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✓ Prémios “Distinção CNOIV” 2022

Atribuídos nas áreas:

- Enologia
- Nutrição e Saúde
- Viticultura

✓ Prémio “Inovação CNOIV” 2022

Prémio “Distinção CNOIV Enologia”



Article

Effect of Barrel-to-Barrel Variation on Color and Phenolic Composition of a Red Wine

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Abstract: Tangible variation of sensory characteristics is often observed in wine aged in similar barrels. Barrel-to-barrel variation in barrel-aged wines was investigated in respect of the most important phenolic compounds of oenological interest. A red wine was aged in 49 medium-toasted oak (*Quercus petraea*) barrels from four cooperages, for 12 months. The resulting wines were evaluated for chromatic characteristics, anthocyanin-related parameters, total phenols, flavonoids and non-flavonoids phenols, flavan-3-ol monomers, and oligomeric and polymeric proanthocyanidins. PCA and ANOVA were applied to investigate the relationships between barrels and to assess cooperage and individual barrel effect. These cooperages influenced the wine similarly during aging. Anthocyanin-related parameters showed the highest variation, 25–39%, other phenolics varied 3–85%, and with two exceptions, chromatic characteristics changed 1.7–3%. The relationship between the number of barrels and the expected variation for each analytical parameter was calculated, as reference for future measurements involving barrel lots, either in wine production or experimental design.



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Phenolic changes during wine aging are a dynamic process yielding a huge variety of colorless products and pigments [3]. Their relative quantity depends on many factors [6].

Prémio “Distinção CNOIV Nutrição e Saúde”



Review

Valorization of Winemaking By-Products as a Novel Source of Antibacterial Properties: New Strategies to Fight Antibiotic Resistance

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Abstract: The emergence of antibiotic-resistance in bacteria has limited the ability to treat bacterial infections, besides increasing their morbidity and mortality at the global scale. The need for alternative solutions to deal with this problem is urgent and has brought about a renewed interest in natural products as sources of potential antimicrobials. The wine industry is responsible for the production of vast amounts of waste and by-products, with associated environmental problems. These residues are rich in bioactive secondary metabolites, especially phenolic compounds. Some phenolics are bactericidal/bacteriostatic against several pathogenic bacteria and may have a synergistic action towards antibiotics, mitigating or reverting bacterial resistance to these drugs. Complex phenolic mixtures, such as those present in winemaking residues (peppers, skins, stalks, leaves, and especially seeds), are even more effective as antimicrobials and could be used in combined therapy, thereby contributing to management of the antibiotic resistance crisis. This review focuses on the potentialsities of winemaking by-products, their extracts, and constituents as chemotherapeutic antibacterial agents.

Keywords: grape by-products; antibacterial activity; antibiotic resistance; phenolic compounds



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Prémios “Distinção CNOIV Viticultura”

✓ Artigo Científico publicado em 2020 no “Physiologia Plantarum” journal: "An apoplastic fluid extraction method for the characterization of grapevine leaves proteome and metabolome from a single sample" de um coletivo de autores representado por Joana Figueiredo;

✓ Artigo Científico publicado em 2021 no “Journal of Experimental Botany”: "Transcriptional, hormonal, and metabolic changes in susceptible grape berries under powdery mildew infection" de um coletivo de autores representado por Ana Margarida Fortes.

Physiologia Plantarum

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An apoplastic fluid extraction method for the characterization of grapevine leaves proteome and metabolome from a single sample

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The analysis of complex biological systems keeps challenging researchers. The main goal of systems biology is to decipher interactions between components of a system. This requires large-scale analytical approaches including transcriptomics, proteome and metabolome and more specialized OMICS such as epigenomics and lipidomics. Studying disease resistance in plants is a good example of this kind of dynamics. Plant apoplast, the cellular compartment external to the plasma membrane including the cell wall, is particularly demanding to analyze. Despite its complexity, it is a key compartment for plant defense against off-growth to biotic stress. Its dynamics is still poorly known due to the lack of efficient extraction processes adequate in such plant system. Analyzing whole plant apoplast is a challenge that can be overcome by extracting apoplastic fluid. In this work we propose a new method to extract apoplastic fluid from grapevine leaves. Among the most important that one needs to do is a wide characterization of the apoplast to a essential for a deeper understanding of its physiology and cellular mechanisms. Here, we describe, for the first time, a semi-automated workflow for the extraction of grapevine apoplastic proteins and metabolites from leaves on a single sample, compatible with high-throughput analysis. Protein and metabolite profiles from non-infected (*Vitis vinifera* L.) grapevines and “Renau” was directly used for proteomic and metabolomic analysis. The proteome was analyzed by LC-MS/MS and 2D-PAGE. Two hundred proteins were identified, being 100 unique biological functions. The metabolome profile through PGC-MS allowed the identification of 514 unique putative compounds revealing a broad spectrum of molecular classes.

