SP4 and SP1, which exhibited lower L* values and hue angles associated with red–purple coloration, showed significantly higher contents of phenolic compounds, flavonoids, and anthocyanins, with SP4 standing out in particular. These genotypes also presented the highest antioxidant activity values in the ABTS and FRAP assays. Phenolic compounds, especially anthocyanins, have a high capacity to scavenge free radicals and a strong reducing power, which explains the close association between darker flesh coloration and the enhanced antioxidant activity observed (IM; KIM; LEE, 2021; NGCOBO *et al.*, 2024). Genotype SP5 exhibited a hue angle close to 360°, indicating a predominance of reddish tones, along with moderate levels of anthocyanins and flavonoids. This genotype showed high antioxidant capacity, particularly in the phosphomolybdenum assay, suggesting that different classes of reducing compounds act synergistically to enhance total antioxidant activity.

In contrast, SP3, characterized by a high L* value, low chroma, and a hue angle close to 100°, presented the lowest contents of carotenoids and anthocyanins, as well as low antioxidant activity in all assays performed. These results reinforce that flesh color can be used as a rapid and non-destructive indicator of antioxidant potential in sweet potatoes, especially when associated with the content of phenolic compounds (MAKORI; MU; SUN, 2020). The differences observed in pigment profiles and antioxidant activity were also reflected in pronounced variations in the carbohydrate profile and enzymatic activity of the samples (Table 4). Genotypes SP1, SP4, and SP5 stood out for presenting higher total sugar contents, a characteristic that may intensify sweetness perception and enhance consumer sensory acceptance. It is worth noting that elevated sugar levels are often inversely related to starch content and are strongly influenced by both genotype and postharvest metabolism (AMJAD *et al.*, 2020; KROCHMAL-MARCZAK *et al.*, 2020; GUO *et al.*, 2019).

Table 4: Mean values of total sugars, PPO activity, POD activity, total starch, amylose, amylopectin, and resistant starch of five sweet potato genotypes.

Sample	**Total Sugars** *(g glucose/100g)*	**PPO** *(EU/min/g tissue)*	**POD** *(EU/min/g tissue)*	**Total Starch** *(g/100g)*	**Amylose** *(%)*	**Amylopectin** *(%)*	**Resistant Starch** *(g/100g)*
SP1	28.49 ± 8.95^{a}	80.15 ± 1.43^{a}	218.60 ± 20.80^{b}	22.73 ± 2.45^{b}	22.10 ± 4.55^{c}	77.90 ± 4.55^{a}	11.62 ± 2.50^{b}
SP2	4.70 ± 2.81^{b}	6.23 ± 1.26^{b}	207.83 ± 16.88^{b}	45.62 ± 3.89^{a}	18.54 ± 5.19^{c}	81.46 ± 5.19^{a}	4.60 ± 2.09^{c}
SP3	18.42 ± 3.11^{a}	17.13 ± 2.02^{c}	114.00 ± 18.49^{c}	15.37 ± 4.01^{c}	27.86 ± 7.28^{bc}	72.14 ± 7.28^{ab}	17.97 ± 1.14^{a}
SP4	23.31 ± 4.80^{a}	67.38 ± 7.38^{d}	281.94 ± 12.53^{a}	19.77 ± 3.07^{bc}	39.31 ± 3.76^{b}	60.69 ± 3.76^{b}	15.56 ± 0.66^{a}
SP5	27.72 ± 5.42^{a}	33.48 ± 3.86^{e}	184.33 ± 15.33^{b}	15.42 ± 2.60^{c}	59.54 ± 10.30^{a}	40.46 ± 10.30^{c}	2.30 ± 0.55^{c}

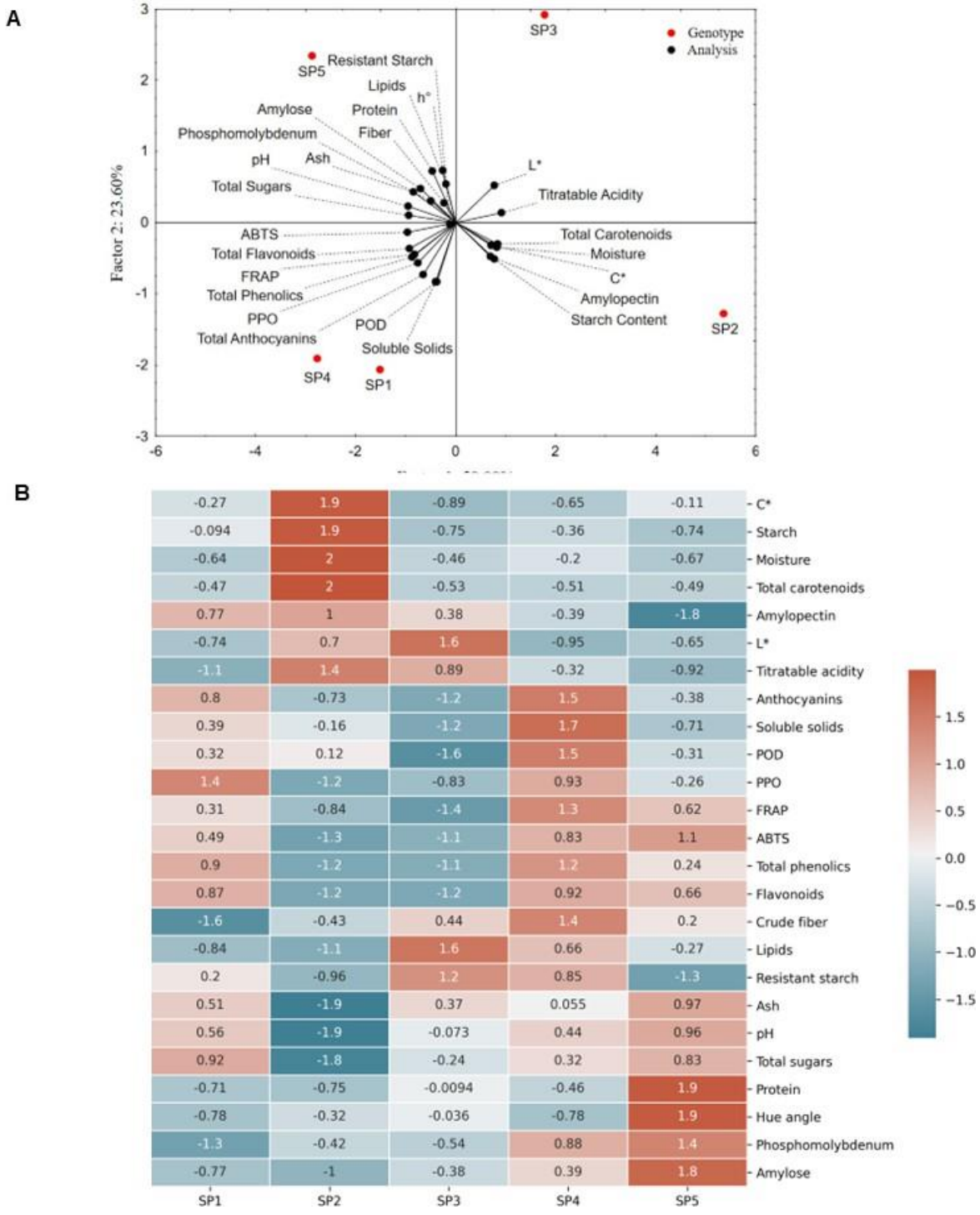
Note: Values are described as mean ± standard deviation ($n = 5$). Means followed by different letters in the same column differ significantly by Tukey's test ($p < 0.05$). PPO: Polyphenol oxidase; POD: Peroxidase; EU: Enzyme Units. Codes: SP1 – UFLA R1440 (purple-fleshed); SP2 – UFLA 286 (white-fleshed); SP3 – UFLA B556 (white-fleshed); SP4 – UFLA 1192 (purple-fleshed); and SP5 – BRS Cotinga (purple-fleshed)

Genotype SP2 exhibited the highest total starch content and the lowest sugar concentration, confirming its predominantly starchy profile. This behavior is technologically advantageous for applications that require high thickening capacity and viscosity development. In contrast, genotypes SP3 and SP5 showed lower starch contents, consistent with their higher levels of soluble sugars.

