A systems approach to model the relationship between aflatoxin gene cluster expression, environmental factors, growth and toxin production by Aspergillus flavus

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A microarray analysis was used to examine the effect of combinations of water activity (\(a_w\), 0.995–0.90) and temperature (20–42°C) on the activation of aflatoxin biosynthetic genes (30 genes) in Aspergillus flavus grown on a conducive YES (20 g yeast extract, 150 g sucrose, 1 g MgSO\(_4\).7H\(2\)O) medium. The relative expression of 10 key genes (\(aflF\), \(aflD\), \(aflE\), \(aflM\), \(aflO\), \(aflP\), \(aflQ\), \(aflX\), \(aflR\) and \(aflS\)) in the biosynthetic pathway was examined in relation to different environmental factors and phenotypic aflatoxin B1 (AFB1) production. These data, plus data on relative growth rates and AFB1 production under different \(a_w\) × temperature conditions were used to develop a mixed-growth-associated product formation model. The gene expression data were normalized and then used as a linear combination of the data for all 10 genes and combined with the physical model. This was used to relate gene expression to \(a_w\) and temperature conditions to predict AFB1 production. The relationship between the observed AFB1 production provided a good linear regression fit to the predicted production based in the model. The model was then validated by examining data-sets outside the model fitting conditions used (37°C, 40°C and different \(a_w\) levels). The relationship between structural genes (\(aflD\), \(aflM\)) in the biosynthetic pathway and the regulatory genes (\(aflS\), \(aflJ\)) was examined in relation to \(a_w\) and temperature by developing ternary diagrams of relative expression. These findings are important in developing a more integrated systems approach by combining gene expression, ecophysiological influences and growth data to predict mycotoxin production. This could help in developing a more targeted approach to develop prevention strategies to control such carcinogenic natural metabolites that are prevalent in many staple food products. The model could also be used to predict the impact of climate change on toxin production.

Keywords: aflatoxin genes; systems biology; water activity; temperature; aflatoxins; predictive modelling

1. INTRODUCTION

Aflatoxins are produced by Aspergillus section Flavi group species and are thought to be one of the most cancerous natural substances known. Economically and biologically the most important fungal species able to produce aflatoxins are Aspergillus flavus and Aspergillus parasiticus [1]. The aflatoxin biosynthesis gene cluster of A. parasiticus has been completely elucidated [2–4]. Indeed, a whole-genome microarray of A. flavus has been used to study the regulation of aflatoxin biosynthesis genes [5]. Generally, the aflatoxin biosynthesis genes of A. flavus and A. parasiticus are highly homologous and the order of the genes within the cluster has been shown to be the same [6]. Aspergillus flavus strains produce only aflatoxin B1 (AFB1) and B2, whereas A. parasiticus produce aflatoxins B1, B2, G1 and G2 [7,8].

The biosynthesis of mycotoxins is strongly dependent on growth conditions such as substrate composition [9] or physical factors, including pH, water activity, temperature or modified atmospheres [10–14]. Water activity (\(a_w\)) is a measure of the amount of freely available water in a substrate for microbial growth and is related to pure water, which has an \(a_w\) of 1 or 100 per cent equilibrium relative humidity. This \(a_w\) is related to the total moisture content (m.c.) of a specific substrate by a

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moisture sorption curve [15]. Depending on the particular combination of external growth parameters, the biosynthesis of aflatoxin can either be completely inhibited or the pathway fully activated. Knowledge about these relationships enables an assessment of which parameter combinations can control aflatoxin biosynthesis and which are conducive to phenotypic aflatoxin contamination. For example, a mathematical model which delineated the relationship between pH, propionic acid concentration and temperature on aflatoxin biosynthesis by A. parasiticus was described by Molina & Giannuzzi [11]. However, with the exception of these data at the phenotypic level, very little information is available on the influence of abiotic factors on the regulation of the aflatoxin biosynthesis genes. Sweeney et al. [16] developed a reverse transcription polymerase chain reaction (RT-PCR) to analyse the expression of the aflR and ord1 genes of the aflatoxin pathway in relation to various nutritional media. Price et al. [17] used a whole-genome microarray approach to analyse the influence of substrate composition and pH on the activation of aflatoxin biosynthesis genes. O’Brien et al. [5] using the whole-genomic microarray found that conducive and non-conducive temperatures affected functioning of the genes, with transcription levels of aflR and aflR proteins present at lower concentrations at 37°C than 35°C for a strain of A. flavus.

