



Cercosporin production by *Cercospora coffeicola* isolates: spectrophotometry and HPLC quantification and image analysis

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Abstract

Cercosporin has excellent properties of photosensitization that have been widely used in organophotocatalyst and photodynamic therapy as well as an antimicrobial agent. Therefore, there is a need to quantify it accurately with accessible methods. A comparative analysis of cercosporin quantification obtained by spectrophotometry (SPEC) and high-performance liquid chromatography (HPLC) was performed for nineteen *Cercospora coffeicola* isolates from different coffee-producing municipalities in Brazil. Image analysis of cercosporin crystals was performed in isolates with either high or low production of the toxin. Our results show that SPEC and HPLC are equally valid for the cercosporin evaluation of *C. coffeicola* cultures grown in vitro. The isolates with high cercosporin production had a higher crystal number and size when compared to the one with low cercosporin production.

Keywords Microscopy · Toxin · High-performance liquid chromatography · Methods

Introduction

Perylenequinones are a class of photoactivated polyketide mycotoxins produced by fungal plant pathogens that notably produce reactive oxygen species with visible light (Newman and Townsend 2016). The cercosporin produced by *Cercospora* and some *Pseudocercospora* and *Colletotrichum* species is the best-studied perylenequinone (Jonge et al. 2018; Gunasinghe et al. 2016). Cercosporin is a highly coveted

red–purple polyketide produced by fungal hyphae for its excellent properties of photosensitization, being, therefore, widely investigated for its photophysics, photochemistry and photobiology aspects (Guedes and Eriksson 2007; Daub and Chung 2009; Souza et al. 2019; Zhou et al. 2021). Furthermore, it has shown potential in medicine regarding the cytotoxic effect on human tumor cells (Mastrangelopoulou et al. 2019). *Cercospora coffeicola*, the causal agent of brown eye spot in coffee trees—a disease that can cause a reduction yield of up to 30%, is the fungus that produces cercosporin (Pozza et al. 2010; Vale et al. 2019).

A simple and accessible method for the extraction and quantification of cercosporin by spectrophotometry (SPEC) was proposed by Jenns et al. (1989) and is used for cercosporin quantification in several *Cercospora* species, such as *C. coffeicola* (Vale et al. 2019; Souza et al. 2019). Cercosporin quantification has also been performed by high-performance liquid chromatography (HPLC) for *Cercospora beticola*, *Cercospora* cf. *flagellaris*, *Colletotrichum fioriniae*, *Pseudocercospora capsellae* (Gunasinghe et al. 2016; Jonge et al. 2018; Rezende et al. 2020). However, there are no reports of studies comparing the cercosporin concentration in SPEC x HPLC. Therefore, the goal of this study was to perform a comparative quantification of cercosporin

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produced by different *C. coffeicola* isolates using two different methodologies, SPEC and HPLC. Additionally, cercosporin crystals obtained from representative isolates (with low and high cercosporin production) were displayed by laser confocal microscopy.

Material and methods

Sample preparation

Nineteen monoconidial isolates of *C. coffeicola* were obtained from the fungal specimen collection of the Laboratory of Parasitism Physiology, Federal University of Lavras, Minas Gerais State, Brazil. The isolates were cultured on 9-cm-diameter Petri dishes containing 9 mL of PDA (potato dextrose agar) culture media maintained in a BOD (Bio-Oxygen Demand) incubator adjusted for a 12-h photoperiod at 25 °C for 12 days (Vale et al. 2019).

