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**Development, Chemometric-Assisted Optimization and in-House  
Validation of a Modified Pressurized Hot Water Extraction  
(PHWE) Method for Multi-Mycotoxin Analysis**

By

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## EXECUTIVE SUMMARY

Improvement in analytical methods, including extraction procedures has been a recurrent topic in mycotoxin research due to the fact that mycotoxins are ubiquitous, potent and notoriously difficult to eradicate from the food and feed supply chain. Effective management of these toxicants rely on stringent regulation and routine surveillance of food commodities via efficient analysis, hence the continuous need for improved methods. This research work describes for the first time the optimization, validation and application of a modified pressurized hot water extraction (PHWE) method for the simultaneous extraction of multiple mycotoxins and subsequent quantification on ultra-high performance liquid chromatography coupled to a tandem mass spectrometer (UHPLC-MS/MS). The research was performed in three phases which are presented as chapters (*i.e.*, Chapters Three to Five), in this thesis.

The first part of the research aimed to establish the thermal degradation patterns of mycotoxins and determine their relative stability under different temperature and time conditions. This was performed in order to determine the feasibility of the application of PHWE for the extraction of the mycotoxins since this extraction technique involves the use of heat. Using a set of statistically pre-determined experimental conditions (103 to 217 °C, and 6.72 to 63.28 min for temperature and time, respectively), simultaneous optimization of the thermal degradation of 15 different mycotoxins in pure form and when spiked into maize was achieved. The mycotoxins studied included aflatoxins (AFs), fumonisins (FBs), zearalenone and its analogues  $\alpha$ -zearalenol and  $\beta$ -zearalenol (ZEAs), ochratoxins (OTs), T-2 toxin (T-2), alternariol monomethyl ether (AME) and sterigmatocystin (STEG). The global optimum degradation condition (*i.e.*, minimum temperature and time required for complete degradation of all mycotoxins) was computed as 217 °C/63.28 min and 211 °C/54.71 min for pure mycotoxin standards and spiked maize matrix, respectively. Based on the results obtained, it was inferred that the studied mycotoxins demonstrated sufficient thermal stability to undergo PHWE which typically employs temperatures ranging from 50 to 200 °C and extraction times ranging from 5 to 20 min.

The second part of this research work focused on the development, optimization and validation of a modified PHWE method for the simultaneous extraction of multi-mycotoxins from maize. This part of the research was aimed at providing technical solutions to some eminent challenges of conventional methods of mycotoxin extraction, such as, use of large volumes of harmful organic

solvents, high cost, long and tedious procedures as well as, as the inherent challenges of simultaneously extracting multiple mycotoxins in a single step. The adoption of advanced chemometric optimization models coupled with a co-solvent-modification of the PHWE system proved vital to achieve satisfactory recoveries across the analytes. The recovery values ranged from 71 to 124%, with the exception of ochratoxin A (OTA) and  $\alpha$ -ZEL which had recoveries of 58 and 14%, respectively. These values were comparable to those of at least three other methods which are solvent-based, validated and well referenced in literature. The linearity (0.986 to 0.999), intra-day precision (0 to 27%) and inter-day precision (3 to 34%) values of the modified PHWE method were also good relative to European Commission (EC), *Codex Alimentarius* (CODEX) and the Association of Official Analytical Chemists (AOAC) guidelines for analytical method performance. Furthermore, a pilot-scale application of the method on 25 maize flour samples purportedly naturally contaminated with mycotoxins was successful.

The third phase of this research work describes the broader application of the modified PHWE method for the estimation of mycotoxin levels in different commercially available food commodities. Ninety-one (91) samples of maize, sorghum and millet obtained from 5 agroecological zones in Nigeria were analyzed for mycotoxins using the modified PHWE method. For further authentication, the same samples were analyzed using a validated solvent extraction method which served as a control for cross-validation. Scrutiny of the results using principal component analysis (PCA) and orthogonal projections to latent structures discriminate analysis (OPLS-DA) indicated that there were no significantly different patterns in the data obtained using the two methods. Accordingly, the results revealed that all of the maize samples (n=16), 32% (n=38) of sorghum and 35% (n=37) of millet samples were positive for at least one of the 15 tested mycotoxins. Amongst the toxins, fumonisins (FBs) were the most prevalent in terms of incidence rate and contamination levels. Aflatoxin (AF) contamination was also relatively high in the samples. In maize, mean contamination levels for aflatoxin B<sub>1</sub> (AFB<sub>1</sub>) and sum of aflatoxins ( $\Sigma$ AFs) was 54 and 56  $\mu$ g/kg, respectively. Eleven out of 16 of the maize samples were contaminated above the EC maximum level of 2 and 4  $\mu$ g/kg for AFB<sub>1</sub> and  $\Sigma$ AFs, respectively. Generally, mycotoxins were more prevalent in maize, followed by sorghum and then millet. Co-occurrence of two or more mycotoxins, particularly AFs+FBs, were observed in some of the cereal samples, which re-affirmed the seriousness of the mycotoxin issue in Nigeria and the need for effective and sustainable intervention approaches to address this issue.