Using a mycotoxin microarray with sub-arrays for specific mycotoxins, developed by Schmidt-Heydt & Geisen [18], the impact of key environmental factors (aflR, temperature) were shown to significantly affect the aflatoxin gene clusters. The ratio of the key regulatory genes (aflR and aflS) being important in encoding the enzymes in the synthetic pathway of both A. flavus and A. parasiticus [19,20]. Other studies have also demonstrated the impact that such environmental factors may have, especially marginal stress conditions, on gene cluster expression and phenotypic toxin production for a number of species [21]. Recently, Schmidt-Heydt et al. [22] showed that, for Fusarium culmorum and Fusarium graminearum, it is possible to integrate such microarray data on relative TRI gene expression under different environmental conditions, growth and deoxynivalenol (DON) production and develop models that can be used to predict DON concentrations for the first time. No such integrated systems approach has been attempted for A. flavus.

In A. flavus, the clustered pathway genes have been detailed, and in some cases new gene names have recently been given [3,4]. Some of the key genes in the aflatoxin biosynthesis include aflD (old name; norB), aflD (nor-1) and aflE (nor-A), which encode a dehydrogenase and two reductases which convert norsolorinic acid into demethylsterigmatocystin; aflM (ver-1) is a dehydrogenase which converts versicolorin A to demethylsterigmatocystin; aflO (omtB) is an O-methyltransferase I or O-methyltransferase B, which is involved in the conversion of demethylsterigmatocystin to sterigmatocystin and dihydro-demethylsterigmatocystin to dihydrosterigmatocystin; aflP (omtA) is an O-methyltransferase A or II which converts sterigmatocystin to O-methylsterigmatocystin to dihydro-O-methylsterigmatocystin; other genes such as aflQ (ordA) and aflX (ordB) have been shown to be involved in the final part of the biosynthetic pathway, as oxidoreductase-P450 monooxygenase and monooxygenase oxidase. The two key regulatory genes which are important in transcription activation are aflR, which is involved in both aflatoxin and sterigmatocystin production, and aflS (=aflJ), which is involved in the regulation of aflatoxin.

We have utilized the mycotoxin microarray sub-array for the aflatoxin genes as a tool for examining the changes that interacting environmental factors may have on the relative expression of A. flavus gene clusters, as well as effects on growth and phenotypic aflatoxin production. The objectives of this study were to (i) examine the effect of aw × temperature conditions on growth, AFB1 and relative expression of 10 key genes (aflD, aflE, aflF, aflM, aflN, aflP, aflQ, and aflX, and the regulatory genes aflR and aflS) in the biosynthetic pathway using the mycotoxin gene microarray; (ii) to quantify the amounts of AFB1 produced under these interacting conditions; (iii) to mathematically model the relationship between expression of these genes, environmental factors, growth and AFB1 production; (iv) to validate the model with datasets outside the range of the model and (v) to examine the possible ternary interactions and relationships between some genes in the early part (aflD, aflM) of the biosynthetic pathway and key regulatory genes (aflR, aflS) in relation to aw, temperature and AFB1 production.

2. MATERIALS AND METHODS

2.1. Fungal strain used

The A. flavus strain (NRRL 3357) was previously used in molecular ecology studies [19]. This was kindly provided by Dr D. Bhatnagar, USDA, New Orleans, LA, USA. It was stored at 4°C and sub-cultured on a 2 per cent maize meal agar when required. It has a known AFB1 production capacity [19].

2.2. Growth studies

These were carried out with a conducive YES medium (20 g yeast extract, 150 g sucrose, 1 g MgSO4·7H2O, 1 l). The agar medium was modified with glycerol to adjust the water availability to 0.99, 0.95, 0.90 and 0.85 aw. The modification was done by first modifying the water with glycerol (46.1, 230, 506, 782 g l⁻¹) and then substituting this mixture as if adding water. The advantage of using glycerol is its stability over the experimental temperature range for modifying aw. The accuracy of the modifications was confirmed using an Aqualab 3TE instrument (Decagon, Pullman, WA, USA) and found to be within ±0.005 of the target aw.

