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2	INFLUENCE OF ENVIRONMENTAL FACTORS ON TENUAZONIC ACID
3	PRODUCTION BY Epicoccum sorghinum: AN INTEGRATIVE APPROACH OF
4	FIELD AND LABORATORY CONDITIONS
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Abstract

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Sorghum is the fifth most cultivated and consumed grain in the world. However, this grain is frequently contaminated with toxins from fungi. The present study evaluated the effects of environmental factors on tenuazonic acid (TeA) production by Epicoccum sorghinum in the field and in controlled laboratory conditions. In this study, 50 sorghum grain samples were collected from summer and autumn growing seasons and analyzed for TeA contamination using LC-MS/MS. To further understand the ecophysiology of this fungus, an isolated strain of E. sorghinum from the field was investigated for its development and TeA production under controlled environmental conditions in the laboratory. In the ecophysiological investigation, the effects of water activity (0.90, 0.95, 0.99) and temperature (18, 22, 26 and 30 °C) were evaluated on the radial growth, enzymatic production and expression of TASI, which is the gene involved in TeA production. Results showed that in the field, the summer season presented the highest TeA average level in the grains (587.8 µg/kg) compared to level found in the autumn (440.5 µg/kg). The ecophysiological investigation confirmed that E. sorghinum produces more actively TeA under environmental conditions simulating the summer season. Optimum growth, maximum TAS1 gene expression, and higher extracellular enzymatic production were observed at 26°C with a water activity of 0.99. Pearson correlation analyses showed that the production of TeA highly correlates with fungal growth. The present study demonstrates that abiotic factors in a combined approach of field and laboratory conditions will assist in predicting the driving environmental factors that could affect growth of E. sorghinum and TeA production in sorghum grains.

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60 **Keywords:** Sorghum; Ecophysiology; Gene expression; *Phoma sorghina*; LC-MS/MS

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1. Introduction

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64 Sorghum is a crop with increasing global importance in food, animal feed, energy 65 production and other diverse industrial uses [1]. According to the USDA [2], sorghum 66 production worldwide in 2016/2017 was estimated to be 62.36 million metric tons, which 67 represented an increase of 4.03 million tons compared to 2015/2016. However, one of the 68 major biotic constraint to sorghum improvement and productivity is fungal 69 contamination, especially in the field when grain development can coincide with 70 favorable weather conditions for fungal growth and subsequent mycotoxin formation [3]. 71 Among the diverse fungi reported to contaminate sorghum grain, Epicoccum sorghinum 72 (also known as *Phoma sorghina*), is commonly described as one of the major fungal 73 contaminants at pre- and post-harvest stages [3,4,5,6]. This fungus is a producer of 74 tenuazonic acid (TeA), a mycotoxin that is considered a potent inhibitor of protein 75 biosynthesis and has been reported to cause acute toxicity to several animals [7,8,9]. Moreover, TeA is considered to be responsible for causing Onyalai, a human 76 77 hematological disorder [10]. 78 In recent years, TeA has gained considerable attention in the scientific community due 79 to their frequent contamination in food and animal feed. However, most available data 80 about TeA occurrence has been linked to the presence of Alternaria spp., while little is 81 known about TeA production by E. sorghinum. In 2011, the European Food Safety 82 Authority [11] published a report on the risks of *Alternaria* toxins for animal and public 83 health. TeA was considered unlikely to be of human health concern. However, only a 84 few data on the occurrence of TeA in food commodities were available at that time and 85 the TeA uptake estimation was based on chronic dietary exposure of adult populations 86 More recently Rychlik et al. [13] determined that TeA contamination on

sorghum/millet-based food represents a potential risk to infant health. These recent