Overall, PHWE seems promising as a suitable and greener alternative to traditional methods of mycotoxin extraction. Research in this area is envisaged to allow bioanalytical scientists working in the field of mycotoxicology to conveniently and efficiently extract mycotoxins in various agricultural products without the need for harmful and expensive organic solvents, as well as, promote analytical techniques that are more environmentally friendly and sustainable.

**Keywords:** Mycotoxins, thermal stability, method development, chemometric-assisted optimization, pressurized hot water extraction.



## DECLARATION

I, Sefater Gbashi, hereby declare that the composition of this doctoral thesis and the work herein described was carried out entirely by myself unless otherwise indicated. None of the material has been submitted previously, in whole or in part, for degree purposes at any other University or institution. All other sources used have been duly cited in text and acknowledged by complete references.



## **DEDICATION**

I dedicate this piece of work to God Almighty, the very essence of my existence and the sovereign ruler over the affairs of humanity. Also, to my family and late dad for the love and support.



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## RESEARCH OUTPUT

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Gbashi, S., Madala, N. E., Adekoya, I.O., De Saeger, S., De Boevre, M., Adebo, O. A., and Njobeh, P. B. (2018). The socio-economic impact of mycotoxin contamination in Africa. In: P. B. Njobeh (Ed.), *Fungi and Mycotoxins - Their Occurrence, Impact on Health and the Economy as well as Pre- and Postharvest Management Strategies* (pp. 1-20). Rijeka, Croatia: InTech.

### Journal articles

Gbashi, S., Madala, N. E., De Saeger, S., De Boevre, and Njobeh, P. B. (2019). Numerical optimization of the temperature-time degradation of multi-mycotoxins. *Food and Chemical Toxicology*, 125, 289-304.

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The logo of the University of Johannesburg is a watermark in the background. It features a stylized sunburst at the top, two birds with spread wings on either side of a central shield-like shape, and the text 'UNIVERSITY OF JOHANNESBURG' below it.

## LIST OF ABBREVIATIONS

<b>%+ve</b>	Percentage of positive samples
<b>%EtOH</b>	Percentage ethanol
<b>15-ADON</b>	15-acetyldeoxynivalenol
<b>3-ADON</b>	3-acetyldeoxynivalenol
<b>AAD</b>	Average absolute deviation
<b>A<sub>f</sub></b>	Accuracy factor
<b>AF</b>	Aflatoxin
<b>AFB's</b>	Aflatoxin B <sub>1</sub> and Aflatoxin B <sub>2</sub>
<b>AFB<sub>1</sub></b>	Aflatoxin B <sub>1</sub>
<b>AFB<sub>2</sub></b>	Aflatoxin B <sub>2</sub>
<b>AFG's</b>	Aflatoxin G <sub>1</sub> and Aflatoxin G <sub>2</sub>
<b>AFG<sub>1</sub></b>	Aflatoxin G <sub>1</sub>
<b>AFG<sub>2</sub></b>	Aflatoxin G <sub>2</sub>
<b>AFM<sub>1</sub></b>	Aflatoxin M <sub>1</sub>
<b>AFM<sub>2</sub></b>	Aflatoxin M <sub>2</sub>
<b>AFs</b>	Aflatoxins
<b>AME</b>	Alternariol monomethyl ether
<b>ANOVA</b>	Analysis of variance
<b>AOAC</b>	The Association of Official Analytical Chemists
<b>AOH</b>	Alternariol
<b>API</b>	Atmospheric-pressure ionization



<b>ARS</b>	Agricultural Research Service (USDA)
<b>BEA</b>	Beauvericin
<b>B<sub>f</sub></b>	Bias factor
<b>CCD</b>	Central composite design
<b>CE</b>	Collision energy
<b>CIT</b>	Citrinin
<b>CO<sub>2</sub></b>	Carbon dioxide
<b>CODEX</b>	<i>Codex Alimentarius</i>
<b>Corr.</b>	Correlation
<b>DALYs</b>	Disability-adjusted life years
<b>DAS</b>	Diacetoxyscirpenol
<b>DCM</b>	Dichloromethane
<b>DF</b>	Desirability factor
<b>DL</b>	Desolvation line
<b>DNA</b>	Deoxyribonucleic acid
<b>DON</b>	Deoxynivalenol
<b>DRS</b>	Derived savannah
<b>DTSC</b>	Department of Toxic Substances Control (California)
<b>EAs</b>	Ergot alkaloids
<b>EC</b>	European Commission
<b>ELISA</b>	Enzyme-linked immunosorbent assay
<b>ENNs</b>	Enniatins
<b>ESI<sup>+</sup></b>	Electron spray ionization