Spores from a 7-day-old culture grown at 25°C were dislodged with a sterile loop and placed in 10 ml of sterile water + 0.05% Tween 20, a surfactant, in a 25 ml Universal bottle. The spores were counted and a 10⁶ spores ml⁻¹ concentration prepared. The 9 cm Petri plates containing media treatments were all overlaid with sterile 8.5 cm cel-lophane discs (P400, Cannings Ltd, Bristol, UK) and then centrally inoculated with a 5 µl spore suspension. Replicates (five per treatment) were incubated at
20, 25, 30 and 35°C for model design and temperatures outside the model boundaries; 37, 40 and 42°C were used to validate the model. Growth was measured daily by taking two diametric measurements at right angles to each other for a period of 9 days. Previous kinetics studies suggested that this was an optimum time under some conditions for gene expression using RT-PCR [21]. At the end of this period, the whole colony biomass was scraped from the cellophane surface into Eppendorf tubes and frozen at \(-80°C\).

2.3. Isolation of RNA from samples

To perform microarray experiments, RNA was isolated using the RNAeasy Plant Mini kit (Qiagen, Hilden, Germany). An amount of 1 g of the mycelium was ground with a mortar and pestle in liquid nitrogen. Two hundred and fifty milligrams of the resulting powder were used for isolation of total RNA. The powder was suspended in 750 µl of lysis buffer, mixed with 7.5 µl of 

\(\beta\)-mercaptoethanol and 100 glass beads with a diameter of 1 mm (B. Braun Biotech International GmbH, Melsungen, Germany) in a 2 ml RNA-free micro reaction tube. The extracts were mixed thoroughly and incubated for 15 min at 55°C and 42 kHz in an S10H ultrasonic bath (Elma, Singen, Germany). All further procedures were essentially the same as suggested by the manufacturer of the kit.

2.4. Microarray experiments

cDNA synthesis and labelling were performed using the Micromax Direct Labelling kit (Perkin Elmer Life and Analytical Science, Inc., Boston, USA). For this purpose, 50 µg of DNase I-treated total RNA was used according to the specifications of the kit. After cDNA synthesis and labelling, the cDNA was purified with the QiAQuick Min Elute kit (Qiagen, Hilden, Germany). The labelled and purified cDNA was dried in a vacuum concentrator (Speed Vac, Savant Instruments, Farmingdale, USA), re-suspended in 60 µl of hybridization buffer (Scienion, Berlin, Germany), heated for 2 min at 95°C, placed on ice to prevent strand rearrangement and hybridized for 18 h at 42°C to the microarray using an automatic hybridization station (Perkin Elmer). After hybridization, the array was scanned with a confocal laser system (Scanarray lite, Perkin Elmer) at a resolution of 5 µm. The analysis of the results was performed using the Scanarray software (Perkin Elmer). The results were normalized using the Lowess algorithm (locally weighted scatter plot smoothing) together with subtraction of the background signal. As a control, the constitutively expressed \(\beta\)-tubulin gene was used.

2.5. Aflatoxin analyses

2.5.1. Derivatization procedure. Agar plugs (4–5 plugs, approx. 0.5 g) were cut out of the agar medium across the 9 cm Petri plates. These were placed into 2 ml Eppendorf tubes and weighed. Aflatoxins were extracted by adding 1 ml of chloroform and shaking for 1 h. The biomass was discarded after centrifugation and the chloroform was evaporated to dryness. The residue was derivatized [23] using the following method:

- 200 µl high-performance liquid chromatography (HPLC) grade hexane was added to the residue in a 2 ml Eppendorf tube.
- 50 µl of trifluoroacetic acid (TFA) was added and vortexed for 30 s; Eppendorf tubes were left for 5 min
- 950 µl of water : acetonitrile (9 : 1) was added
- Eppendorf tubes were vortexed for 30 s.
- They were left for 10 min for separation of the layers. The upper layer was discarded. The extracts were filtered through Nylon 13 mm, 0.2 µm filter (SMI-Lab Hut Ltd, UK) directly into amber HPLC vials (Jaytec Biosciences Ltd, UK).