Analysis of starch fractions revealed significant differences in the amylose and amylopectin proportions among the genotypes. SP5 stood out for its higher amylose content, whereas SP1 and SP2 showed higher proportions of amylopectin. It is noteworthy that elevated amylose levels are associated with reduced digestibility and increased formation of resistant starch, which is considered beneficial for glycemic control and intestinal health (SUN *et al.*, 2022; GUO *et al.*, 2025). In turn, genotypes SP3 and SP4 presented the highest resistant starch contents, indicating their potential use as functional ingredients (PAN *et al.*, 2025). Enzymatic activities also differed significantly among the analyzed genotypes. SP1 exhibited the highest polyphenol oxidase (PPO) activity, indicating greater susceptibility to enzymatic browning, which may limit its application in minimally processed products and require rapid thermal inactivation to preserve color. In contrast, SP2 and SP3 showed low PPO activity, suggesting greater color stability. SP4 displayed the highest peroxidase (POD) activity, an enzyme known for its high thermal resistance, indicating that more intense thermal treatments may be necessary to achieve complete inactivation during processing (TARANTO *et al.*, 2017).

Principal component analysis (PCA) explained 73.6% of the total variance in the first two components, with 50.0% attributed to Factor 1 (PC1) and 23.6% to Factor 2 (PC2), indicating an adequate representation of data variability (Figure 3).

Figure 3- (A) PCA biplot illustrating the dispersion of physicochemical and functional variables among five sweet potato genotypes; (B) Multivariate clustering analysis displayed as a heatmap, highlighting qualitative disparities among the genotypes.



PC1 promoted a clear separation among the genotypes, primarily distinguishing SP2, which was associated with higher values of chroma (C*), lightness (L*), carotenoid content, starch, and amylopectin. In contrast, SP1 and SP4 were positioned on the negative side of PC1 and were correlated with total phenolics, anthocyanins, flavonoids, and higher antioxidant activity (ABTS and FRAP). PC2 contributed to further separation of the genotypes based on nutritional and structural composition. SP5 was associated with amylose, resistant starch, dietary fiber, and protein, suggesting greater functional and nutritional potential. SP3 was characterized by its association with higher lightness and hue angle, reflecting lower pigment contents and reduced antioxidant activity.

The heatmap (Figure 3B) presents the standardized distribution (z-scores) of physicochemical, nutritional, and bioactive parameters among the five sweet potato genotypes (SP1–SP5), providing a clear visualization of variety-specific patterns and associations among the analyzed variables, thereby corroborating the results observed in the PCA. SP2 stood out by exhibiting higher values of chroma (C*), starch, moisture content, and total carotenoids, indicating roots with greater color saturation and starch accumulation typical characteristics of orange-fleshed materials.

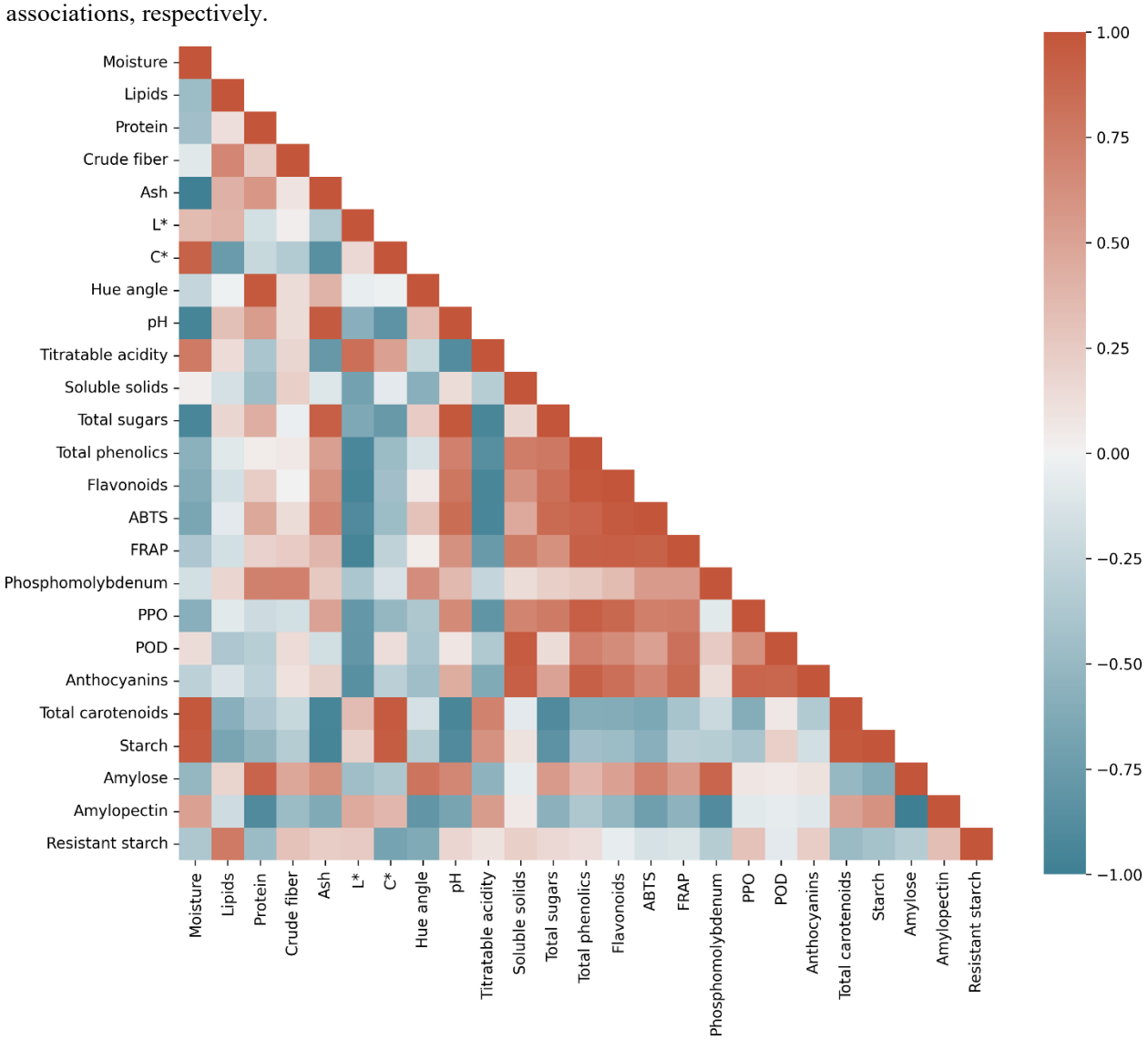
Orange-fleshed sweet potatoes are known to contain significantly higher levels of total carotenoids, particularly β-carotene, which contributes to the intense orange coloration and enhanced nutritional quality (LAVERIANO-SANTOS *et al.*, 2022). Moreover, studies reporting the relationship between flesh color and carotenoid content across different sweet potato cultivars corroborate the association between chromatic intensity and elevated carotenoid levels, reinforcing their potential for industrial applications and biofortification strategies (AINA *et al.*, 2009; PILON *et al.*, 2021).

In contrast, SP4 showed higher contents of anthocyanins, soluble solids, and parameters related to antioxidant activity (FRAP, ABTS, total phenolics, and flavonoids), in addition to higher activities of peroxidase (POD) and polyphenol oxidase (PPO). This profile is characteristic of purple-fleshed genotypes, in which phenolic compounds especially anthocyanins are the primary contributors to antioxidant potential (MAQSOOD *et al.*, 2025; NEUNFELD *et al.*, 2022). The clustering of these variables highlights the close association between phenolic metabolism and antioxidant capacity, reinforcing the functional value of this genotype. SP3 exhibited higher contents of lipids, resistant starch, and lightness (L*), accompanied by lower levels of phenolic

compounds. This profile suggests a composition more oriented toward structural carbohydrates and lipophilic components. Such characteristics may influence both technological and nutritional properties, particularly due to the higher resistant starch content.

SP5 stood out for presenting the highest values of protein, amylose, hue angle, antioxidant capacity determined by the phosphomolybdenum assay, ash content, pH, and total sugars. The concomitant increase in amylose and protein suggests a starch composition with potential implications for glycemic response and technological functionality. Moreover, the high antioxidant capacity assessed by the phosphomolybdenum method indicates the presence of non-phenolic antioxidants, suggesting a broader spectrum of redox-active compounds (PRIETO; PINEDA; AGUILAR, 1999). SP1, in turn, displayed intermediate characteristics, with moderate values of amylopectin, anthocyanins, antioxidant capacity, and fiber-related parameters. This balanced profile indicates a more neutral composition, without a marked specialization in either starch accumulation or enrichment in bioactive compounds. Overall, PCA and heatmap analyses demonstrate that the evaluated genotypes differ according to distinct metabolic priorities, involving starch composition (amylose/amylopectin ratio), pigment biosynthesis (carotenoids and anthocyanins), and pathways associated with antioxidant activity. These differences highlight the influence of genetic background on the nutritional, functional, and technological attributes of sweet potato roots. The integrated visualization reinforces the potential of specific genotypes for targeted applications, such as functional foods, industrial processing, or breeding programs focused on nutritional quality and enrichment in bioactive compounds. The Pearson correlation matrix (Figure 4) revealed significant relationships among the physicochemical, nutritional, and bioactive attributes of the sweet potato genotypes, uncovering patterns that reflect root physiology and are consistent with the results obtained from the other multivariate analyses.