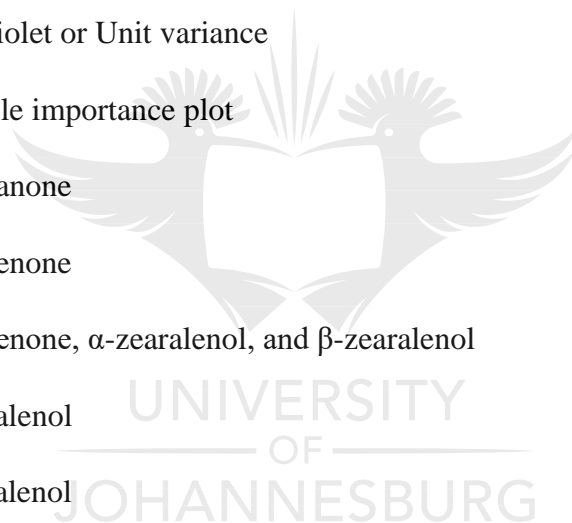
<b>EtOH</b>	Ethanol
<b>EU</b>	European Union
<b>FA</b>	Formic acid
<b>FAO</b>	Food and Agriculture Organization (UN)
<b>FB<sub>1</sub></b>	Fumonisin B <sub>1</sub>
<b>FB<sub>2</sub></b>	Fumonisin B <sub>2</sub>
<b>FB<sub>3</sub></b>	Fumonisin B <sub>3</sub>
<b>FBs</b>	Fumonisins
<b>FDA</b>	Food and Drug Administration (US)
<b>FID</b>	Flame ionization detection
<b>FUS-X</b>	Fusarenon-X
<b>GC</b>	Gas chromatography
<b>GDP</b>	Gross domestic product
<b>HACCP</b>	Hazard and critical control point
<b>HBV</b>	Hepatitis B virus
<b>HLWE</b>	Hot liquid water extraction
<b>HPLC</b>	High performance liquid chromatography
<b>HRF</b>	Humid rain forest
<b>HRMS</b>	High resolution mass spectrometry
<b>HWE</b>	Hot water extraction
<b>IA</b>	Immuno-affinity
<b>IAC</b>	Immuno-affinity column
<b>IARC</b>	International Agency for Research on Cancer

<b>ICH</b>	International conference on harmonization
<b>ID</b>	Inner diameter
<b>IT</b>	Ion trap
<b>LC</b>	Liquid chromatography
<b>LC-MS/MS</b>	Liquid chromatography coupled to tandem mass spectrometry
<b>LLOQ</b>	Lower limit of Quantification
<b>LOD</b>	Limit of detection
<b>LOQ</b>	Limit of quantification
<b>MAE</b>	Microwave-assisted extraction
<b>ME</b>	Matrix effect
<b>MLS</b>	Method of least square
<b>MON</b>	Moniliformin
<b>MRM</b>	Multiple reaction monitoring
<b>MS</b>	Mass spectrometry
<b>MS/MS</b>	Two mass spectrometers in tandem
<b>N.D.</b>	Not detected or Not determined
<b>NA</b>	Not applicable
<b>NGS</b>	Northern guinea savannah
<b>NI</b>	Not investigated
<b>NIV</b>	Nivalenol
<b>NMISA</b>	National Metrological Institute of South Africa
<b>OD</b>	Outer diameter
<b>OPLS-DA</b>	Orthogonal projections to latent structures discriminate analysis

<b>OTA</b>	Ochratoxin A
<b>OTB</b>	Ochratoxin B
<b>OTC</b>	Ochratoxin C
<b>OTD</b>	Ochratoxin D
<b>OTs</b>	Ochratoxin A and ochratoxin B
<b>PA</b>	Penicillic acid
<b>PAT</b>	Patulin
<b>PCA</b>	Principal component analysis
<b>PCs</b>	Principal components
<b>PDA</b>	Photo-diode array detector
<b>PHW</b>	Pressurized hot water
<b>PHWE</b>	Pressurized hot water extraction
<b>PLPWE</b>	Pressurized low polarity water extraction
<b>Q1</b>	Quadruple 1
<b>Q1 Pre bias</b>	Quadruple one pre-rod bias
<b>Q2(cum)</b>	Cumulative predictive capacity
<b>Q3</b>	Quadruple 3
<b>Q3 Pre bias</b>	Quadruple three pre-rod bias
<b>qToF</b>	Quadrupole time-of-flight
<b>QuEChERS</b>	Quick, Easy, Cheap, Effective, Rugged, and Safe
<b><math>R^2</math></b>	Coefficient of determination
<b><math>R^2</math> Adj</b>	Adjusted coefficient of determination
<b><math>R^2X</math>(cum)</b>	Cumulative ratio of the variation of the X variables