2.5.2. Sample analysis. Sample extracts were analysed by HPLC using a Waters 600 E system controller, 470 fluorescence detector (Millipore Waters Corporation, MA, USA) (\(A_{exc} = 360\) nm; \(A_{em} = 440\) nm) and a C18 column (Phenomenex Luna ODS2 150 × 4.6 mm, 5 µm) all under the control of Waters Millennium²³² software. The analysis was performed at a flow rate of 1 ml min\(^{-1}\) of the mobile phase (30% methanol : 60% water : 10% acetonitrile) and the run time was 25 min. A 200 µl stock solution of an aflatoxin mixed standard in methanol (Supleco, Bellefonte, USA), containing 200 ng of B1, 60 ng of B2, 200 ng of G1 and 60 ng of G2, was dried under nitrogen gas and derivatized as for samples. Four concentrations (AFB1: 50–200 ng ml\(^{-1}\)) were prepared for HPLC injection to make a standard curve (\(r^2 = 0.9999\)). The limit of detection for AFB1 using HPLC was 0.8 ng g\(^{-1}\) medium.

2.6. Data analysis and model development

This study has used a mixed-growth-associated product formation model [24], which takes account of both specific growth rate and metabolite accumulation. This includes the fact that product formation is a combination which is given by equation (3.1). This has previously been used for production of compounds such as xanthan gum and a range of secondary metabolites of pharmaceutical interest.

2.7. Generation of ternary contour surfaces of interactions between gene expression and environmental factors, and on AFB1 production

In order to plot the ternary contour surfaces of the genetic expression, a standardized signal from the microarray was calculated as follows for \(a_w\) and for temperature to relate the relative abundance of mRNA of the structural genes (e.g. \(a_{fR}, a_{fS}\)) to the regulatory genes (\(a_{fR}, a_{fS}\)):

\[
\begin{align*}
\frac{f(a_w)}{a_{fID} + a_{fIR} + a_{fIS}} &= \frac{a_{fR}}{a_{fID} + a_{fIR} + a_{fIS}}, \\
\frac{a_{fS}}{a_{fID} + a_{fIR} + a_{fIS}} &= a_{fID} + a_{fIR} + a_{fIS}
\end{align*}
\]
\[ f(\text{temperature}) = \frac{a\text{flD}}{a\text{flD} + a\text{flR} + a\text{flS}} + \frac{a\text{flR}}{a\text{flD} + a\text{flR} + a\text{flS}} \frac{a\text{flS}}{a\text{flD} + a\text{flR} + a\text{flS}} \]

where the standardized value = actual value - minimum value/maximum value - minimum value.

For AFB1 production, the model is

\[ f(\text{aflatoxin (µg g}^{-1})) = \left( \frac{a\text{flD}}{a\text{flD} + a\text{flR} + a\text{flS}} \right) \frac{a\text{flR}}{a\text{flD} + a\text{flR} + a\text{flS}} \frac{a\text{flS}}{a\text{flD} + a\text{flR} + a\text{flS}} \]

3. RESULTS

3.1. Effect of environmental factors on growth and AFB1 production by the strain of A. flavus

Figure 1a shows the effect of interacting conditions of \( a_w \) and temperature on growth of the \( A. \ flavus \) strain used in this study. This shows that the optimum was at 0.99 \( a_w \) and 30–35°C, with a good growth at 0.95 \( a_w \) and 25–40°C. At the driest conditions examined, 0.85 \( a_w \), growth only occurred at 30–37°C.

Figure 1b shows the effect of these parameters on AFB1 production. This shows a very different pattern from that for growth. Very little, if any, AFB1 was produced at 40°C, except at 0.95 \( a_w \). It is interesting to note that, at sub-optimal growth conditions, AFB1 production occurred at 20–37°C with often higher production at 0.99–0.98 \( a_w \). These datasets were used in conjunction with the relative gene expression of the 10 genes encoding for enzymes involved in the biosynthesis of AFB1 for modelling their relationship.