Spectrophotometric analysis

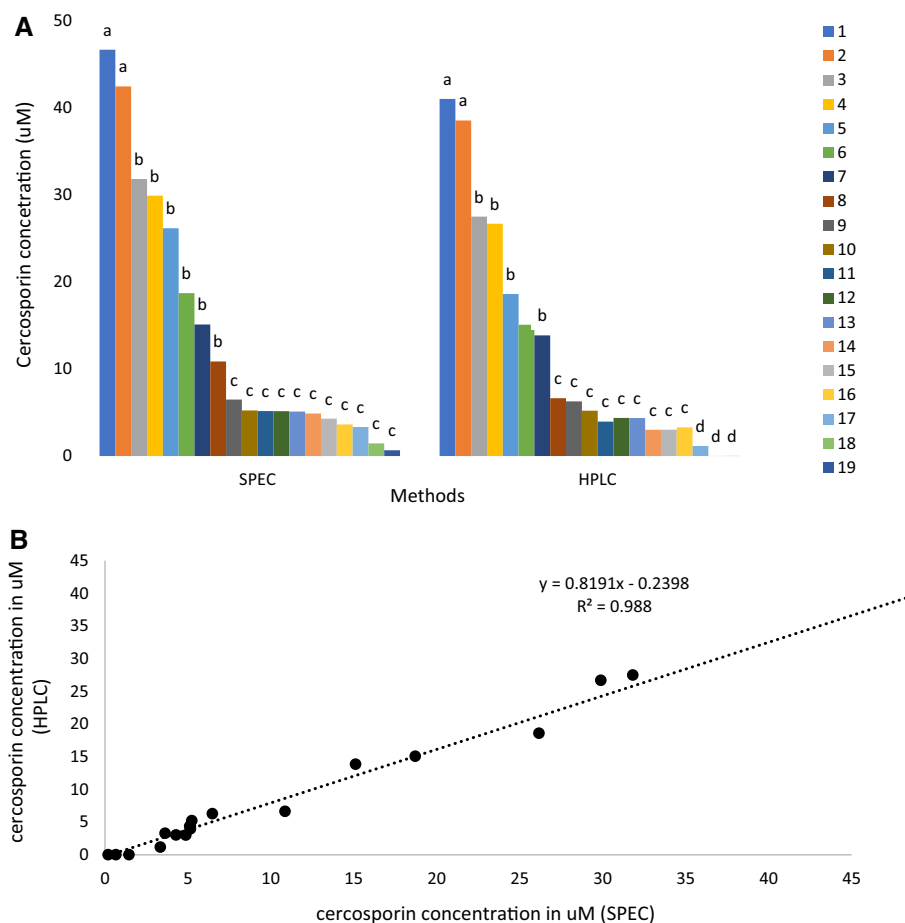
Four mycelial plugs (6 mm diameter) collected from each Petri dish colony were immersed in 8 mL of 5 N KOH and

maintained in the dark for 4 h (Jenns et al. 1989). Afterward, the SPEC analysis was performed using a spectrophotometer reader PowerWave XS (Biotek®) at an absorbance of 480 nm (Jenns et al. 1989). The cercosporin concentration was calculated using a molar absorption coefficient (ϵ) of 23,300 $\text{mM}^{-1} \text{cm}^{-1}$.

HPLC analysis

Concerning the HPLC analysis, the equipment used was an LC-20AT pump, DGU-20A5 degasser, SIL-20A HT automatic injector, CTO-20^a, detector UV-Vis SPD-20^a and CBM-20A interface model. The column was Shim-pack CLC-ODS (15 cm \times 6.0 mm D.I., 5 μm) connected to pre-column Eclipse XDB-C18 (4.6 \times 12.5 mm, 5 μm). The chromatographic method used was gradient mode analysis with a mobile phase composed of 5% (v/v) acetic acid in water (eluent A), acetonitrile (eluent B) at 1.5 mL min^{-1} . A linear gradient is adapted from Gunasinghe et al. (2016) ranging from 50 to 70% of eluent B for the first eight minutes followed by a change to 100% of eluent B within a period of one minute and maintained for six more minutes. Afterward, a new change to 50% of eluent B with the linear gradient within 10 min was performed for column rebalance. The analytical

Fig. 1 Comparison cercosporin concentrations in 19 *Cercospora coffeicola* isolates quantified by SPEC and HPLC methods (a). Bars followed by the same letters do not differ significantly at Scott Knott's test ($p \leq 0.05$). Correlation cercosporin concentrations of 19 *C. coffeicola* isolates in SPEC method versus HPLC method (b)



curve for cercosporin quantification was built using a standard stock solution of this toxin from *Cercospora hayii* (C6696 Sigma-Aldrich) at concentration 4×10^{-4} mol.L⁻¹. Standards and samples were filtered into a 0.45- μ m-pored filter syringe (Millipore®) before injection of 20 μ L into the chromatograph (in triplicate). The cercosporin quantification in the samples was calculated based on the peak retention time and compared to the standard curve of this toxin.