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findings raised more concerns about health and safety of the TeA mycotoxin. As part of effective crop protection strategy, the understanding of the ecophysiology of fungal pathogens as well as the occurrence of mycotoxins triggered by environmental conditions, are essential to better understand and prevent mycotoxin contaminations. Our recent study described the identification of the TeA biosynthetic gene (TASI) in Epicoccum sorghinum [14]. This study enabled us to investigate the TeA biosynthesis in more detail in the present study. Moreover, there are no data on the ecophysiology of E. sorghinum as well as the effect of environmental factors linking the TeA occurrence in the field. Therefore, this study aims to integrate molecular and ecological approaches to better understand the key abiotic factors in TeA production by E. sorghinum. For that, we

evaluated whether growing seasons (summer and autumn) affect the occurrence of TeA mycotoxin in sorghum grains. In Brazil, these seasons have different temperatures and humidity levels. Therefore, controlled laboratory experiments simulating field conditions with a field isolate of E. sorghinum was also investigated under different temperatures

and water activities (a_w). These two environmental parameters were correlated with

fungal growth and gene expression of TeA as well as enzymatic activity.

2. Material and methods

2.1. Field study

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Cultivation and sampling of sorghum grains occurred from November 2012 to May 2013 to determine the influence of growing seasons (summer and autumn) on the occurrence of TeA in sorghum grains. A total of 50 sorghum grain samples (25 from each growing season) were collected in a sorghum plantation owned by the São Paulo Agency for Agribusiness Technology (APTA) (Votuporanga, the state of São Paulo, latitude 20° 28'

113 S, longitude 50° 04' W). APTA uses the best practice for sorghum cultivation in Brazil. 114 The cultivar DKB 550 (Dekalb seeds), commonly grown in Brazil, was used for both 115 growing seasons. The sowing of summer and autumn crops occurred in November of 116 2012 and February of 2013, respectively, with a distance of 0.5 m between rows and a 117 final population of 180 000 plants ha⁻¹. 118 For sampling, a stratified random sampling design was followed [15]. The experimental 119 area used for both growing seasons was divided into five uniform plots. The samples were 120 composed of five panicles randomly collected from each plot. The panicles were hand-121 harvested and pooled, and 100g of each sample was immediately analyzed for fungal 122 contamination and water activity (a_w) and then stored at 4°C until mycotoxin analyses. 123 The water activity was determined by automatic analysis using an Aqualab CX-2 124 apparatus (Decagon Devices, Pullman, WA, USA). 125 The prevailing climatic factors during the sample collection periods, including 126 temperature (°C) and precipitation (mm), were monitored by the Climatological Station 127 (CIIAGRO), located at Votuporanga, SP, Brazil. The data were obtained daily during 128 both growing seasons, from sowing to harvest time.

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2.2 Frequency of E. sorghinum

From each sample, 30 sorghum grains were surface-disinfected with a sodium hypochlorite solution (1%) and then plated (10 grains per Petri dishes) onto a potato dextrose agar (Oxoid, Basingstoke, UK) supplemented with chloramphenicol (100 mg 1⁻¹). The plates were incubated at 25°C in the dark for five days. Colonies of *Epicoccum* spp. developing from the sorghum grains were then counted and morphologically identified according to *Phoma* Identification Manual [16]. Colonies were identified using morphological criteria, such as colony aspect and micromorphological features. The identification at the species level was performed using molecular analysis of ITS region

of the rRNA gene, as described by Oliveira et al. [17]. The results are reported in percentage of infected grains.

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2.3. Tenuazonic acid analysis

143 The sorghum samples were analyzed for TeA mycotoxin contamination utilizing high-144 performance liquid chromatography-tandem mass spectrometry (HPLC-MS/MS) based 145 on the method described by Oliveira et al. 2017 [17]. 146 Briefly, samples of 5 g of ground sorghum grain were homogenized for 90 min with 15 147 mL of acetonitrile:water (1:1, v/v), acidified with 110 μL of formic acid. After 148 centrifugation (5 min at 4000 rpm), an aliquot of 100 µL of supernatant was taken and 149 diluted with 900 µl of water. TeA was determined by API 5000 LC-MS/MS system 150 (Applied Biosystems, Foster City, CA, USA) equipped with an Ion Electrospray 151 Ionization (ESI) source in the negative ionization mode. The column used was a 50 mm 152 x 4.6 mm x 1.8 µm SB C-18 (Agilent). Multiple-reaction monitoring (MRM) was used 153 for TeA determination. The precursor peak of TeA (m/z 196.0) and two products peaks 154 m/z 139 (DP - 75, CE -26 V, CXP -19 V) m/z 112.0 (DP - 75, CE -34 V, CXP -15 V) 155 were monitored to accomplish both quantitation and qualification criteria. A binary 156 gradient at a flow rate of 0.4 mL/min was performed with solvent A (water) and solvent