Figure 4- Pearson correlation matrix among physicochemical and enzymatic variables of sweet potato genotypes. Correlation coefficients range from -1 (blue) to +1 (red), indicating negative and positive associations, respectively.



A strong positive correlation was observed among total phenolics, flavonoids, anthocyanins, and antioxidant capacity assessed by the ABTS and FRAP assays, indicating that the antioxidant potential of the samples is largely explained by the accumulation of these bioactive compounds. Similarly, polyphenol oxidase (PPO) and peroxidase (POD) activities showed direct correlations with these same groups, suggesting higher enzymatic activity in genotypes richer in phenolic pigments. In contrast, starch-related variables such as total starch, amylopectin, and resistant starch were positively correlated with each other and also with total carotenoids, indicating that genotypes with higher contents of structural carbohydrates tend to exhibit greater carotenoid concentrations. Color parameters (L*, C*, and h°) were positively

correlated with titratable acidity and moisture content, suggesting that lighter roots with greater chromatic saturation generally present higher water content and acidity. Conversely, lipids, protein, and crude fiber showed negative correlations with several bioactive components, reflecting distinct nutritional profiles among the evaluated genotypes. Overall, the correlation pattern demonstrates that the genotypes express integrated sets of traits, reinforcing the groupings observed in the heatmap and principal component analysis (PCA), and highlighting the coexistence of profiles oriented toward higher antioxidant capacity, starchy composition, or specific nutritional attributes.

4 CONCLUSION

The evaluation of five sweet potato genotypes revealed wide phenotypic diversity, with distinct nutritional and functional profiles indicating specific technological aptitudes for each genotype. Multivariate analysis enabled the classification of the genotypes into three main profiles. SP4 and SP1 were characterized by a bioactive and antioxidant profile, exhibiting high contents of phenolic compounds, flavonoids, and anthocyanins, which showed strong positive correlations with antioxidant capacity (ABTS and FRAP), highlighting their potential for functional foods and natural colorants, although SP4 requires careful processing due to its high peroxidase activity. SP2 presented a starchy and industrial profile, with the highest contents of starch, moisture, and total carotenoids; its yellow–orange flesh and high chroma (C*) indicate strong potential for provitamin A biofortification and industrial applications requiring thickening capacity and purée production. In contrast, SP5 showed a nutritional and metabolic profile, distinguished by higher protein and ash contents and a high proportion of amylose, while SP3 and SP4 stood out for their resistant starch content, suggesting benefits for intestinal health and glycemic control. Overall, these findings support the strategic selection of sweet potato genotypes for breeding programs and for the development of value-added food products, aiming to fully exploit the nutritional and functional potential of this crop.

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ARTIGO 2 – Volatile Composition and Aromatic Implications in Sweet Potato Genotypes

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The characterization of Brazilian sweet potato genotypes enables the identification of chemical profiles and specific volatile compounds, contributing to the valorization and increased commercial potential of this crop. This study characterized the volatile organic compound (VOCs) profile of five sweet potato genotypes with different flesh colors (purple, orange, and white). Four genotypes developed by the breeding program of the Federal University of Lavras (UFLA) and the commercial cultivar BRS Cotinga were evaluated. Prior to volatile extraction, shredded sweet potato tuberous roots were placed in a headspace vial and heated in a water bath at 100 °C for 30 minutes to simulate steam cooking and release volatile compounds. The procedure was applied uniformly across all genotypes. Volatile compounds were extracted using solid-phase microextraction (SPME) coupled with gas chromatography-mass spectrometry (GC-MS). A total of 72 VOCs were detected, classified into eight chemical groups, with aldehydes and terpenoids predominating. Different volatile compounds were associated with metabolic pathways such as lipid oxidation, carotenoid degradation, Strecker reactions, and thermal release of glycosylated terpenes. Multivariate analysis, including variable importance in projection (VIP) scores and heatmaps, enabled discrimination of genotypes. Notably, β-ionone and β-cyclocitral were identified as potential volatile markers for the orange-fleshed genotype, reflecting carotenoid degradation pathways, while phenylacetaldehyde and benzaldehyde were more abundant in purple-fleshed genotypes, suggesting Strecker degradation as a predominant biosynthetic route. These findings provide information for breeding programs aimed at selecting genotypes with differentiated sensory profiles.

Keywords: Ipomoea batatas; volatile organic compounds; SPME-GC-MS; multivariate analysis; Strecker reaction; carotenoid degradation

Introduction

Sweet potato (Ipomoea batatas (L.) Lam.) is one of the most relevant food crops worldwide, playing a significant role in food security and climate-change adaptation due to its broad adaptability, relatively short growth cycle, and high yield potential (Sapakhova et al., 2023). In addition to its agronomic relevance, sweet potato is a nutritionally dense crop, providing complex carbohydrates with a low glycemic index, dietary fiber, minerals, and bioactive compounds that confer functional and health-promoting properties.

The species exhibits great genetic variability, resulting in diverse chemical compositions, tuberous root shapes, and flesh colors, including white, yellow, cream, orange, and purple (Amoanimaa-Dede et al., 2020). Purple-fleshed roots contain anthocyanins, phenolic pigments associated with antioxidant capacity and potential human health benefits (Zhao et al., 2024). Conversely, orange-fleshed cultivars are characterized by the presence of carotenoids, especially β-carotene, a vitamin A precursor and a substrate for the formation of volatile compounds derived from the thermal degradation of this pigment (Nabot et al., 2024). On the other hand, white-fleshed roots contain low concentrations of pigments and are primarily composed of starch and sugars, which have been suggested to produce simpler and less intense aromatic profiles (R. Zhang, Tang, Jiang, Mo, & Wang, 2025), although direct comparative sensory confirmation remains limited in the literature.

The chemical composition of each genotype, including sugars, amino acids, fatty acids, and pigments, directly influences the formation of volatile organic compounds (VOCs) during thermal processing. Cooking induces a series of thermochemical reactions that are the main pathways for VOC formation, including Maillard reactions, Strecker degradation of amino acids, carotenoid degradation, lipid oxidation, and thermal release of glycosylated terpenes (Abugu, Allan, Johanningsmeier, Iorizzo, & Yencho, 2025; Shen et al., 2024).

Maillard reactions between reducing sugars and amino acids generate aldehydes and furans that contribute to sweet, caramelized, and roasted aromas, frequently

associated with the flavor of boiled or baked sweet potatoes (R. Zhang, Tang, Jiang, Mo, & Wang, 2021). In orange genotypes, carotenoid degradation is the key mechanism in the formation of high-sensory-impact norisoprenoids, such as *β*-Ionone and *β*-cyclocitral, compounds recognized for their characteristic fruity-floral aroma (Kammona, Othman, Abdullah, & Abu Bakar, 2015). Thermal lipid oxidation contributes to the formation of short- and medium-chain aldehydes and alcohols, often associated with herbaceous, green, and fruity notes (Yao, Zhang, Jia, et al., 2024). Furthermore, amino acid degradation can lead to the formation of various compound classes, mainly aldehydes such as benzaldehyde and phenylacetaldehyde, known for their contributions to sweet, fragrant, and floral aromas (Jiang et al., 2023; Shen et al., 2024).

Volatile compounds directly influence consumer acceptance, as aroma is one of the most important attributes in quality perception (Al-Khalili, Pathare, Rahman, & Al-Habsi, 2025). Volatile profiles exhibiting sweeter, floral, and fruity notes tend to be more acceptable, whereas earthy or herbaceous aromas may result in lower acceptability. Thus, understanding how the chemical characteristics of each genotype influence VOC formation is essential to expand knowledge regarding the volatile compounds present in different sweet potato genotypes. This knowledge supports breeding programs aimed at selecting and developing genotypes with sensory profiles that are more attractive to consumers.

Brazil is one of the world's major centers of sweet potato genetic diversity, harboring a wide range of landraces and improved varieties with distinct flesh colors, chemical compositions, and sensory profiles that remain largely unexplored in the scientific literature (Veasey et al., 2008; H. Y. Zhang & Zhao, 2024).

Despite this remarkable diversity, studies characterizing the volatile composition of Brazilian sweet potato varieties are scarce, as Asian and African genotypes have received far greater attention in published research (Abugu et al., 2025). This gap limits the understanding of the aromatic profile and the particularities of national varieties. Therefore, comparative analyses are needed to clarify important relationships between these factors and the resulting aroma. In this context, the present study aimed to identify

and compare the volatile organic compound profile of five sweet potato genotypes, three purple-fleshed, one orange-fleshed, and one white-fleshed, using gas chromatography-mass spectrometry (GC–MS), providing a foundation for advances in breeding, food processing, and the development of products with higher sensory quality.