<b>R2Y(cum)</b>	Cumulative ratio of the variation of the Y variables
<b>Ret. time</b>	Retention time
<b>RPM</b>	Revolutions per minute
<b>RSD</b>	Relative standard deviation
<b>RSD<sub>R</sub></b>	Inter-day precision also referred to as between-day (intermediate) precision
<b>RSD<sub>r</sub></b>	Intra-day precision
<b>RSM</b>	Response surface methodology
<b>S/N</b>	Signal to noise ratio
<b>SFE</b>	Supercritical fluid extraction
<b>SGS</b>	Southern guinea savannah
<b>SHS</b>	Sahel savannah
<b>sIgA</b>	Secretory Immunoglobulin A
<b>SIM</b>	Single ion monitoring
<b>SOLV-DS</b>	Solvent extraction followed by dilute and shoot injection
<b>SOLV-EXT</b>	Solvent extraction
<b>SOLV-SPE</b>	Solvent extraction followed by clean-up using different SPE cartridges
<b>SPE</b>	Solid phase extraction
<b>STEG</b>	Sterigmatocystin
<b>SWE</b>	Subcritical water extraction
<b>T1L</b>	Linear effect of temperature
<b>T1L by T2L</b>	Interaction effect temperature and time
<b>T1Q</b>	Quadratic effect of temperature
<b>T-2</b>	T-2 toxin

<b>T2L</b>	Linear effect of time
<b>T2Q</b>	Quadratic effect of time
<b>THs</b>	Trichothecenes
<b>TLC</b>	Thin layer chromatography
<b>USD</b>	US dollars
<b>UN</b>	United nations
<b>UHPLC</b>	Ultra-high performance liquid chromatography
<b>UPLC</b>	Ultra-performance liquid chromatography
<b>UV</b>	Ultraviolet or Unit variance
<b>VIP</b>	Variable importance plot
<b>ZAN</b>	Zearalanone
<b>ZEA</b>	Zearalenone
<b>ZEAs</b>	Zearalenone, $\alpha$ -zearalenol, and $\beta$ -zearalenol
<b><math>\alpha</math>-ZEA</b>	$\alpha$ -zearalenol
<b><math>\beta</math>-ZEA</b>	$\beta$ -zearalenol



## LIST OF SYMBOLS AND UNITS

<b>%</b>	Percentage
<b>±</b>	Plus or minus
<b>≤</b>	Less than or equal to
<b>≥</b>	Greater than or equal to
<b>°C</b>	Degree Celsius
<b>µg</b>	Microgram
<b>µg/g</b>	Microgram per gram
<b>µL</b>	Microlitre
<b>µm</b>	Micrometer
<b>C18</b>	Octadecyl
<b>C2</b>	Ethyl
<b>C8</b>	Octyl
<b>Channels/sec</b>	Channels per second
<b>CN</b>	Cyanopropyl
<b>Da</b>	Dalton
<b>eV</b>	Electron volts
<b>ε</b>	Dielectric constant
<b>g</b>	Gram(s)
<b>h</b>	Hour(s)
<b>H<sub>2</sub>SO<sub>4</sub></b>	Sulphuric acid
<b>KCl</b>	Potassium chloride
<b>L/min</b>	Litres per minute
<b>m/z</b>	Mass to charge ratio
<b>Min</b>	Minute(s)



<b>mL</b>	Millilitre
<b>mL/min</b>	Millilitre per minute
<b>mM</b>	Millimolar
<b>mm</b>	Millimeter
<b>mm/yr</b>	Millimeters per year
<b>NH<sub>2</sub></b>	Aminopropyl
<b>psi</b>	Pounds per square inch
<b>r</b>	Pearson's bivariate coefficient
<b>S/N</b>	Signal-to-noise ratio
<b>sec</b>	Second(s)
<b>V</b>	Volts
<b>µg/g</b>	Microgram per gram
<b>µg/kg</b>	Microgram per kilogram





## THESIS OUTLINE

This thesis describes studies on the design, optimization, validation and applicability of a modified pressurized hot water extraction (PHWE) method for the analysis of mycotoxins in food commodities. The experiments described herein were conducted in the Department of Biotechnology and Food Technology, University of Johannesburg (South Africa) and partly at the Centre of Excellence in Mycotoxicology and Public Health, Department of Bioanalysis, Ghent University (Belgium). The thesis consists of six chapters; a brief outline of each of the chapters is presented below.