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2.3.1 Method validation

Method performance characteristics such as recovery, linearity, limits of detection (LOD) and limits of quantification (LOQ) were evaluated. For the recovery test, free TeA samples of sorghum grain were spiked with a standard solution at two concentrations (100 μg/kg and 200 μg/kg), in triplicates. A calibration curve was obtained using six TeA standard concentrations (20, 200, 400, 600, 800, and 1000 μg/kg).

B (methanol), following the conditions described by Oliveira et al. 2017 [17].

The mean recoveries for both concentrations were 96.3% and 99.7%, respectively. Good linearity was achieved with a correlation coefficient higher than 0.999. LOD (signal to noise ratio = 3) and LOQ (signal to noise ratio = 10) were 4 and 10 μ g/kg, respectively and showed the suitability of the method for the TeA determination in sorghum grains.

2.4. Assessment of eco-physiology of E. sorghinum isolated

2.4.1. Fungal strain and growth media

The TeA producer strain *Epicoccum sorghinum* P48 was used in this study. It was previously isolated from the same sorghum field studied and the species identification and ability to produce TeA was confirmed using molecular tools and LC-MS/MS [17]. The strain was grown on oatmeal agar (Difco, Detroit, Michigan) for 7 days at 25 °C and maintained in 15% glycerol at -80 °C in the Department of Microbiology at the University of Sao Paulo. The nucleotide sequence is available in the GenBank database under the accession number: KT31009.

For the experimental conditions, such as growth rate, *TAS1* gene expression and enzymatic production a sorghum-base medium was used. This medium was prepared by blending 4% (w/v) ground sorghum grains in sterile water and then adding 2% (w/v) agar [18]. Except for enzymatic analysis, in which a sorghum-base broth was used instead of agar, since the API-ZYM method cannot be used in agar plates. For the aw, we used the sorghum-base agar supplemented or not with glycerol to obtain aw of 0.90 (280 ml/L); 0.95 (152 ml/L) and 0.99 (nothing added). Water activity was determined by an Aqualab CX-2 apparatus (Decagon Devices, Pullman, USA).

2.4.2. Growth rate

A 5-mm-diameter mycelial disk from the margin of a 7-day-old growing colony of E.

sorghinum strain was used to centrally inoculate all treatments. The plates containing

medium with different aw values (0.90, 0.95, 0.99) were incubated at 18, 22, 26 and 30°C for 7 days; the experiments were performed in triplicate. Assessments of radial growth were made daily by measuring two right-angled diameters of the colonies. The diameters were plotted against time, and radial growth rates (mm/day) were obtained from the slope of linear regressions [19].

2.4.3. *TAS1* gene expression

2.4.3.1. RNA extraction and cDNA synthesis

Petri plates (diameter 90 mm) containing autoclaved media treatments were overlaid with sterile cellophane membranes to facilitate removal of the mycelium for RNA extractions. The total RNA was extracted from mycelium of each of the three replicates using the RNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA), according to the manufacturer's instructions. First strand cDNA was synthesized using the High Capacity cDNA Reverse Transcription kit (Applied Biosystems, Carlsbad, CA, USA), according to the manufacturer. The synthesis was performed in a Veriti thermal cycler (Applied Biosystems) using the following conditions: hybridization step of 10 min at 25 °C, reverse transcriptase (RT) step of 120 min at 37 °C and 5 min at 85 °C. The cDNA samples were stored at – 20 °C.