The linearity was adjusted using the correlation coefficient from the analytical curve (straight line) fitted from cercosporin analytical data in the pre-chosen concentration range.

The limit of detection (LOD) and limit of quantitation (LOQ) were calculated according to the International Conference on Harmonization guidelines: LOD = 3.3 SDb/a and LOQ = 10.0 SDb/a, where SDb represents the standard deviation of the y-intercept and a is the calibration curve slope.

Spectroscopic analysis

The spectroscopic analysis was made with the isolate 19 (higher cercosporin producer). All NMR measurements were done in a Bruker 14.1 T (600 MHz for hydrogen frequency) AVANCE III equipment with 5 mm TCI cryoprobe head, using deuterated chloroform as a solvent and keeping the temperature at 25 °C during all the experiments.

Image analysis of cercosporin crystals

A laser confocal microscope was used for image analysis of cercosporin crystals. Agar plugs containing mycelium of two isolates with contrasting cercosporin production (low and high) were aseptically transferred to freshly prepared malt extract agar MEA (MEA: 20.0 g L⁻¹ malt extract, 20.0 g L⁻¹ glucose, agar 15.0 g L⁻¹ and peptone 1.0 g L⁻¹) and incubated for three weeks in an incubator at 20 °C (Gunasinghe et al. 2016). Fragments with 0.5 cm diameter were positioned above coverslips for observation using an inverted scanning laser confocal Zeiss Observer Z1 LSM780 with the Zen 2012 software. The image acquisition was performed done using EC Plan-Neofluar 100 \times /1.3 oil M27 objective, 1024 \times 1024 resolution, Ch2 detector, beam splitter MBS 543 nm, pinhole 106 μ m, 543 nm excitation laser at 20%, master gain 600, digital gain 1, digital offset gain -46 and emission filter range at 600–710 nm. Bright-field images were acquired using the T-PMT detector, master gain 423, digital gain 1 and digital offset gain -62. The images were edited using the Fiji-ImageJ and Corel Draw software.

Experimental design and statistical analysis

The experiment was conducted in a randomized complete block design with 19 treatments (isolates) evaluated in two methods (SPEC and HPLC) and three replicates. The experimental plot consists of three Petri dishes. The means of the treatments were grouped by the Scott–Knott test ($p \leq 0.05$).

Results and discussion

Our results showed that cercosporin produced by the 19 *C. coffeicola* isolates varied substantially among isolates, ranging from 0.2 to 48.65 μ M to SPEC and 1.15 to 37.26 μ M to HPLC (Fig. 1a). The amount variability of cercosporin produced by *C. coffeicola*, *C. piaropi*, *Cercospora cf. alchemillicola* and *Pseudocercospora capsellae* isolates has already been reported by other authors using the SPEC method (Gunasinghe et al. 2016; Silva 2018; Vale et al. 2019). Cercosporin biosynthesis is affected by external factors such as light, temperature, pH, nutrient supply and incubation time (Jenns et al. 1989; Vale et al. 2019; Zhou et al. 2021). Since the factors mentioned above have been standardized in the present study, possibly the isolates have intrinsic factors that influence the production of the toxin in hyphae, resulting in different cercosporin concentrations. The selection of isolates with the ability to produce cercosporin associated with enhancers (e. *Bacillus velezensis*, *Lysinibacillus* sp.) will allow more potential industrial applications with cercosporin (Zhou et al. 2021).

The cercosporin quantification obtained by SPEC and HPLC showed a significant linear association between the methods, indicating a direct relationship between them (Fig. 1b). The HPLC method was validated since it presented selectivity, linearity, limits of detection (8.8 E-7 mol/L) and limits of quantification (2.9 E-6 mol/L), retention time mean of 4.8 min and robustness, which generated reproducible and reliable results in the quantification of cercosporin (Fig. 2). The spectrophotometry effectiveness for cercosporin quantification must be emphasized for its speed, easy execution and low cost of reagents and equipment compared to the HPLC method (Kumar et al. 2010).

Regarding the SPEC analysis, the most common problems found in applying this methodology are specificity and selectivity since other substances can absorb UV radiation in the same wavelength (Oliveira et al. 2010). Our results indicate that both methods can be used for cercosporin quantification and the chosen one depends on the study objective and available equipment in the laboratory.