### Chapter One

This introductory chapter provides a general overview of the research subject and rationale. The chapter starts off by presenting relevant background information, describing the problem under investigation and the context within which this study was conducted. Important terms used in the study are defined, while also highlighting the theoretical assumptions (hypothesis), aim and objectives of the study.

### Chapter Two

This chapter reviews relevant literature within the context of the research focus, situates the research objectives in the framework of the wider academic community of mycotoxicology, and gives credence to the research rationale by identifying the knowledge gaps that the research seeks to explore. The concept of mycotoxins, their chemical characteristics, occurrence and significance is described. Various conventional methods of mycotoxin extraction including their pros and cons is reviewed. The principles and applications of mass spectrometry (MS) in mycotoxin analysis is also presented. The chapter further describes the process of method development and parameters that must be considered when validating an analytical method. The concept, mechanism and dynamics of PHWE, its advantages, disadvantages and applicability are also exhaustively appraised. The chapter ends by describing various chemometric tools applicable in the development of sample preparatory procedures and bioanalytical chemistry. Some aspects of this chapter have been published under two titles: the first is a book chapter titled *Subcritical water extraction and its prospects for aflatoxins extraction in biological materials*, which is published in InTech. The second publication is titled *The socio-economic impact of mycotoxin in Africa*, which is also published as a book chapter by the same publisher.

### **Chapter Three**

Chapter Three describes experiments on a systematic study of the thermal stability and degradation patterns of multi-mycotoxins as a function of temperature and time using a numerical optimization approach called the central composite design. The experimental design, methodology and a detailed interpretation and discussion of the results thereof are clearly described. The work described in this chapter has been published online in Food and Chemical Toxicology.

### **Chapter Four**

The chapter's primary focus is on the development, optimization and validation of a modified PHWE method for the extraction of multi-mycotoxins and subsequent analysis on UHPLC-MS/MS. The chapter describes the adoption of a chemometric optimization approach for this purpose. Method validation was performed according to standard guideline parameters by the European Commission (EC), *Codex Alimentarius* (CODEX), The Association of Official Analytical Chemists (AOAC), and the International Conference on Harmonization (ICH). Comparison of the validated PHWE method was made against a number of established solvent extraction methods. The Chapter further describes a pilot scale application of the validated PHWE method in the analysis of locally sourced food samples (*i.e.*, maize meal) for possible mycotoxin contamination.

### **Chapter Five**

A comparative application of PHWE and a solvent-based extraction method for the quantitative estimation of mycotoxin levels in staple cereals (maize, sorghum and millet) from different agroecological zones in Nigeria is presented in Chapter Five. In addition to providing practical application for the PHWE method, inference is drawn from the results of this study to determine the current risk and situation of mycotoxin prevalence in the country.

### **Chapter Six**

This chapter reaffirms the research focus (*i.e.*, problem statement and aim) of this thesis and puts the entire research experiments presented in Chapters Three to Five into perspective via an overall discussion of the issues addressed in the chapters. The contributions of the thesis to existing knowledge, recommendations and directions for future research is also provided.