2.4.3.2. Quantitative real-time PCR (qRT-PCR)

The transcription profiles of the TeA biosynthetic gene (*TAS1*) and of β-tubulin gene (*TUB2*), as a reference gene, were analyzed by using qRT-PCR. The primers were designed using the NCBI tool for qRT-PCR Primer Design (http://www.ncbi.nlm.nih.gov/tools/primer-blast/) and are listed in table 1. For the *TAS1* primer design, a search in the NCBI database was performed (www.ncbi.nim.nih.gov) for similar proteins of the *TAS1* gene recently obtained from the sequenced genome of *E*.

sorghinum P48 strain [14]. Homolog proteins of TAS1 were found sharing over 83% identity with domain structures of TAS1 gene (C-A-PCP-KS). Base on that, TAS1 specific pairs of primer for E. sorghinum were designed from a sequence of KS domain found in E. sorghinum genome, which was described as an indispensable domain for TASI activity. The pair of primers used to amplify TUB2 gene was designed from a TUB2 sequence of the E. sorghinum genome in a similar manner as the TAS1 primers. The qRT-PCR assays were carried out using 2X Power SYBR Green PCR master-mix (Invitrogen, U.S.A.), according to the manufacturer. Primer optimization was performed following the manufacturer guidelines. The comparative $\Delta\Delta$ Ct method was used for the analysis of the qRT-PCR including the melting curve (Step One Plus Real time PCR system, Applied Biosystems). The PCR efficiencies for both genes were performed using the suggested protocol from the manufacturer. Briefly, the cDNA of positive control templates was diluted to the factor of 10 with 6 points and TAS1 and TUB2 primers were run at the same time to check for the qPCR validation and efficiency. The qPCR parameters obtained in this study were acceptable to the conditions required to quantify the relative gene expression using the $2^{-\Delta\Delta CT}$ method (Fig. S1) [20]. The ΔCt and $\Delta\Delta Ct$ were calculated from the Ct value obtained from the results of qRT-PCR following the calculation described by the manufacturer of Applied Biosystems. Samples were performed in triplicate at the same time with negative controls (without cDNA template) and using the thermal cycle and the reaction mix described in Table 1. The results were expressed in terms of fold change vs samples.

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2.4.4. Extracellular enzymatic production

The effects of different temperatures on the extracellular enzymatic production of *E. sorghinum* were evaluated by API-ZYM® system (Bio-Me'rieux, Marcy l'Etoile, France). Five culture discs (5 mm) from each of *E. sorghinum* isolates were transferred

243 to flasks containing sorghum-base broth and were incubated at 22°C for 10 days [21,22]. 244 The growth media were filtered with 0.22 µm Millex filters (Merck Millipore 245 Ltd., Tullagreen, Carrigtwohill, Ireland) and the filtrates were used to determine 246 production of 19 extracellular enzymes with the API-ZYM® system (Bio-Merieux, 247 Marcy l'Etoile, France). Briefly, 65 µL of each fungal culture broth were deposited in the 248 20 well-plates, and the plates were maintained at 30°C for 4 h in the dark. Thereafter, a 249 drop of ZYM A reagent (25 g of Tris-hydroxymethyl aminomethane + 11 mL of 250 hydrochloric acid 37% + 10 g of sodium lauryl sulphate + 100 mL of H₂O) and ZYM B 251 reagent (0.12 g 'Fast Blue BB' + 40 mL of methanol + 60 mL dimethyl sulphoxide) were 252 added to each well. The results were determined in nanomoles (nmol) of the hydrolyzed 253 substrate according to the intensity of the color reaction on a scale of 1-5, i.e., 1=5 nmol, 254 2 = 10 nmol, 3 = 20 nmol, 4 = 30 nmol and 5 = >40 nmol. All of the measurements were 255 taken in duplicate, and the sorghum-base broth was used as the negative control.