3.2. Modelling the relationship between environmental factors, gene expression and AFB1 production

We have used a mixed-growth-associated product formation model, with specific rate of product formation given by the equation where \[24\]

\[ q_P = \alpha \mu + \beta, \]  

(3.1)

where \( q_P \) is the total production of AFB1 produced; \( \alpha \) and \( \beta \) are constants of AFB1 production associated with primary and secondary metabolism and \( \mu \) is the specific growth rate.
The specific rate of product formation is proportional to the total biomass and the rate of product formation,
\[
q_p = \frac{1}{X} \frac{dP}{dt}.
\] (3.2)

The rate of product formation for a growth-associated product is related to the initial biomass \( (X_0) \) and the specific growth rate \( (\mu) \) and the time \( (t) \).

Thus, combining equations (3.1) and (3.2), we get
\[
\frac{dP}{dt} = (a\mu + \beta)X = \frac{1}{X} \frac{dX}{dt}.
\] (3.3)

and
\[
\frac{dP}{dt} = X_0e^{\mu t}.
\] (3.4)

The rate of microbial growth is characterized by the specific growth rate, defined as
\[
\mu = \frac{1}{X} \frac{dX}{dt}.
\] (3.5)

After integration form \( t = 0 \) to \( t \) (days) and \( X(0) = X_0 \) to \( X(t) = X \)
\[
X = X_0e^{\mu t}, \quad X_0 = Xe^{-\mu t}.
\] (3.6)

Substituting equations (3.6) and (3.3), we get
\[
\frac{dP}{dt} = (a\mu + \beta)X_0e^{\mu t}.
\] (3.7)

A temperature-dependent rate coefficient for growth represented by Arrhenius's empirical equation is given by
\[
\mu = e^{-E_a/RT},
\] (3.8)

where \( E_a \) is the activation energy and \( R \) is the universal constant of the gases (\( 8.31 \times 10^{-3} \text{J K}^{-1} \text{mol}^{-1} \)) and \( T \) is the absolute temperature (in K). If we assume that the rate of production is affected directly by fungal growth rate and activation energy, we obtain the following:
\[
\frac{dP}{dt} = (a\mu + \beta)X_0e^{\mu t} \cdot e^{-E_a/RT}.
\] (3.9)

Based on previous experiments (data not shown) it was observed that the activation energy could be adjusted as a quadratic function as follows:
\[
E_a = b_1 a_w.
\] (3.10)

Thus
\[
\frac{dP}{dt} = (a\mu + \beta)X_0e^{(-b_1 a_w/RT)}e^{\mu t}
\] (3.11)

and
\[
\int_0^t \frac{dP}{dt} = (a\mu + \beta)X_0e^{(-b_1 a_w/RT)} \int_0^t e^{\mu t} \, dt.
\] (3.12)

After integration, we obtain
\[
P = \left(\frac{\alpha + \beta}{\mu}\right)X_0e^{(-b_1 a_w/RT)}e^{t-1}.
\] (3.13)

For assessing the relationship between physiological and thermodynamic conditions and AFB1 production and the expression of the gene clusters involved in toxin production, the physical model was combined with the gene expression data as a linear combination. The generic cluster can be described as a linear function:
\[
[g] = a_1 a_f D + a_2 a_f R + a_3 a_f S + a_4 a_f E + a_5 a_f M + a_6 a_f O + a_7 a_f P + a_8 a_f Q + a_9 a_f X + a_{10} a_f F
\] (3.14)

where \( a_i \) to \( a_{10} \) are the parameter estimates from the linear combination of the expression of genes so that \([g]\) represents the sum of the effect of the individual genes expressed under specific conditions. The final model which considers \( a_w \), temperature, growth rate and gene expression on the regulation of AFB1 is given by
\[
P = [g] \times \left(\frac{\alpha + \beta}{\mu}\right)X_0e^{(-b_1 a_w/RT)}(e^{\mu t} - 1).
\] (3.15)