## CHAPTER ONE

### 1. INTRODUCTION

#### 1.1 BACKGROUND

The pervasive contamination of agricultural commodities by mycotoxins has become a serious global concern because of their severe impact on health and the economy (Lizárraga-Paulín *et al.*, 2011; Makun *et al.*, 2012). These toxins are low-molecular weight secondary metabolites of fungi origins, principally those belonging to the genera *Aspergillus*, *Penicillium*, *Claviceps* and *Fusarium* (Njobeh *et al.*, 2010; Zain, 2011; Garba *et al.*, 2017). Prevalence of mycotoxins does not only constitute a public health hazard, it also affects livelihood, food security, income and causes significant economic losses (Daniel *et al.*, 2011; Enyiukwu *et al.*, 2014; Gbashi *et al.*, 2018). These toxins have been identified as the most significant chronic dietary risk factor, superior to other natural inherent plant toxins, synthetic contaminants, food additives, or pesticide residues (Kuiper-Goodman, 1998; Bennett and Klich, 2003). In fact, one of the mycotoxins, aflatoxin B<sub>1</sub> (AFB<sub>1</sub>) has been recognized as the most potent naturally occurring carcinogen known to man (Makun *et al.*, 2012). In 2010, over 130 people died in Kenya and another episode in mid-2011 in South Africa over 220 dogs died after consuming respectively, maize and pet food contaminated with high levels of aflatoxins (AFs) (Lewis *et al.*, 2005; Daniel *et al.*, 2011; Mwanza *et al.*, 2013). About 25% of the global food and feed produce is contaminated by mycotoxins (Enyiukwu *et al.*, 2014), and very often, contamination of agricultural commodities by mycotoxins results from a cumulative process, which begins from pre-harvest through post-harvest stage and continues throughout the entire food production chain (Wilson & Abramson, 1992; Gbashi *et al.*, 2018). Some factors that drive mycotoxin contamination along the food and feed supply chain are the favorable climatic conditions for fungi growth, poor agricultural practices, poverty, limited data on their occurrence and effects, as well as inadequate regulatory mechanisms (Mejía-Teniente *et al.*, 2011; Njobeh & Olotu, 2017). It has been estimated that approximately 4.5 billion people in the world are at the risk of being chronically exposed to mycotoxins (Bryden, 2007; Turner *et al.*, 2007). As a result of their widespread proliferation and associated deleterious effects, there is a growing concern over their intake via consumption of contaminated food and feed by humans and animals alike. This has led to more stringent guidelines and regulatory limits of these toxins, especially with the globalization of the food supply chain, and consequently, necessitating the need

for routine surveillance of these toxicants in agricultural commodities (Krska *et al.*, 2008; Rahmani *et al.*, 2009). In this regard, there has been an ever increasing demand for more efficient and robust analytical methods for the determination of mycotoxins, particularly with respect to safer, cheaper and quicker methods (Rahmani *et al.*, 2009; Gbashi *et al.*, 2017c).

## 1.2 PROBLEM STATEMENT

Extraction is an important step in mycotoxin analysis. It is almost inevitable irrespective of the protocol adopted. Although different methods exist for extracting mycotoxins from food and feed such as solvent extraction, solid-phase extraction (SPE) and immuno-affinity column (IAC) extraction amongst others, there are concerns over human and environmental health regarding safety in their applications (Teo *et al.*, 2010; Gbashi *et al.*, 2017d). These conventional methods are also tedious and time-consuming (Choi *et al.*, 2003), requiring relatively large volumes of organic solvents, which are expensive and hazardous (Santana *et al.*, 2009; Teo *et al.*, 2010). Bearing in mind these concerns, the design of a greener method that is efficient, cheap, fast and relatively easy to use is eminent. Pressurized hot water extraction (PHWE) seems promising in this regard. Better results, recoveries and effectiveness have been reported for PHWE as compared to other traditional methods for extracting different bioactive compounds (Hawthorne *et al.*, 2000; Kubátová *et al.*, 2001; Bart, 2005). It is intended herein to explore the possibilities of designing and adopting a modified PHWE method as an alternative to conventional methods for multi-mycotoxin extraction from various food commodities.

## 1.3 JUSTIFICATION

Analysis is an important component of mycotoxin control and management. The quality of analytical results has often been directly linked to the efficacy of the extraction process utilized. At present, available extraction methods for mycotoxins analysis remain largely limiting in many ways, particularly in terms of human and environmental safety, cost, time and labor intensity. This study sets out to address these issues by adopting an innovative, green and efficient extraction approach, PHWE, for mycotoxin analysis in agricultural commodities. To the best of our knowledge, there has been no report on the use of PHWE for mycotoxins analysis. However, the adoption of PHWE for multi-mycotoxin extraction has some envisageable challenges such as the possibility of degradation of some of the analytes due to the thermal conditions involved during

PHWE. Also, due to the diverse physicochemical properties of the different classes of mycotoxins, there may be limited extractability of some of the mycotoxins in a single-step multi-mycotoxin extraction procedure. In this regard, it is critical to adequately optimize the PHWE system using appropriate models for optimum performance of the method.

#### **1.4 HYPOTHESIS**

It has been hypothesized in this research work that: (1) using optimization models, it would be possible to establish the thermal degradation patterns and ascertain the thermal stability of mycotoxins within a range of temperatures relevant to PHWE; (2) by means of advanced chemometric tools, and perhaps, a co-solvent, it would be possible to design and optimize a PHWE method for the simultaneous extraction of multiple mycotoxins followed by quantification on ultra-high performance liquid chromatography and tandem mass spectrometry (UHPLC-MS/MS); (3) the optimized PHWE method would perform adequately relative to standard guideline parameters for validation of analytical methods; (4) practical applicability of the validated PHWE method would be achievable for the analysis of naturally contaminated food samples for possible mycotoxin contamination.