The results of spectroscopic analysis of cercosporin from *C. coffeicola*: ¹H NMR spectrum (600 MHz, CDCl₃) δ 0.65 (d 6.11), 2.91 (dd 6.11,13.25), 3.39 (sext 6.37), 3.59 (dd 7.13, 13.25), 4.21 s, 5.75 s, 7.08 s and 14.83 s. ¹³C {¹H}

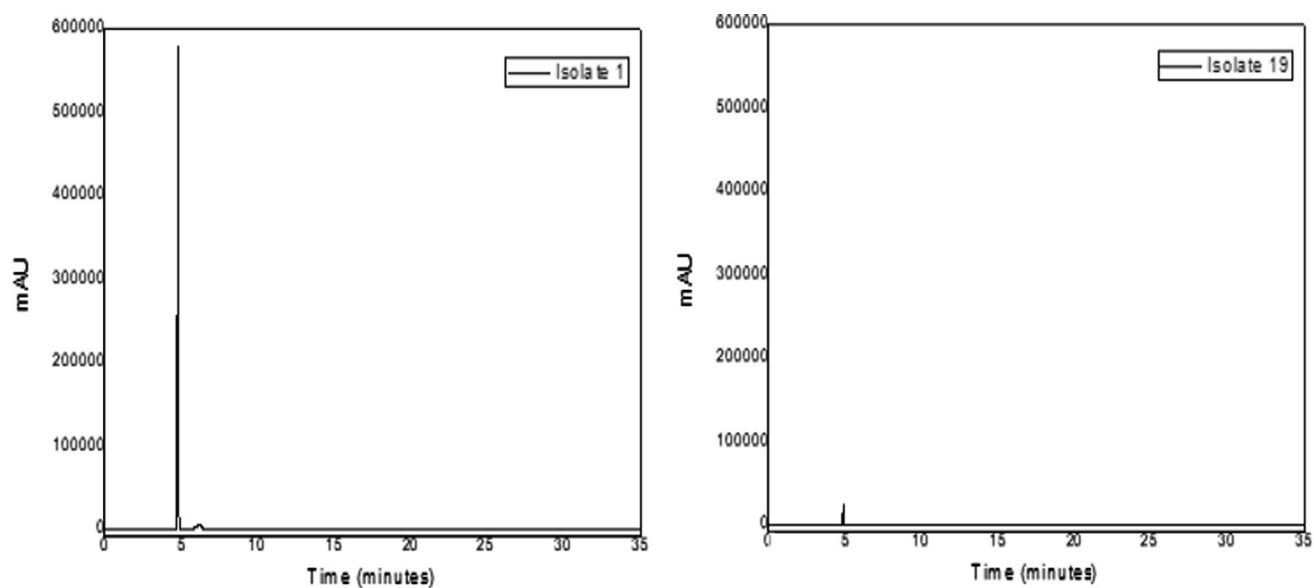


Fig. 2 Chromatograms obtained from HPLC analysis for isolate 1 (high producer cercosporin) and isolate 19 (low producer cercosporin)