Materials and Methods

Plant material and sweet potato processing

The experiment evaluated the volatile organic compound (VOC) profile of four genotypes developed by the breeding program of the Universidade Federal de Lavras (UFLA) and one commercial cultivar, BRS Cotinga (Figure 1). The plant material was obtained from a field experiment established at the Center for UFLA Development and Technology Transfer (CDTT/ESAL/UFLA), planted in December 2024, and harvested 150 days after planting. The experiment was located at Palmital Farm, in the municipality of Ijaci, Minas Gerais, Brazil (altitude: 918 m; latitude: 21°14′16″ S; longitude: 45°08′00″ W). For each genotype, five intact medium-sized sweet potato tubers (100–150 g) were cleaned, sliced, frozen, and subsequently stored at −80 °C before analysis by gas chromatography–mass spectrometry (GC–MS).

Figure 1. Sweet potato genotypes evaluated in the study, identified by experimental codes: UFLA R1440 (SP1), 2021-Dialelo-286 (SP2), UFLA B556 (SP3), 2020-Uruguaiana-1192 (SP4), and the commercial cultivar BRS Cotinga (SP5).

Extraction of volatile compounds

For the extraction of volatiles, the parameters described by R. Zhang et al. (2025) were used with adaptations. The volatile compounds were extracted by the solid phase microextraction technique (SPME) and tentatively identified by Gas Chromatography Mass Spectrometry. For sample preparation, 1 g of frozen, shredded sweet potato was placed in a 20 mL headspace vial. The vial was then sealed with a crimp cap and a PTFE/silicone septum to prevent the loss of volatile compounds. All analyses were performed in three replicates. Subsequently, the samples were heated in a water bath at 100 °C for 30 minutes to simulate steam cooking and release volatile compounds. The volatile compounds present in the samples were extracted by solid-phase microextraction (SPME) with a divinylbenzene/carboxene/polydimethylsiloxane (DVB/CAR/PDMS) fiber for 30 minutes at 80°C. Next, the volatile components extracted and retained in the SPME fiber were desorbed at the GC injection port for 3 minutes at 250 °C in splitless mode. The fiber was conditioned at a temperature of 270°C for 30 minutes before use. GC–MS analysis was performed using a GC–MS QP2010 Plus gas chromatography–mass spectrometry system (Shimadzu, Japan) equipped with an RTX-WAX capillary column (polyethyleneglycol, PEG; 30 m × 0.25 mm × 0.25 μm). A constant helium flow rate of 1.0 mL · min^{-1} was used for chromatographic separation. The oven temperature program was as follows: initial temperature of 35 ˚C held for 2 min; ramp of 5 ˚C.min^{-1} to 190 ˚C, held for 1 min; ramp of 20 ˚C · min^{-1} to 250 ˚C, held for 2 min; with a solvent delay of 1 min. The mass spectrometer was operated in electron impact (EI) ionization mode at 70 eV and 230 ˚C in fullscan mode, with a mass-to-charge ratio (*m/z*) range of 35 and 450.

Identification and quantification of volatile compounds

Data acquired from the GC–MS analysis were preprocessed using GCMS Solution software (Shimadzu, Japan) for peak selection and mass spectral deconvolution. The compounds were tentatively identified based on the comparison of mass spectra and retention indices (RI) against the Wiley 8 mass spectral library and specific literature from Adams (2007). The RI of each compound was calculated using alkane standards (C5–

C20; Supelco, Sigma-Aldrich, PA, USA). The aroma descriptions of most compounds were obtained from those reported in the Flavornet (Acree & Arn, 2004). The constituent concentrations (%) were calculated by the total area of their respective peaks, related to the total area of all the constituents of the sample (area normalization). Since no internal standard, response factor correction, or external calibration curve was applied, the data should be considered semi-quantitative and interpreted only as relative abundances.

Statistical analysis

The results were expressed as mean ± standard deviation. Data were subjected to analysis of variance (ANOVA), followed by Tukey's test ($p < 0.05$), using Sisvar software, version5.8. A p-value < 0.05 was considered statistically significant. Multivariate statistical plots were generated using Python, including partial least squares discriminant analysis (PLS-DA) and heatmaps.

Results and discussion

Profiling of Volatile Organic Compounds of Five Sweet Potato Genotypes

The analysis of volatile organic compounds (VOCs) in five sweet potato genotypes allowed the identification of a broad chemical profile. A total of 72 VOCs were detected (Table 1). These compounds were classified into eight chemical classes, including alkanes, alcohols, aldehydes, ketones, esters, furans, monoterpenes, and sesquiterpenes. Terpenoids (monoterpenes and sesquiterpenes) and aldehydes stood out as the main constituents of the volatile profile of the studied genotypes (Table 1 Figure 2A).

These results corroborate previous studies (Shen et al., 2024; Y. Wang & Kays, 2001; Yao, Zhang, Jia, et al., 2024; R. Zhang et al., 2023, 2021), reinforcing that terpenoids and aldehydes are the main chemical classes responsible for the characteristic aromatic profile of sweet potato. The wide diversity of VOCs present in sweet potato indicates that its aroma results from complex interactions among multiple volatile compounds (Y. Wang & Kays, 2000). Factors such as genotype, flesh color, and cooking

conditions affect the distribution of these chemical groups (Shen et al., 2024; J. B. Sun, Severson, Schlotzhauer, & Kays, 1995; Y. Wang & Kays, 2001; Yao, Zhang, Jia, et al., 2024; R. Zhang et al., 2021).

Table 1. Volatile compounds, classes, related odor, retention index (RI), relative concentration (% Area) of Different Genotypes