#### **1.5 AIM**

The aim of this research work was to develop, optimize and validate a modified pressurized hot water extraction (PHWE) method, and adopt same for multi-mycotoxin analysis in food commodities.

#### **1.6 OBJECTIVES**

The objectives of this research were:

- i. To optimize the temperature-time degradation of multi-mycotoxins.
- ii. To develop, optimize and validate a modified PHWE method for the extraction of multi-mycotoxins in maize.
- iii. To adopt the validated PHWE method for the extraction and subsequent estimation of multi-mycotoxin levels in various commercially available food commodities from Nigeria and South Africa.

## CHAPTER TWO

### 2. MYCOTOXINS

#### 2.1 DEFINITION AND CONCEPT OF MYCOTOXINS

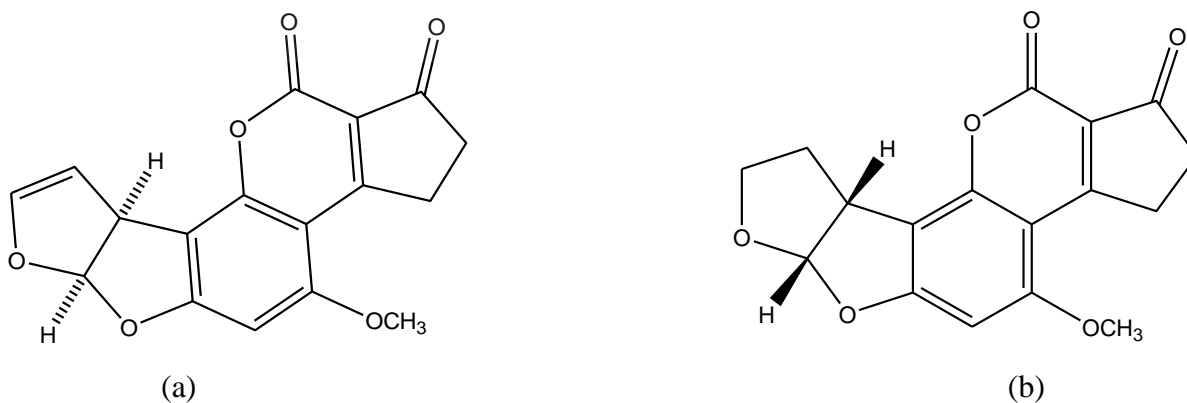
Mycotoxins can simply be described as toxic biochemical compounds produced by fungi (Adeyeye, 2016). These compounds are diverse secondary metabolites synthesized by certain fungi species that are ubiquitous in the food supply chain, contaminating pre- and post-harvest crops, as well as, processed food and feed commodities (Njobeh *et al.*, 2010b; Abia *et al.*, 2013; Chilaka *et al.*, 2016). Fungal genera most frequently associated with mycotoxin production include *Aspergillus*, *Penicillium*, *Fusarium* and *Alternaria*, that are notable for their toxigenicity and disease-causing effects amongst humans and animals (Gbashi *et al.*, 2018).

Production of mycotoxins by fungi depends on a number of factors including environmental conditions, physical damage to the crop, and the nature of the food substrate (Kokkonen *et al.*, 2010; Magan *et al.*, 2011; Pitt *et al.*, 2013). A single fungal species may synthesize more than one mycotoxin, while a specific mycotoxin may be produced by more than one fungal species all depending on favorable environmental conditions (Bayman & Baker, 2006; McCormick *et al.*, 2011; Ismaiel & Papenbrock, 2015). Tropical climatic conditions such as in sub-Saharan Africa particularly favors the proliferation of mycotoxins. Over 300 mycotoxins have been characterized in literature, however, only a few have received significant attention due to their health and economic importance. Some of the economically important mycotoxins include aflatoxins (AFs), fumonisins (FBs), ochratoxins (OTs), zearalenone (ZEA) and its analogues  $\alpha$ -zearalanol ( $\alpha$ -ZEL) and  $\beta$ -zearalanol ( $\beta$ -ZEL), T-2 toxin (T-2), HT-2 toxin (HT-2), sterigmatocystin (STEG), alternariol monomethyl ether (AME), deoxynivalenol (DON), citrinin (CIT), and patulin (PAT). These mycotoxins and some of the emerging mycotoxins are described in detail in the succeeding sections of this chapter.