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2.5. Statistical analysis

To compare the frequency of E. sorghinum and TeA content between summer and autumn growing seasons, t-test was used (P < 0.05). The effects of temperature, a_w and their interaction were evaluated by the two-way ANOVA for growth rate and TASI gene expression. The differences among mean values were performed by Tukey's Multiple Comparisons Test at a 99% confidence level. To better correlate the temperature and a_w with growth and TeA production we used Pearson correlations. All the analysis was performed in OriginTM software (OriginLab, Inc.).

3. Results

3.1. E. sorghinum and TeA occurrence in the field

Mycological and mycotoxin analysis of the sorghum grains grown during the twogrowing season (summer and autumn) are shown in Table 2. In both growing seasons E. sorghinum was the major fungal species isolated, however, the natural variation of environmental factors of each season affected the frequency of E. sorghinum. For instance, 74% and 87.4% of the sorghum grains samples from summer and autumn season, respectively, were contaminated with E. sorghinum (P = 0.00005224). The highest average level of TeA was found in sorghum grains cultivated during the summer (587.8 μg/kg), with contamination levels ranging from 165.4 to 1647.5 μg/kg; while in autumn, the average of TeA levels was 440.5 μ g/kg (198.6 - 1154.9 μ g/kg) (P = 0.5680). These growing seasons present very distinct environmental conditions (Table 2). For instance, the summer temperature average (26.3°C) was 4 °C higher than in autumn (22.4) °C). The total rainfall was similar in both seasons (10.5 mm - summer; 9.2 mm - autumn). However, the percentage of rainy days observed during the summer (38.3%) was higher than in autumn (16.6%). Precipitation is known to have a direct effect on the aw levels in sorghum grain. This was confirmed by the samples collected during the two seasons. For instance, in the summer the a_w was around 0.98, as opposed to autumn that was 0.55.

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3.2 Ecophysiology of E. sorghinum

To better understand the impacts of a_w and temperature in the development and production of TeA by this fungus, laboratory controlled experiments were performed with different conditions of a_w and temperatures. These conditions were selected based on the climatological data collected in the field during summer and autumn seasons.

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3.2.1. Mycelium growth

Fig. 1 shows the radial growth rate of the *E. sorghinum* strain on sorghum media in response to different a_w (0.90-0.99) and temperatures (18-30°C). The results indicated

that mycelium growth occurred over the temperature and a_w ranges investigated. The optimum growth condition occurred at 0.99 a_w and 26°C (5.7 mm/day). The results also confirmed that the combination of the lowest temperature and driest conditions (0.90 a_w ; 18°C) tested were less favorable to *E. sorghinum* growth compared to higher values (0.99 a_w ; 30°C). Statistical analysis of variance (ANOVA) showed that all single factors (a_w , temperature, and their interaction) were significant on the radial growth rate (P < 0.01), except for 22°C and 30 °C at 0.95 a_w . The correlations of temperature and a_w with growth and TeA production was also confirmed by the Pearson correlation (Fig. 2). In agreement with the high TeA level found in sorghum grain grown on summer, a high and positive correlation was found between growth and *TAS1* gene expression in a combination of hot and humid conditions (26 - 30 °C and 0.99 a_w) (Fig. 2; Table S1).

3.2.2. *TAS1* gene expression

The results of the relative gene expression of the *TAS1* in *E. sorghinum* strain grown on sorghum medium under different combination of temperature and a_w is shown in Fig. 3. The highest expression of *TAS1* was observed at 26 °C and at 0.99 a_w , which was also the same optimum condition found for mycelium growth and agree with the highest TeA levels found in sorghum grains grown on summer season. These parameters also correlated well in the Pearson correlation with 0.87 and 1.00 for the 0.99 a_w and 26 °C, respectively (Fig. 2; Table S.1.). At lower temperatures (18° and 22°C), the transcriptional level of the *TAS1* was noticeably lower compared to the 26°C, except for 0.90 a_w . At 30°C, a considerable decrease of transcription was observed at 0.90 a_w . However, at 0.99 a_w , the expression followed the same pattern of 18° and 22°C. Moreover, it is interesting to note that the influence of a_w in *TAS1* gene expression was more pronounced at higher than at lower temperatures. Statistical analysis of variance (ANOVA) showed that all

single factors (a_w , temperature, and their interaction) were significant (p < 0.01) on the TASI gene expression, except for 0.90 a_w at 18, 22 and 26 °C.