Compound	Class	Odor	RI	SP1	SP2	SP3	SP4	SP5
3-ethyl-2-methyl-1,3-Hexadiene	Alkane	-	728	-	-	3.39±0.78a	-	-
Trans-3-methyl-1-(-2-cyclohexenyl)but-1-ene	Alkane	-	1110	-	-	0.69±0.06a	-	-
5-METHYL-5-ETHYLDECANE	Alkane	fruity, woody, sweet	1272	1.08±0.095a	-	-	-	-
Tridecane <n->	Alkane	-	1300	-	-	0.52±0.13a	-	-
Ethanol	Alcohol	sweet	460	-	-	0.6±0.03a	-	-
1-Hexanol	Alcohol	floral, green	867	3.82±0.15a	1.45±0.61b	0.86±0.17b	0.7±0.03b	0.5±0.01b
1-Octen-3-ol	Alcohol	mushroom	989	0.73±0.265b	-	7.35±0.64a	3.22±0.09ab	-
2-Octen-1-ol, (Z)-	Alcohol	fatty, sweet, fruity	1070	-	1.02±0.03a	-	-	-
1-Octanol	Alcohol	nutty and mushroom	1070	1.05±0.16a	2.03±0.12a	3.22±0.03a	1.51±0.09a	2.34±0.26a
3-Octanol, 3,7-dimethyl-	Alcohol	floral, citrus	1193	0.50±0.14a	-	-	-	-
Oct-3-en-2-ol	Alcohol	mushroom, nutty, earthy	980	1.29±0.055a	-	-	-	-
Terpinen-4-ol	Alcohol	nutmeg, mustard	1177	-	-	0.58±0.01ab	-	5.89±1.13a
l-α-Terpineol	Alcohol	oil, anise, mint	1189	-	0.63±0.01a	-	-	-
3-Methylbutanal	Aldehyde	malty, nutty, chocolate	654	6.65±1.45a	0.57±0.07c	-	1.65±0.35bc	3.60±1.10b
Hexanal	Aldehyde	grass, tallow, fatty	801	4.95±1.53a	5.9±1.96a	4.59±0.55ab	1.45±0.25b	1.64±0.53b
2-Hexenal, (E)-	Aldehyde	apple, green	855	0.45±0.05a	-	-	-	-
Heptanal	Aldehyde	fatty, citrus, rancid	903	0.75±0.145b	3.49±1.31a	1.82±0.35ab	0.55±0.05b	0.84±0.13b
2-Heptenal, (Z)-	Aldehyde	soapy, fatty, almond	901	0.83±0.015ab	0.56±0.09b	2.02±0.24a	0.47±0.0b	0.71±0.14ab
Benzaldehyde	Aldehyde	almond, burnt sugar	961	10.05±0.765b	3.15±0.44c	4.89±0.54c	17.43±1.36a	16.60±0.05a
Octanal	Aldehyde	soapy, fatty, lemon, green	1005	-	1.03±0.52a	1.32±0.35ab	0.99±0.07ab	0.92±0.04ab
Heptadienal <2,4-trans,trans->	Aldehyde	nutty, fatty	1012	-	-	2.37±0.57a	-	-
Phenylacetaldehyde	Aldehyde	sweet, perfume	1045	-	-	5.20±1.72b	-	29.62±0.92a
Benzeneacetaldehyde	Aldehyde	honey, sweet	1043	10.76±2.06b	3.08±1.74c	-	26.53±4.12a	-
2-Octenal, (E)-	Aldehyde	green, nutty, fatty	1065	0.97±0.035b	1.34±0.10b	3.12±0.59a	0.90±0.04b	-
n-Nonanal	Aldehyde	fatty, citrus, green	1103	5.38±0.9a	9.39±1.45a	13.50±3.65a	7.09±0.48a	3.45±2.86a
3,4,8-TRIMETHYL-2-NONENAL	Aldehyde	green, fatty, cucumber	1348	-	1.67±0.23a	-	-	-
n-Decanal	Aldehyde	soap, orange peel, tallow	1206	1.21±0.04a	1.53±0.02a	1.11±0.12a	1.95±0.56a	4.64±3.2a
Vanillin	Aldehyde	vanilla	1660	2.85±0.74a	-	-	1.99±0.02ab	1.89±0.25b
Dodecanal <n->	Aldehyde	sour, fatty	1409	-	-	-	-	2.14±1.41a
Dihydroactinidiolide	Furanone	ripe apricot	1475	-	1.36±0.23a	-	-	-
2-Heptanone	Ketone	soapy	890	-	1.27±0.4a	-	-	0.34±0.01b
1-Octen-3-one	Ketone	mushroom, earthy	980	1.99±0.325a	-	-	0.77±0.14b	-
3-Octanone	Ketone	herbal, butter, resin	988	2.55±0.85a	-	1.72±0.15a	-	0.54±0.04a
6-METHYL-5-HEPTEN-2-ONE	Ketone	citrus, fruity	896	-	1.78±0.05a	-	-	-
Cyclohexanone <2,2,6-trimethyl->	Ketone	minty, spicy	1123	-	0.9±0.03a	-	-	-
3-Nonen-2-one	Ketone	oily, spicy, waxy	1110	-	0.28±0.01b	0.45±0.01a	-	-
Geranylacetone	Ketone	floral, green	1453	0.93±0.045b	6.33±1.40a	1.47±0.09b	0.89±0.24b	0.51±0.08b
Hexanoate <ethyl->	Ester	apple peel, fruit	998	6.01±2.64a	5.05±1.98a	3.83±2.08a	6.37±1.56a	5.50±0.87a
Geranyl propionate	Ester	sweet, fruity, balsamic	1384	-	0.93±0.02a	0.53±0.1a	0.56±0.01a	-
4-hexyl-1,3-Benzenediol	Phenol	seaweed, violet, floral, raspberry	1643	-	-	-	0.78±0.01a	-
2,4-Di-tert-butylphenol	Phenol	woody, balsamic	1515	1.44±0.065a	-	-	-	-
Furan <2-pentyl->	Furan	green bean, butter	988	2.27±0.78b	4.56±1.30a	6.39±0.51a	1.09±0.31b	1.023±0.29b
Isoterpinolene	Monoterpene	floral, herbal, citrus	1085	-	0.51±0.07a	-	-	-
l-Limonene	Monoterpene	lemon, orange	1024	-	-	-	0.99±0.01a	-
l-Phellandrene	Monoterpene	mint, spices	1005	-	-	-	-	0.61±0.02a

l-β-Pinene	Monoterpene	pine, resin	979	-	-	-	-	1.68±0.95a
α-Terpinene	Monoterpene	lemon	1017	-	-	-	-	1.34±0.09a
Linalool	Monoterpene	floral, lavender	1095	-	0.89±0.06a	0.59±0.01a	0.40±0.04a	0.59±0.07a
Myrtenol	Monoterpene	woody, pine, balsamic, sweet, mint	1195	6.51±1.46a	-	4.79±1.37ab	3.85±0.22ab	3.03±2.24ab
β-Cyclocitral	Monoterpene	mint	1116	-	7.74±0.49a	-	-	-
β-Citronellol	Monoterpene	citronella, floral	1225	0.48±0.07a	-	-	-	-
Nerol	Monoterpene	sweet	1228	9.65±1.29a	6.44±1.65a	4.28±0.64a	11.37±0.99a	5.81±1.99a
β-Cyclohomocitral	Monoterpene	camphor	1390	-	2.23±0.49a	-	-	-
Myrtanol <trans->	Monoterpene	herbaceous, camphor	1206	3.87±0.77a	-	1.66±0.48b	1.74±0.2b	1.40±0.58b
α-linalol	Monoterpene	floral	1099	-	-	1.74±0.39a	-	-
β-Ionone <(E)-	Monoterpene	seaweed, violet, floral, raspberry	1491	-	12.64±0.22a	-	-	-
α-Cubebene	Sesquiterpene	citrus, fruity	1351	0.52±0.025a	-	0.51±0.01a	-	-
α-Copaene	Sesquiterpene	woody, spicy	1376	2.19±0.965a	-	4.53±2.03a	0.85±0.36a	1.07±0.41a
β-Elemene	Sesquiterpene	herbal, waxy, fresh	1038	-	-	0.64±0.18a	-	-
β-Cubebene	Sesquiterpene	citrus, fruity	1387	-	-	1.86±0.83a	-	1.32±0.01a
γ-Elemene	Sesquiterpene	green, woody, oil	1391	0.38±0.005a	-	-	-	-
α-Guaiene	Sesquiterpene	woody, balsamic	1437	0.95±0.05a	-	0.88±0.01a	0.54±0.01b	-
Germacrene D	Sesquiterpene	woody, spicy	1480	-	-	0.87±0.01a	-	-
α-Humulene	Sesquiterpene	woody	1452	0.74±0.26ab	-	0.98±0.41a	0.50±0.14b	-
γ-Muurolene	Sesquiterpene	herbal, woody, spice	1476	-	-	0.98±0.41a	-	-
α-Muurolene	Sesquiterpene	woody	1496	-	-	2.41±0.57a	-	0.71±0.04b
β-Selinene	Sesquiterpene	herbal	1486	1.40±0.105a	-	-	-	-
δ-Guaiene	Sesquiterpene	woody	1439	-	-	-	0.40±0.01a	-
α-Gurjunene	Sesquiterpene	woody, balsamic	1412	0.55±0.05b	6.33±0.63a	6.86±1.98ab	4.21±0.81ab	0.68±0.02b
β-Maaliene	Sesquiterpene	woody, herbal	1490	5.53±1.385a	-	-	-	-

Odor descriptions were obtained from the literature based on database information (Flavornet, https://www.flavornet.org/flavornet.htm). Means within the same row followed by different lowercase letters are significantly different according to Tukey's test ($p < 0.05$). SP1, UFLA R1440; SP2, 2021-Dialelo-286; SP3, UFLA B556; SP4,2020-Uruguaiana-1192; SP5, BRS Cotinga.

To evaluate the importance and variation of VOC profiles among the five sweet potato genotypes, a variable importance in projection (VIP) score plot with a heatmap was generated (Figure 2B). The integrated evaluation of the VIP score plot and the heatmap revealed marked differences in the volatile profiles among the five evaluated genotypes. In PLS-DA (Figure 2B), compounds with VIP values > 1.0 were considered discriminant, as they contributed significantly to the separation among groups (Wold, Sjöström, & Eriksson, 2001). As shown in the figure, several terpenes, aldehydes, and ketones exhibited the highest VIP values. In contrast, others, such as phenylacetaldehyde, displayed low values (<0.2), indicating that they are not relevant for discriminating among genotypes. These results support the idea that the mere presence of a compound does not imply discriminative power; rather, its importance depends on the weight assigned by the multivariate model.

Among the most differentiated compounds (VIP > 1), the highlights were (Z)-2-heptenal, heptanal, trans-2-octenal, octanal, 3-methylbutanal, 2-heptanone, 3-nonen-2-one, 6-methyl- 5-hepten-2-one, 2,2,6-trimethylcyclohexanone, *β*-ionone, 1-octen-3-ol, myrtenol, *α*-linalool, *α*-terpineol, *β*-cyclocitral, dihydroactinidiolide, geranylacetone, 2-pentylfuran, vanillin, and isoterpinolene. These volatiles exhibited contrasting patterns in the heatmap, indicating significant variation in relative abundance among genotypes, thereby confirming their role as key chemical markers.