Abbreviations: APF, apoplastic fluid; C16:0, palmitic acid; C16:1, trans-3-hexadecenoic acid; C17:0, margaric acid; C18:0, stearic acid; C18:1, oleic acid; C20:0, arachidic acid; C20:1, linoleic acid; C22:0, behenic acid; C22:1, behenic acid; C24:0, behenyl acetate; C24:1, behenyl oleate; FA, fatty acid; MS, mass spectrometry; MZ, mass-to-charge ratio; PGC, proton-coupled gas chromatography; PGC-MS, proton-coupled mass spectrometry; PGC-MS/MS, signal peptide; VAC, vacuum; VACUUM, vacuum-infiltration centrifugation.

Joana Figueiredo and Ana Rita Gouveia have contributed equally to this work.

Ana Rita Matos, Marta Sousa Silva, Andreia Figueiredo are co-senior authors on this work.

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RESEARCH PAPER

Transcriptional, hormonal, and metabolic changes in susceptible grape berries under powdery mildew infection

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Abstract

Grapes (*Vitis vinifera*) berries are extremely sensitive to infection by the biotrophic pathogen *Erysiphe necator*, causing powdery mildew disease with deleterious effects on grape and wine quality. The combined analysis of the transcriptome and metabolome associated with this biotrophic infection has not been previously carried out in any fruit. To obtain a detailed picture of hormonal and metabolic responses to infection, we collected healthy and naturally infected *V. vinifera* cv. Carignan berries were collected at two developmental stages: late green (EL2) and early varaison (EL3). RNA sequencing was performed using RNA-seq and GC-electroforese. Metabolite analysis was performed using LC-MS/MS and LC-Capillary electrophoresis. The pathogen infection was able to activate defense mechanisms with the involvement of salicylic acid and jasmonic acid and to accumulate defense-associated metabolites (e.g. phenylpropanoids). The defensive strategies also included the synthesis of secondary metabolites (e.g. terpenoids). However, the pathogen infection was not enough to restrict fungal growth. The fungal metabolic program during infection involves secretion of effectors related to effecter-triggered susceptibility, carbohydrate-active enzymes and activation of sugar, fatty acid, and nitrogen uptake pathways. The metabolic response to infection was mainly driven by the presence of metabolites such as gallic, sinapic, and catechins acids and resveratrol, which can be used to monitor early stages of infection.

Keywords: Erysiphe necator, grapevine, hormonal profiling, metabolome, plant defense, powdery mildew, transcriptional susceptibility, metabolite analysis

Acknowledgments: CA/Green, carbonyl-active enzymes; EL2, late green stage; EL3, early varaison stage; ETI, effector triggered immunity; PAMP: pathogen-associated molecular pattern; PM, powdery mildew; PR1, pattern-recognition receptor; STI, DAMP: triggered immunity.

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Prémio “Inovação CNOIV”

- ✓ Artigo Científico publicado em 2020 na revista da especialidade “Scientific Reports”: "Integrating metabolomics and targeted gene expression to uncover potential biomarkers of fungal/oomycetes associated disease susceptibility in grapevine" de um coletivo de autores representado por Marisa Maia;

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Integrating metabolomics and targeted gene expression to uncover potential biomarkers of fungal/oomycetes-associated disease susceptibility in grapevine

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Vitis vinifera, one of the most cultivated fruit crops, is susceptible to several diseases particularly caused by fungus and oomycete pathogens. In contrast, other *Vitis* species (American, Asian) display different degrees of tolerance/resistance to these pathogens, being widely used in breeding programs to introgress resistance traits in elite *V. vinifera* cultivars. Secondary metabolites are important players in plant defence responses. Therefore, the characterization of the metabolic profiles associated with disease resistance and susceptibility traits in grapevine is a promising approach to identify trait-related biomarkers. In this work, the leaf metabolic composition of eleven *Vitis* genotypes was analyzed using an untargeted metabolomics approach. A total of 190 putative metabolites were found to discriminate resistant/partial resistant from susceptible genotypes. The biological relevance of discriminative compounds was assessed by pathway analysis. Several compounds were selected as promising biomarkers and the expression of genes coding for enzymes associated with their metabolic pathways was analyzed. Reference genes for these grapevine genotypes were established for normalization of candidate gene expression. The leucanthocyanidin reductase 2 gene (*LAR2*) presented a significant increase of expression in susceptible genotypes, in accordance with catechin accumulation in this analysis group. Up to our knowledge this is the first time that metabolomic constitutive biomarkers are proposed, opening new insights into plant selection on breeding programs.

Grapevine (*Vitis vinifera* L.) is one of the most cultivated fruit plants in the world, with an important economic impact in wine and table grape industries. Of the 80 known and globally distributed *Vitis* species^{1,2}, *Vitis vinifera* L. is the mostly used in viticulture. As a result of its easy cultivation, vineyard longevity and numerous applications, in 2018, the global surface area for grapevine production was 7.4 Mha³. Grapevine cultivation requires specific knowledge about the main diseases and pests that affect the crop, such as downy mildew (*Pseudomonas* (Berk. & Curt.) Berk. et de Toni), powdery mildew (*Erysiphe necator* syn. *Uncinula necator* (Schweinf.) Burrell), gray mold (*Botrytis cinerea* Pers.) and black rot (*Gymnosporangium juniperi* (Ellis) Vials & Ravaz).

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