where \( P \) is the AFB1 production (\( \mu g \text{ g}^{-1} \)) and \( b_1, \alpha \) and \( \beta \) are parameter estimates from the model and \( \mu \) was calculated based on a period of 9 days’ growth and the assumption that growth occurs in cylindrical fungal hyphal extension with a constant radius simplified as follows:
\[
\mu t = \ln \left(\frac{X_f}{X_i}\right) = \ln \left(\frac{m_i \times \rho \pi \times r_A^2 \times L_f}{m_f \times \left(\frac{v_f}{m_f}\right) \pi \times r_A^2 \times L_i}\right)
\] (3.16)

where \( X_i \) and \( X_f \) are final and initial biomass, \( m_i \) and \( m_f \) are initial and final fungal mass, \( v_i \) and \( v_f \) are the initial and final fungal fungal voxel volume, \( r_A \) is the A. flavus hyphal radius and \( L_f \) and \( L_i \) are the radial growth and \( \rho \) is the fungal density.

Table 1 shows the actual mean data \( n = 3 \) for AFB1 production and that predicted by the model in relation to different combinations of temperature and \( a_w \), the gene expression data and the relative mean growth rate.

Table 2 shows the ANOVA for the fit of the model and the regressed coefficients and the corrected totals. This suggests that the model showed a good fit to the data and was statistically significant. Table 3 shows the overall estimates and the dependence for the main areas that are related to the model. All the parameters are statistically significant at \( p < 0.01 \). The model fit for the observed versus the predicted effects on AFB1 production (\( \mu g \text{ g}^{-1} \)) gave a good correlation between the parameters \( (r^2 = 0.9495; \text{residual square difference } R_{\text{mod}} = 0.0440) \). The model was used to construct contour maps of the relationship between environmental factors, growth and AFB1 production (figure 2a, b). This shows that the optimum growth was at about 27°C and 0.98 \( a_w \). The marginal conditions for growth were in the region \( <0.90a_w \) and temperatures \( <20°C \) and \( >35°C \). For
AFB1 production, the optimum conditions were at 0.98–0.99 aw and 25–33°C.

3.3. Validation of the model

The model was subsequently tested to examine whether it could be used at temperatures of 37 and 40°C at different aw levels. These conditions were not originally included in the model because of the limited data at these conditions. Table 4 shows the effect on growth rate, and on the observed and predicted AFB1 production under these conditions. At 37°C and 0.90, 0.95 and 0.99 aw, the model predicted slightly higher AFB1 production than that was actually observed. The divergence between the predicted and observed value at 0.95 to 0.99 aw increased from 30 to 56 per cent at this temperature. At 40°C and 0.90 aw, there was very slow growth but no AFB1 produced. This was similar to the predicted value.

3.4. Ternary relationships between gene expression, environmental factors and AFB1 production

By using a standardized signal from the microarray dataset for some of the key structural and regulatory genes, it was possible to examine the relative relationship between the activity of either aflD or aflM and
and for temperature, 

\[
T \,(\degree C) = 47.95 \left( \frac{aflM}{aflM + aflJ + aflS} \right) + 30.52 \left( \frac{aflJ}{aflM + aflJ + aflS} \right) + 17.53 \left( \frac{aflS}{aflM + aflJ + aflS} \right).
\]

(3.19)

(3.20)

The effect of interactions between aflM, aflS and aflR showed that with more available water (e.g. 0.98 \(a_w\)) there was a higher expression of the genes aflM and aflS (figure 4a). In contrast, under drier conditions, there was a higher aflR signal. There was an inverse proportional effect of temperature on the expression of aflM and aflR. Thus, the higher the temperature, the lower aflR and higher aflM gene signal (figure 4b). The expression of aflS was similar across a wide spectrum of temperatures.

Figure 5 shows the relative expression of (i) aflD, aflR and aflS, and (ii) aflM, aflR and aflS in relation to AFB1 production. The relationships were calculated based on

\[
\text{aflatoxin B1 production (\(\mu g\ \text{g}^{-1}\))} = 3.66 \left( \frac{aflD}{aflD + aflR + aflS} \right) - 0.802 \left( \frac{aflR}{aflD + aflR + aflS} \right) + 1.91 \left( \frac{aflS}{aflD + aflR + aflS} \right).
\]

(3.21)
This study has examined the relationship between the growth of *A. flavus* and the impact that environmental factors can have on key structural and regulatory genes and the impact that this will have on AFB1 production. This has shown that temperature and water availability have a profound effect on both gene expression of key biosynthetic genes as well as significantly affecting the phenotypic production of the toxic secondary metabolite actually quantified analytically.