3.2.3. Enzymatic production

The effect of temperature in the extracellular enzymatic production of *E. sorghinum* is shown in Fig. 4. The following five extracellular enzymes were produced: alkaline phosphatase, acid phosphatase; naphthol-AS-BI phosphohydrolase; α -glucosidase and N-acetyl- β -glucosaminidase. These five enzymes were only simultaneously produced at 22°C and 26°C. A thermal stress was observed at the lowest (18°C) and highest (30°C) temperatures tested. Two out of the five enzymes were inhibited, alkaline phosphatase and N-acetyl-b-glucosaminidase at 18°C and naphthol-AS-BI phosphohydrolase and α -glucosidase at 30°C. Moreover, production of acid phosphatase and naphthol-AS-BI phosphohydrolase increased at 18°C, when compared to the other temperatures. We also observed a pigment production when the colonies were cultivated in lower temperatures, with the highest production at 18 °C.

These results suggested that intermediate temperatures (22 and 26 °C) could lead to a more effective grain colonization by this species, and may explain the high frequency of *E. sorghinum* found in sorghum grains grown under the two-growing seasons (22 °C autumn and 26 °C summer).

4. Discussion

It is well known that environmental factors modulate fungal development and mycotoxin production, especially those related to climate change, which directly cause an impact on food security and quality [23]. In Brazil, sorghum cultivation occurs mainly as succession planting, especially in succession to summer crops, from September to March. In a recent study, based on the zoning of climatic conditions, it was determined that 53% of the

national territory are able to produce this crop, with the potential to increase the production up to 54 times [24]. However, there is no data on the influence of sowing period concerning food safety aspects, such as fungal and mycotoxin contamination. In our study, natural TeA contamination was found in sorghum grain grown in both growing seasons (summer and autumn). However, environmental conditions prevailing in the summer showed to be more favorable to TeA contamination. During this season, the sorghum grains were exposed to warm and rainy weather with a mean temperature 4 °C higher than autumn and precipitation percentage more than double the value of the autumn season (Table 2). The precipitation clearly influenced the aw in the sorghum grains, keeping high a_w levels (0.91) during the summer season. According to Srivastava et al. [25] changing planting or harvest dates of sorghum crops can be an effective and low-cost option to reduce pests and diseases in crops, Currently, there are no regulations worldwide for TeA in food; however, the average of TeA level found in sorghum grains grown in summer (587.8 µg/kg) was higher than the regulatory limit proposed by Bavarian Health and Food Safety Authority (500 µg/kg the TeA content in sorghum-based infant food) [13]. Therefore, a correct choice of sowing date, especially during a cooler and dry season, can play an important role in reducing the TeA contamination in sorghum crop. To our knowledge, very little information on the ecophysiology of E. sorghinum is available. The only previous work that evaluated the effects of temperature and pH on growth of P. sorghina strains demonstrated that the optimum temperature for mycelium growth was 28°C [26]. On the other hand, Alternaria spp., an important TeA producer, has been studied extensively over the last decade. Several studies have examined the response of Alternaria spp. under different environmental conditions [19,27] and interestingly, comparing to our results, E. sorghinum have a similar pattern of growth and