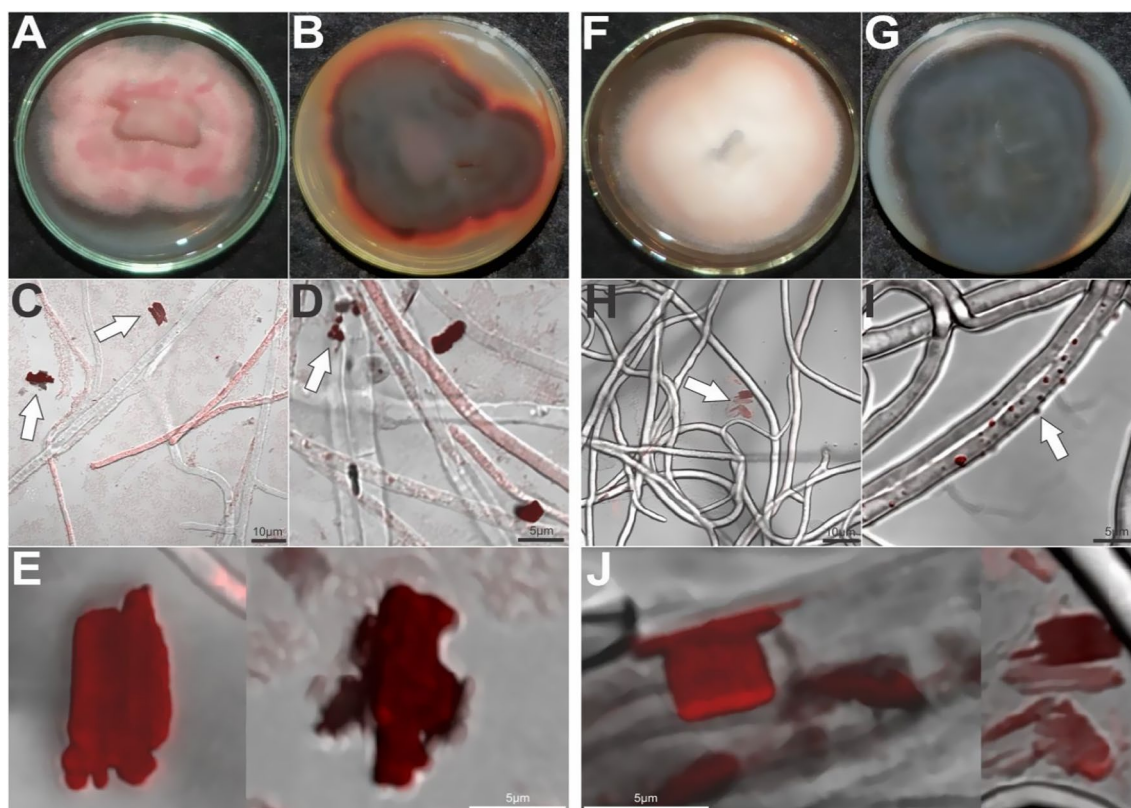


Fig. 3 *Cercospora coffeicola* isolate 1 with high-cercosporin production (a–e) and isolate 19 with a low-cercosporin production (f–j) after incubation at 20 °C under cool fluorescent white light for 3 weeks in

MEA medium. a–b and f–g: Colonies morphology. Laser scanning confocal microscopy: c–d and h–i: aerial mycelia and cercosporin crystals (arrows). e and j: cercosporin crystals magnification

(125 MHz, CDCl₃) 23.4, 42.2, 61.2, 68.1, 92.6, 108.2, 109.3, 112.9, 127.9, 130.5, 135.2, 152.8, 163.4, 167.5 and 181.8 (Supplemental Figs. 1 and 2). The NMR data are in agreement with the values reported by Morgan et al. (2010).

Two representative *C. coffeicola* strains with high or low cercosporin production were selected for imaging characterization using laser confocal microscope. For the high producer isolate (1) crystals dispersed in media and adhered to the hyphae surface were observed, with 1.5–5 µm width and 3–10 µm length and with 0.5–1 µm diameter, respectively (Fig. 2a–e). Regarding isolate 19, cercosporin crystals with 1.5–3.5 µm width and 3–5 µm length were dispersed in the culture medium and lower crystals (0.5–1.5 µm diameter) were found adhered to the hyphae surface (Fig. 3d and i, arrow). After release, crystals are deposited in media, and subsequently can aggregate and give rise to larger forms (Fig. 3c and h, arrow). *C. coffeicola* showed similar cercosporin crystals to *Pseudocercospora capsellae* (Gunasinghe et al. 2016) and the quantification of cercosporin showed relation with presence crystals.

Conclusions

HPLC and SPEC methodologies are equally valid for the cercosporin evaluation from cultures of *C. coffeicola* grown in vitro. The isolate with high cercosporin production had a higher crystal number when compared to the one with low cercosporin production.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s11696-021-01965-5>.

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Authors' contributions LGG and MLVR conceived and planned the experiments. WDS and ART carried out HPLC analysis. SIM carried out image analysis of cercosporin crystals. DMSB, JBR and SOA carried out *C. coffeicola* isolates in vitro and spectrophotometric analysis. AGF was responsible for the NMR measurements and ¹H/¹³C attributions. TR carried out samples to spectroscopic analysis. EAP provided material and contributed to interpretation of results. LGG, DMSB and MLVR analyzed the data, finalized the figures and drafted the manuscript. All authors read and approved the final manuscript.

Data availability The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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