The data have shown that, while growth can occur over a wider range of temperatures x water activity levels, AFB1 production is over a narrower range of conditions. Thus optimum conditions for growth of this strain of *A. flavus* were 30–35°C and 0.99 aw, with marginal conditions at 15°C and 40°C at 0.99 aw. For AFB1 production, the optimum conditions were 25–30°C at 0.99 aw and this changed to 30–35°C at 0.95 aw. While few previous studies have considered interactions between environmental conditions, Sanchis & Magan [14] did integrate data based on growth and AFB1 production on different nutritional matrices, and this showed that optimum aw and temperatures on groundnuts were 0.94 and 34°C for growth and 0.99 aw and 32°C for AFB1 production. More recently, an Italian isolate of *A. flavus* from maize was shown to have a wide temperature tolerance range for growth (15–45°C) but much narrower for AFB1 (20–35°C) production [25].

In the present study, expression data were available for the whole aflatoxin gene cluster. However, we decided to use eight key biosynthetic genes and the two regulatory genes that were relevant to the biosynthesis of AFB1 [2,26]. This showed that both temperature and aw influenced their relative expression. Schmidt-Heydt *et al.* [19,20] showed that the ratio of the regulatory genes aflR and aflS may be important, as a low ratio under certain aw x temperature levels resulted in low AFB1 production while higher ratios resulted in significantly higher toxin production in both *A. flavus* and *A. parasiticus*. Because of this, we examined the relative

and for aflM and the regulatory genes

\[
\text{afltoxin B}_1 \text{ production (} \mu\text{g g}^{-1} \text{)} = \\
3.21 \left( \frac{\text{aflM}}{\text{aflM} + \text{aflJ} + \text{aflJ}} \right) - 0.63 \left( \frac{\text{aflR}}{\text{aflM} + \text{aflJ} + \text{aflS}} \right) \\
+ 1.85 \left( \frac{\text{aflS}}{\text{aflM} + \text{aflJ} + \text{aflS}} \right).
\]

(3.22)

4. DISCUSSION

This study has examined the relationship between the growth of *A. flavus* and the impact that environmental factors can have on key structural and regulatory genes and the impact that this will have on AFB1 production. This has shown that temperature and water availability have a profound effect on both gene expression of key biosynthetic genes as well as significantly affecting the phenotypic production of the toxic secondary metabolite actually quantified analytically.

The black circles indicate the experimental data in relation to changes in water activity in the range 0.86–1.00 and (b) temperature in the range 15–55°C. Legends indicate relative expression.

![Figure 3. Ternary diagrams of the relative relationship between expression of aflD, aflR and aflS in response to (a) water activity in the range 0.86–1.00 and (b) temperature in the range 15–55°C.](http://rsif.royalsocietypublishing.org/)

Figure 3. Ternary diagrams of the relative relationship between expression of aflD, aflR and aflS in response to (a) water activity in the range 0.86–1.00 and (b) temperature in the range 15–55°C. Legends indicate relative expression. The black circles indicate the experimental data in relation to gene expression.

The activity of two genes (aflD, aflM) present in the early part of the biosynthetic pathway with the regulatory genes in relation to changes in aw and temperature. This showed that there was some relationship which was influenced by both temperature and water stress.

O’Brien *et al.* [5] analysed the influence of elevated temperature on aflatoxin gene expression. They found
by microarray analysis a differential expression of certain genes at 28°C, which was conducive, compared with 37°C, which was repressive, for aflatoxin biosynthesis in their strain of *A. flavus*. However, in agreement with the data presented here, transcript levels of both *aflR* and *aflS* did not change significantly between these temperatures.