Genotype SP1 showed low predominance of sesquiterpenes (Figure 2A), accounting for only 12.26% of the total volatile area (Table 1), with a greater presence of aldehydes such as benzaldehyde, phenylacetaldehyde, 3-methylbutanal, hexanal, nonanal, and lipid oxidation derivatives, associated with sweet, green, and mild notes (Shahidi & Hossain, 2022). SP2 exhibited an intermediate profile, with relevant contributions from compounds such as *β*-Ionone, *β*-cyclocitral, nonanal, and geranylacetone, composing a more balanced aroma with herbal, fruity, and floral notes (R. Zhang et al., 2023). SP3 stood out for the predominance of sesquiterpenes, which constituted the largest chemical class in terms of number of compounds identified (11 compounds; Table 1), including *α*-gurjunene, *β*-elemene, germacrene D, *β*-cubebene, and *α*-muurolene, indicating greater activity of terpenoid biosynthetic pathways (Dudareva, Klempien, Muhlemann, & Kaplan, 2013) and resulting in a more intense, herbaceous, and woody aromatic profile, also marked by sweet notes.

The SP4 genotype presented elevated concentrations of compounds such as nerol, phenylacetaldehyde, and nonanal, which confer sweet, citrus, and slightly fatty notes. These markers suggest the combined involvement of the mevalonic acid (MVA) and methylerythritol phosphate (MEP) pathways, as well as metabolism derived from simple phenols and fatty acids (Dudareva et al., 2013; Schwab, Fischer, & Wüst, 2015). SP5 showed a complex profile, with emphasis on nerol, trans-myrtanol, n-nonanal, and other aldehydes and sesquiterpenes of high sensory impact, associated with fatty, green, sweet, and herbaceous notes (Abugu et al., 2025). These compounds helped distinguish this genotype from the others.

The uneven distribution of volatiles among the materials reinforces that each genotype possesses a distinct chemical signature, resulting from differential fluxes through biosynthetic pathways that modulate the formation of aldehydes, ketones, and terpenoids (Vranová, Coman, & Gruissem, 2013). The combination of VIP scores and heatmap analysis (Figure 2B) enabled the identification of compounds that play a major role in genotype separation, confirming the suitability of the PLS-DA model for this type of characterization. These findings are relevant for quality assessment, sensory selection, and breeding programs, as the volatile profile directly influences the aromatic properties and industrial application potential of each genotype.

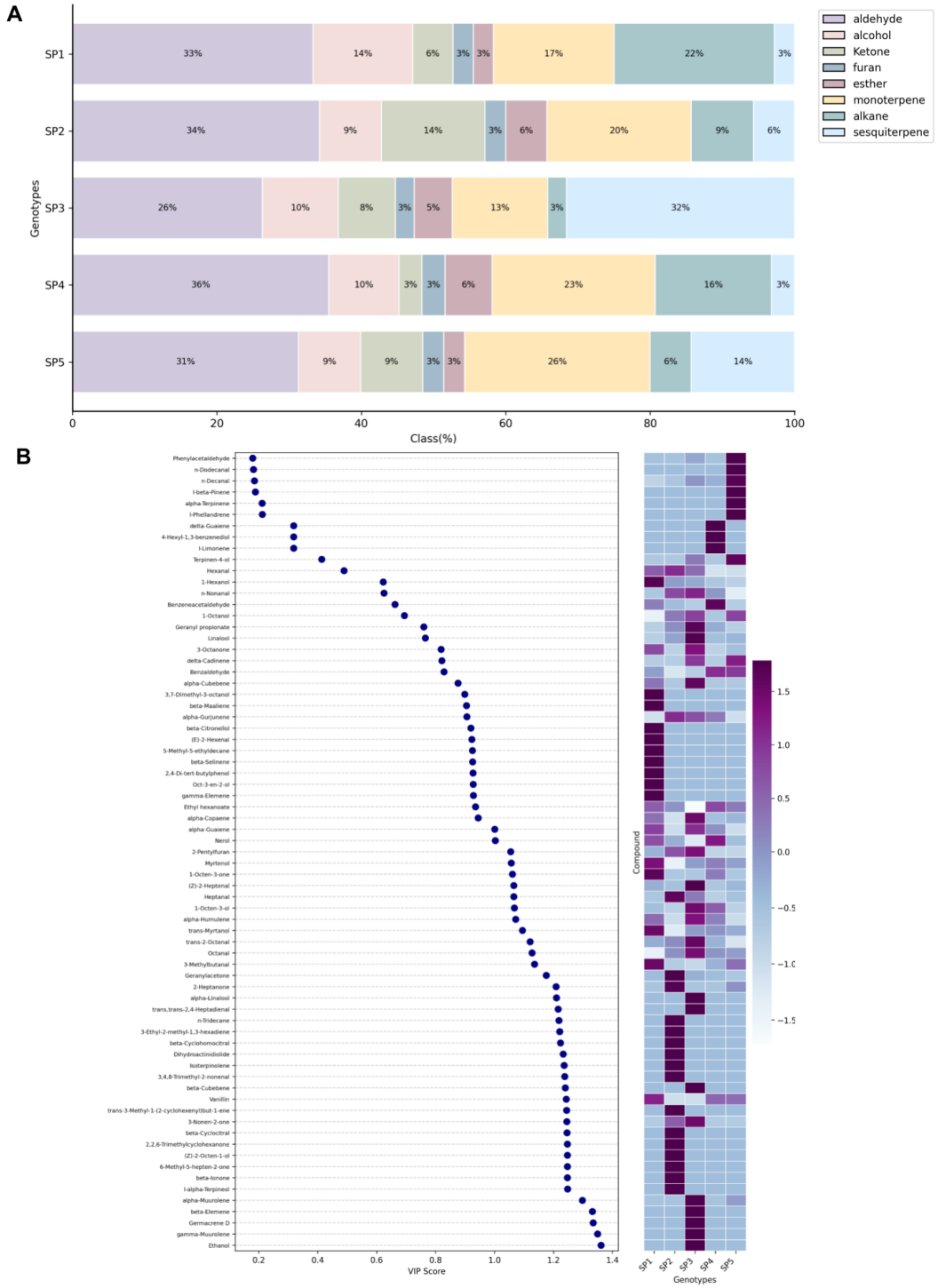

Figure 2. (A) Relative distribution of VOC chemical classes and (B) VIP scores and heatmap of discriminant volatile compounds obtained by PLS-DA for five sweet potato genotypes.

The trends observed in chemical composition become even clearer when analyzing the aroma wheel (Figure 3B), which organizes compounds according to their aroma notes and reveals the predominance of sweet, floral, green, and woody descriptors. These groups are consistent with the observation that many of the identified compounds belong to chemical classes such as aldehydes and terpenes, which are commonly associated with these aromas. When these same groups are projected onto the radar plots (SP1–SP5, Figure 3A), it is proposed that each genotype developed its own aromatic "personality". SP1, for example, contains compounds described with notes by more pronounced sweet notes and woody undertones; SP2 combined compounds described sweet, floral, and green with a slight menthol-like freshness; SP3 contained compounds described in the literature with an odor woody and mushroom like aromas; SP4 exhibited a milder and more subtle profile; whereas SP5 presented compounds together sweet and herbal notes. According to an earlier study by Jiang et al. (2023), sweet potato volatile compounds play a determining role in shaping the final aroma.