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TeA production, especially at elevated a_w and temperature conditions (≥0.95; 26°C). For instance, the optimum condition for mycelia growth of Alternaria has been observed in a range of 25~30°C and 0.98~1 a_w [27]. In terms of TeA production, Megan and Baxter [28] demonstrated that 0.99 was the optimum a_w level for TeA production by A. alternata on sorghum grain. Similar results were found by Oviedo et al. [29], who reported maximum TeA production at 0.98 a_w and between 25 and 30° C for strains of A. alternata on soybean-based agar. Epicoccum sorghinum is an important mold fungus infecting sorghum grains. To overcome the barrier of the grain tissue, an array of extracellular hydrolytic enzymes are produced to facilitate the penetration and subsequent infection on the host tissue [30]. However, thermal stress experienced by the microbial pathogen may impact the dynamics of host/pathogen interactions and ultimately resulting in changes in virulence [31]. Results showed that temperature plays an important role on the enzymatic expression of E. sorghinum (Fig. 4). Alkaline phosphatase and naphthol-AS-BI-phosphohydrolase, important enzymes for the degradation of organic phosphorus compounds found in the lipid layer of the plant cell plasma membrane, were inhibited at 18°C and 30°C respectively, as well as N-acetyl-β-glucosaminidase at 18°C [32]. Moreover, αglucosidase, which hydrolyzes disaccharides and is usually involved in the plant polysaccharides degradation, was inhibited at 30°C [33]. The results suggested that intermediate temperatures (22 and 26 °C) led to maximum enzymatic production, which could lead to more effective grain colonization by this species. In the case of the TeA biosynthetic gene, this is the first study evaluating the effects of environmental factors on TASI gene expression. TASI was recently described in Magnaporthe oryzae, a pathogen of rice, and consists of an NRPS (non-ribosomal peptide

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synthetase) with an unique type PKS-KS domain (polyketide synthase) that biosynthesizes TeA from isoleucine and acetoacetyl-CoA [34].

In the recently sequenced *E. sorghinum* genome, *TAS1* was determined to be highly conserved and had an identical domain described in *M. oryzae*, which is in agreement with the capability of this species to produce TeA [14]. In the current work, temperature and a_w showed a significant effect on *TAS1* expression. It is noticeable that the best condition of the *TAS1* gene expression (26 °C and 0.99 a_w) matches the higher level of TeA detected in the grains grown under the warm and humid conditions found in the summer season. Moreover, the highest *TAS1* expression range includes the optimal conditions for growth and extracellular enzymatic production, suggesting that TeA production by *E. sorghinum* also occur within the range of environmental conditions most favorable for sorghum grain colonization.

Additional studies are needed to better understand the occurrence of TeA in grains in relation to the ecophysiology of TeA fungal producers (*E. sorghinum* and *Alternaria* spp.) with worldwide distribution, and to create an integrated management of field and laboratory data to minimizing the risk of this mycotoxin contamination.

5. Conclusion

This study demonstrated that environmental conditions observed during different growing seasons (summer and autumn) have a direct effect on the TeA contamination of sorghum grains. The average of TeA levels detected in the sorghum samples grown during the summer season was 25 % higher than those detected in autumn. Moreover, the ecophysiological response of *E. sorghinum*, such as mycelium growth, *TAS*1 gene expression and enzymatic production indicated a good agreement with the environmental conditions observed in the field. Hot and humid days seems to play a role in *E. sorghinum*

419 development and consequently, in TeA accumulation in the grains. The results of the 420 combined approach of the environmental factors under field and laboratory conditions 421 has contributed to create an optimum risk assessment for mycotoxin production in 422 sorghum grains and added fundamental knowledge on the environmental conditions 423 inducing TeA biosynthesis. 424 425 **Acknowledgments** 426 This work was supported by the Research Support Foundation of the State of São Paulo 427 (FAPESP/Project 09570-1), Coordination for the Improvement of Higher Level -or 428 Education- Personnel (CAPES/Project 006869/2015-07) and U.S. Department of Energy 429 Biological and Environmental Research Science Focus Area grant (grant no. DE-AC52-430 06NA25396). 431 432 Appendix A: Supplementary data Additional Supporting Information may be found in the online version of this article: 433 434 Fig. S.1 Reference gene validation using serial dilutions with reference gene (TUB2) and 435 target gene (TASI) and checking for the slope of each line. 436 **Table S.1** Person Correlations of the growth versus gene expression at different 437 temperature and water activity levels

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