It is also necessary to consider this study in the context of what might happen when biotic variables are included. Thus, the interaction with ripening maize kernels, especially where plant physiological and nutritional effects may be important, also needs to be considered [26]. Some relevance from the present study can be inferred from the changes in $a_w$ of maize kernels in ripening maize cobs. At the early dough stage, the m.c. is about 40 per cent ($=0.99 a_w$) with no water stress effects, this decreases to 30–35% m.c. at the mid-dough stage ($=0.95 a_w$) and to 20–25% (0.90–0.85 $a_w$) at full maturity over a period of about 4–6 weeks [27]. This will influence infection and colonization by *A. flavus*. Recently, Giorni *et al.* [25] showed that the nutritional media made from maize kernels at different ripening stages had little effect on growth of *A. flavus* and AFB$_1$ production. This suggests that $a_w \times$ temperature stresses may play an important role in influencing both gene expression and aflatoxin contamination in the fungus–plant interface during this period. This may further influence the interaction with other mycobiota which colonize the ripening maize cobs during these critical phases of plant development.

Oxidative stress may also be an important factor as it has been shown that this can stimulate aflatoxin production [28]. For example, antioxidants such as gallic acid found in walnuts were found to inhibit several aflatoxin biosynthetic pathway genes including *aflD* and *aflM* [29]. Kim *et al.* [30] showed that caffeic acid

Figure 4. Ternary diagram of the relative relationship of expression of *aflM*, *aflR* and *aflS* in response to (a) water activity in the range 0.90 and 0.98 and (b) temperature in the range 20–45°C. Legends indicate relative expression of each gene. Black circles indicate the experimental data in relation to gene expression.

Figure 5. Ternary diagram of relative expression of (a) *aflD*, *aflR* and *aflS* and (b) *aflM*, *aflR* and *aflS* on AFB$_1$ production (µg g$^{-1}$), the black circles represent the experimental data in relation to gene expression.
downregulated most of the aflatoxin biosynthetic genes. These studies suggest that several oxidative stress genes such as catalases, superoxide dismutases and mitogen-activated protein kinase genes may be required to overcome such stress. These effects may be further influenced by environmental parameters which may add another layer of complexity to attempts to model the system.

Recently, Abdel-Hadi et al. [31] suggested that relative expression of aflD was an important indicator of colonization under different environmental regimes. They were able to develop a contour map in relation to water and temperature stresses with phenotypic secondary metabolite data to examine the relationship between ecophysiological factors, growth and DON production by strains of *F. culmorum* and *F. graminearum* for the first time. This suggested that it was possible to use quantitative PCR data for specific genes (e.g. TRI5, TRI6) under different environmental conditions to predict DON production using contour maps. However, validation was not possible using this model. The present study has used a mixed growth model to try and relate the relative expression of 10 biosynthetic genes under different interacting environmental factors to growth and AFB1 production. This made it possible to use this approach to develop a predictive model which gave a good relationship between the observed and predicted AFB1 production. Contour maps could be developed to show the relationship between water and temperature on AFB1 production. It also enabled the inclusion of the gene expression data for 10 genes as a linear function to relate this to growth and toxin production under a range of interacting stress conditions. Validation of the mixed growth model was possible under conditions which were not included in the model development. Thus the effect of slight changes in temperature to 35 and 40°C at different water stress levels could be examined. The model gave a better fit under some conditions, but deviated markedly under very wet conditions, which are conducive to growth. The approach could be a powerful tool in examining the impact of climate change factors, including elevated temperature conditions, water stress and elevated CO2 have on growth, gene expression and also potential for toxin production [32].

The development of ternary diagrams to examine the relationship between structural and regulatory genes in relation to environmental conditions and toxin production has not been studied in detail previously. This has shown that the relative expression of aflD or aflM to that of aflR and aflS is important, and are related and influenced by both water and temperature. The fact that aflS expression remains relatively consistent across a range of interacting environmental conditions suggests that this is a key regulatory gene in the biosynthetic pathway for aflatoxin biosynthesis. This approach may enable the links between different genes to be examined in order to better understand how they impact on the phenotypic production of aflatoxins.

We believe that the effective integration of molecular, ecophysiological and secondary metabolite datasets could be critical in predicting the relative risk of mycotoxin contamination under different biotic and biotic stress scenarios which could have an impact on both food quality and security [32].

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**REFERENCES**

Toxin genes, environment and aflatoxin models  A. Abdel-Hadi et al.