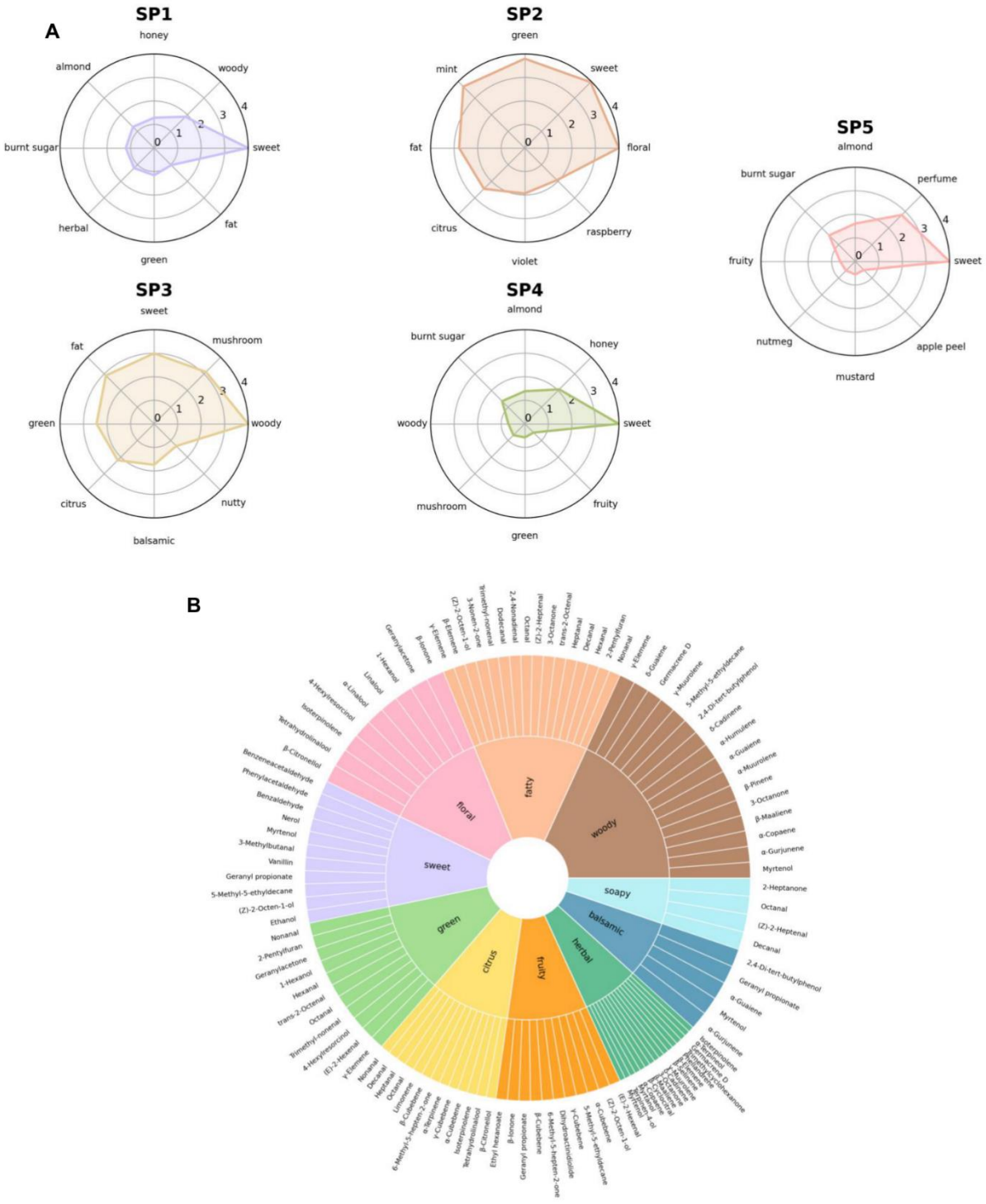

Figure 3. (A) Radar plots illustrating genotype-specific aroma profiles (SP1–SP5) and (B) aroma wheel showing the ten most frequent sensory descriptors associated with volatile compounds in sweet potato genotypes. Odor descriptions were obtained from the literature based on database information (Flavornet, https://www.flavornet.org/flavornet.htm).

Suggested mechanisms for the formation of aroma active volatile organic compounds (VOCs)

The possible formation pathways of some compounds detected in the studied genotypes are described in Table 2. Among them, two are classified as products of Strecker degradation (SD) of amino acids (Jiang et al., 2023; Nakamura, Ono, Yagi, & Miyazawa, 2013; Shen et al., 2024; Y. Wang & Kays, 2000; Yao, Zhang, Jiang, et al., 2024). Another eight compounds are associated with lipid breakdown (Jiang et al., 2023; Y. Wang & Kays, 2001; Yao, Zhang, Jia, et al., 2024); three are known to originate from carotenoid degradation (Jiang et al., 2023; Waché, Bosser-DeRatuld, Lhuguenot, & Belin, 2003; Y. Wang & Kays, 2000, 2001) and six are considered to result from the thermal release of glycosidically bound terpenes (Jiang et al., 2023; Shen et al., 2024; Tsai et al., 2021; Y. Wang & Kays, 2000, 2001; Yao, Zhang, Jia, et al., 2024).

Table 2. Suggested Mechanisms of Formation for Aroma Compounds

Suggested Mechanism of Formation	Aroma Compounds
Strecker degradation of aminoacids	
	Benzaldehyde
	Phenylacetaldehyde
Lipid oxidation	
	2-Pentylfuran
	Butanal
	Hexanal
	Heptanal
	(Z)-2-Heptenal
	Octanal
	Nonanal
	Decanal
Thermal release of glycosidically bound terpenes	
	α-Terpinene
	Linalool
	Myrtenol
	Nerol
	β-Citronellol
	α-Copaene
Carotenoid degradation	
	Geranylacetone
	β-Cyclocitral
	β-Ionone

In Strecker degradation, *α*-dicarbonyl compounds react with phenylalanine to form compounds such as phenylacetaldehyde and benzeneacetaldehyde (Table 2), which are responsible for floral and sweet aromas reminiscent of honey or soft fragrances (Jiang et al., 2023; Shen et al., 2024). In a previous study (Yao, Zhang, Jiang, et al., 2024), sweet potato cultivars with higher phenylalanine contents were also found to exhibit higher

concentrations of phenylacetaldehyde, reinforcing that the final VOC composition is strongly influenced by the amino acid acting as a precursor.

Sweet potato roots contain relevant amounts of unsaturated fatty acids, particularly polyunsaturated fatty acids (PUFAs), with linoleic, linolenic, and oleic acids being the most prominent (S. Wang, Nie, & Zhu, 2016). PUFAs act as key precursors in the formation of several lipid-derived volatile compounds, such as nonanal, decanal, heptanal, and 2-pentylfuran (Table 2), which were detected in the present study and are widely reported in cooked sweet potato (Shen et al., 2024; Tsai et al., 2021; Yao, Zhang, Jia, et al., 2024). These volatiles impart characteristic aroma notes, often described as herbaceous, green, or slightly fatty (Shahidi & Hossain, 2022). Studies indicate that these molecules can be generated both through lipid oxidation pathways and through interactions between lipids and reactive intermediates produced during the Maillard reaction (Abugu et al., 2025; Whitfield & Mottram, 1992).

Raw sweet potatoes contain terpenes in glycosylated forms (bound to sugar moieties), which are stable, nonvolatile, and odorless and function primarily as storage forms (Kays & Wang, 2002). These compounds release volatile terpenes only upon hydrolysis or when the roots are subjected to heating, thereby contributing to aroma development during cooking (Abugu et al., 2025; Rodriguez, Prinyawiwatkul, Aryana, King, & Xu, 2023).

In gas chromatography–olfactometry (GC–O) analyses, monoterpenes were identified, such as α-terpinene and linalool, and associated these compounds with the floral and sweet notes typical of cooked sweet potato (Y. Wang & Kays, 2000). Subsequent studies also reported that linalool and α-terpineol were not present in stored raw roots but became abundant after acid hydrolysis and thermal treatment (Rodriguez et al., 2023; Y. Wang & Kays, 2001).

Several terpene alcohols, including linalool, α-terpineol, citronellol, nerol, and geraniol, have been reported at high concentrations in recent studies on cooked sweet potato (Jiang et al., 2023; Tsai et al., 2021; Yao, Zhang, Jia, Deng, & Wang, 2023). In addition, GC-O analyses of cooked roots identified sesquiterpenes such as α-copaene, which are

associated with earthy, woody, baked potato–like notes and rose-like nuances (Abugu et al., 2025; Horvat, Arrendale, Dull, Chaoman JR., & Kays, 1991; Ohta et al., 1990; Shen et al., 2024).

The volatile compounds derived from carotenoid degradation, such as *β*-Ionone, dihydroactinidiolide (DHA), *β*-cyclocitral, geranylacetone, *β*-damascenone, and 5,6-epoxy-*β*- Ionone, have been found at high concentrations in cooked sweet potato (Jiang et al., 2023; T. Sun, Tadmor, & Li, 2020; Tsai et al., 2021). These volatiles are widely recognized for contributing aroma notes reminiscent of violet, wood, sweet flowers, tea, roses, and fruits in a variety of foods and beverages, including fruits, vegetables, wines, and teas (Winterhalter & Rouseff, 2001).

Among these compounds, *β*-Ionone has been specifically associated with a violet-like aroma when evaluated individually by GC-O (Y. Wang & Kays, 2000). During heating, *β*-Ionone and DHA emerge as some of the first products formed during the thermal cleavage of *β*-carotene in cooked sweet potato roots (Aisman, Syukri, Rini, Jaswandi, & Haiyee, 2024).

Studies also indicate that carotenoid degradation tends to reduce *β*-carotene content while simultaneously increasing the relative production of several VOCs derived from this class, regardless of the evaluated genotype (Aisman et al., 2024; Kays & Wang, 2000; Shen et al., 2024; Yao et al., 2023). These findings reinforce that *β*-carotene acts as a central precursor in the formation of most of these volatile compounds.

Multivariate analyses revealed marked differences in the volatile profiles among the five evaluated genotypes. The heatmap (Figure 4B) illustrates the relative distribution of compounds across genotypes. Lipid degradation-related compounds (such as hexanal, (E)-2-heptenal, and nonanal) were more abundant in SP3 (white-fleshed), which may be associated with oxidative susceptibility in these materials. In contrast, compounds derived from the thermal degradation of carotenoids (*β*-Ionone, *β*-cyclocitral, and geranylacetone) were more concentrated in SP2, a genotype characterized by intense orange flesh color and higher carotenoid content. Additionally, Strecker reaction markers (phenylacetaldehyde and benzaldehyde) were abundant in SP5

(purple-fleshed), indicating a greater contribution of amino acid degradation pathways during heating. These results suggest that each genotype possesses a differentiated volatile chemical composition, directly influenced by the predominant biochemical mechanisms underlying VOC formation.

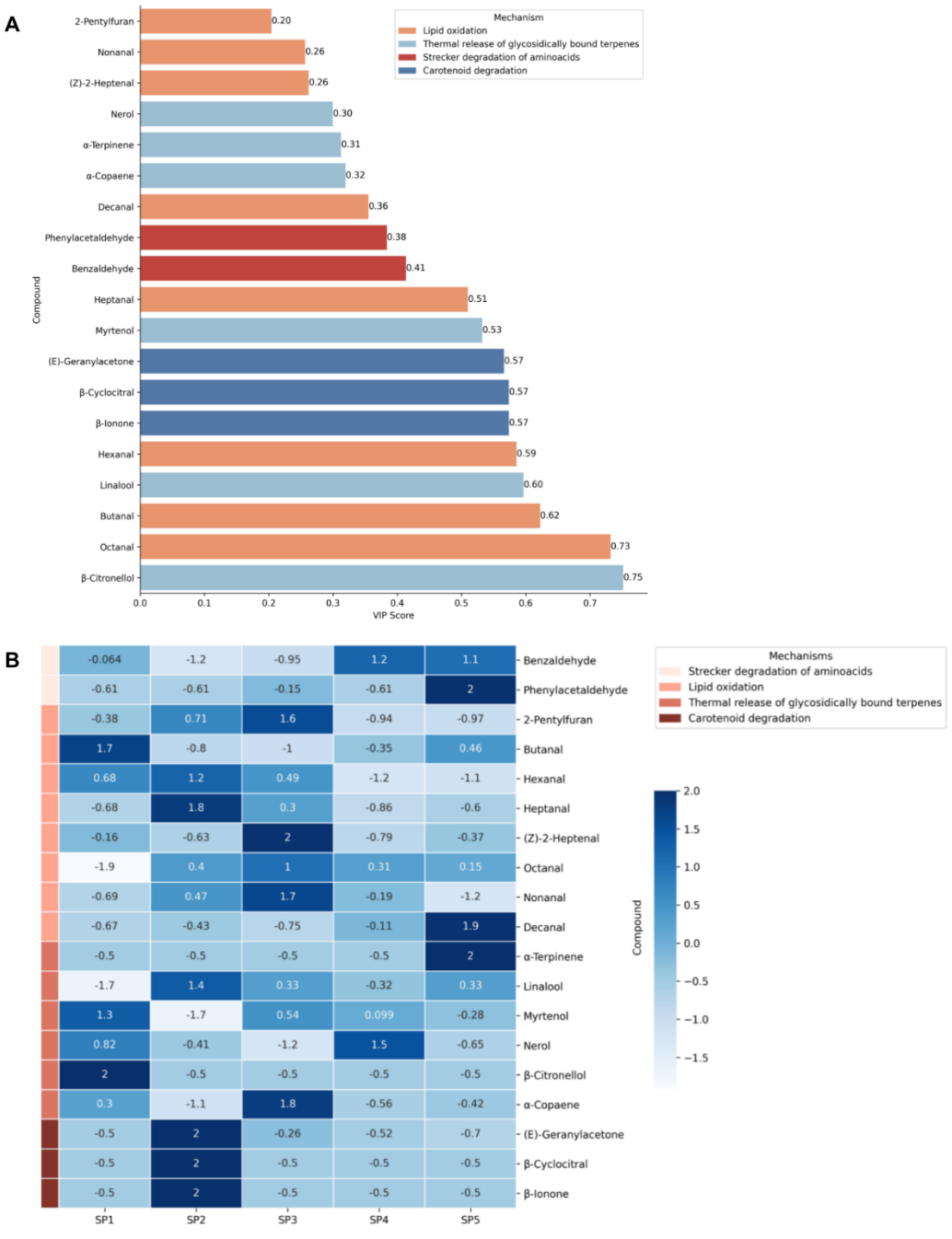

Figure 4. (A) VIP-selected volatile compounds categorized by formation pathways and (B) heatmap illustrating genotype-specific contributions of lipid oxidation, Strecker degradation, terpene release, and carotenoid degradation.

Analysis of VIP values (Figure 4A) suggests that discrimination among genotypes is driven by a set of compounds derived from distinct chemical pathways, reinforcing the multifactorial nature of the volatile profile. Of the selected compounds, those with the highest discriminant importance were associated with lipid oxidation and the thermal release of glycosidically bound terpenes, with *β*-citronellol (VIP = 0.75) and octanal (VIP = 0.73) standing out. These VOCs exhibited greater variation among genotypes and therefore contributed more to the multivariate model. The relevance of these markers is consistent with studies demonstrating the influence of lipid and terpene pathways on the formation of characteristic aromas in pigmented genotypes (Chen et al., 2025; Muchlinski et al., 2020).

In addition, compounds originating from the Strecker pathway, such as benzaldehyde (VIP= 0.41) and phenylacetaldehyde (VIP= 0.38), showed intermediate importance, indicating that although they can contribute to aromatic differentiation, their impact is less decisive than that of lipid- and terpene-derived compounds. Compounds related to carotenoid degradation, including *β*-Ionone (VIP = 0.57), *β*-cyclocitral (VIP= 0.57), and geranylacetone (VIP= 0.57), exhibited moderate VIP values, suggesting that this pathway may contribute to specific aroma nuances.

Conversely, compounds with lower VIP values, such as 2-pentylfuran (VIP= 0.20) and nonanal (VIP = 0.26), showed a limited role in discrimination, reflecting their relatively uniform distribution among the analyzed materials. These results reinforce that only a fraction of the detected VOCs can be decisive in explaining chemical differences among genotypes, in line with the rationale of supervised models previously described in the literature (R. Zhang et al., 2025).

Overall, the integrated evaluation of volatile profiles, multivariate analysis, and proposed formation pathways suggests that each sweet potato genotype has a distinct chemical composition. The observed differences between genotypes arise from the relative contributions of multiple metabolic pathways, such as lipid oxidation, carotenoid degradation, Strecker reactions, and thermal release of glycosidically bound terpenes. These observations can contribute to validating the use of VOC profiling combined with

multivariate analysis for genotype discrimination and aroma differentiation. From an applied perspective, the results reinforce the relevance of volatile composition as a criterion for breeding, sensory quality assessment, and the development of sweet potato-based products with differentiated aromatic profiles.

Acknowledgments

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TERCEIRA PARTE

3 CONSIDERAÇÕES FINAIS

O presente estudo realizou uma caracterização integrada de genótipos de batata-doce, demonstrando que as diferenças físico-químicas, bioquímicas e aromáticas estão fortemente associadas à coloração da polpa e ao fundo genético. Os genótipos de polpa roxa destacaram-se pelo elevado teor de compostos fenólicos e antocianinas, refletindo maior capacidade antioxidante, enquanto as de polpa alaranjada apresentaram altos níveis de carotenoides, confirmando seu potencial como alimentos biofortificados. Genótipos de polpa clara mostraram maior predominância de amido e açúcares, relevantes para aplicações tecnológicas específicas. Diferenças na atividade das enzimas polifenoloxidase e peroxidase indicaram distintos potenciais de escurecimento enzimático e estabilidade térmica, com implicações diretas para o processamento. A identificação de 72 compostos orgânicos voláteis e a aplicação de análises multivariadas permitiram a discriminação clara dos genótipos, evidenciando que as variações químicas se traduzem em perfis aromáticos distintos, associados a diferentes vias metabólicas e atributos sensoriais.

No entanto, como a avaliação sensorial foi inferida a partir do perfil químico dos voláteis, a ausência de análises sensoriais diretas com consumidores ou painéis treinados representa uma limitação do estudo, o que poderia fortalecer ainda mais a correlação entre composição química e percepção sensorial. Assim, estudos futuros são recomendados para incorporar análises sensoriais, testes de aceitação do consumidor, investigações sobre a estabilidade dos compostos bioativos e voláteis ao longo do armazenamento e da cadeia produtiva e métodos de processamento.

A batata-doce apresenta elevado potencial nutricional, funcional e tecnológico, e a caracterização desenvolvida neste trabalho foi eficiente para a discriminação varietal e para a valorização dessa cultura no âmbito da segurança alimentar, da inovação tecnológica e do desenvolvimento sustentável.

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