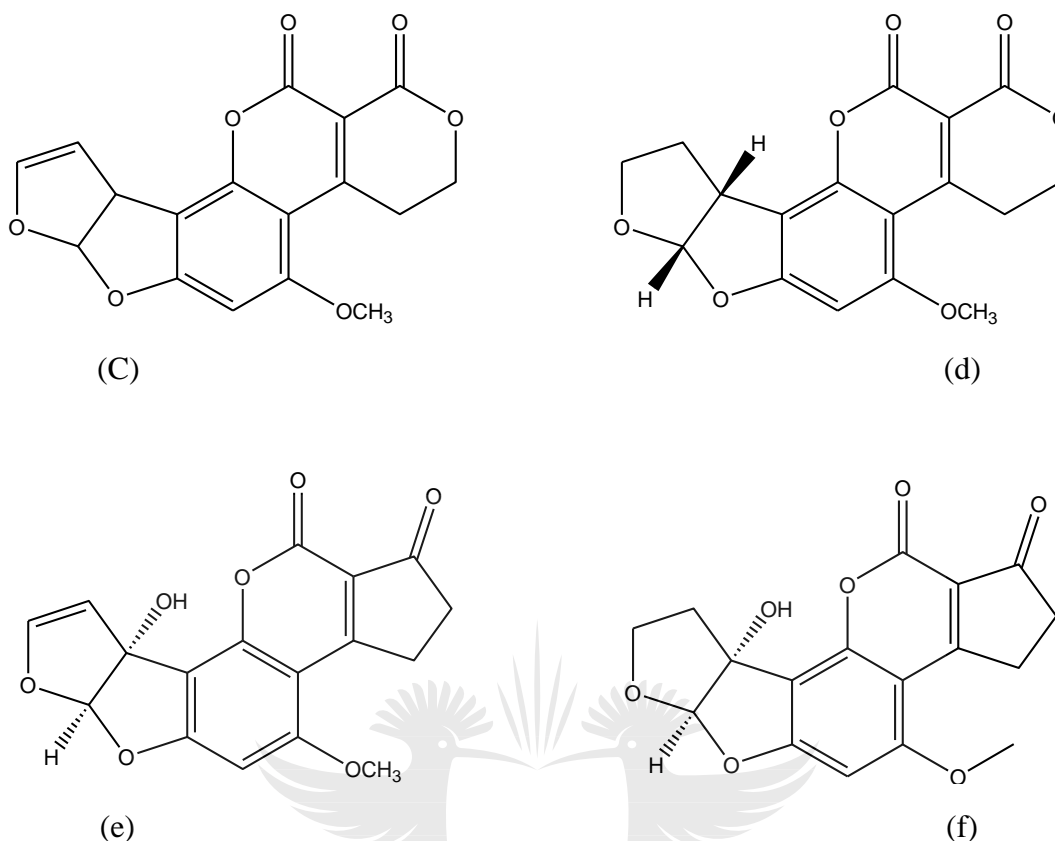
## 2.2 MYCOTOXIN DIVERSITY: STRUCTURAL, PHYSICOCHEMICAL AND TOXICOLOGICAL CHARACTERISTICS

### 2.2.1 Aflatoxins

Aflatoxins are the most perilous group of mycotoxins to humans and animals (Gbashi *et al.*, 2017c). They are produced by toxigenic strains of *Aspergillus flavus*, *A. parasiticus* and *A. niger* (Mircea *et al.*, 2008; Makun *et al.*, 2012; Yang *et al.*, 2014). At least 14 different types of AFs are known to exist in nature, however, the major ones of economic and health significance are AFB<sub>1</sub>, aflatoxin B<sub>2</sub> (AFB<sub>2</sub>), G<sub>1</sub> (AFG<sub>1</sub>), G<sub>2</sub> (AFG<sub>2</sub>), M<sub>1</sub> (AFM<sub>1</sub>) and M<sub>2</sub> (AFM<sub>2</sub>) (Figure 2.1). The molecular structure of AFs generally constitutes highly substituted coumarins containing a fused dihydrofurofuran moiety. The AFB's (*i.e.*, members of the blue fluorescent series) generally feature a fusion of a cyclopentenone ring to the lactone ring of the coumarin moiety, while the AFG's possess a fused lactone ring (Kensler *et al.*, 2011). Aflatoxin B<sub>1</sub> and G<sub>1</sub> contain an unsaturated bond on the terminal furan ring at the 8,9 position. Epoxidation at this position has shown to be essential for their carcinogenicity (Groopman & Kensler, 2005). Aflatoxin M<sub>1</sub> and M<sub>2</sub> are hydroxylated metabolites of AFB<sub>1</sub> and B<sub>2</sub>, respectively, bio-transformed by the liver and found in milk, urine and other body fluids, being less harmful than their precursor toxins (Prado *et al.*, 2008; Bbosa *et al.*, 2013). The intensity of fluorescence (light) emission differs greatly among the four compounds. This property plays a significant role in their quantification by fluorescence techniques (Dhanasekaran *et al.*, 2011).





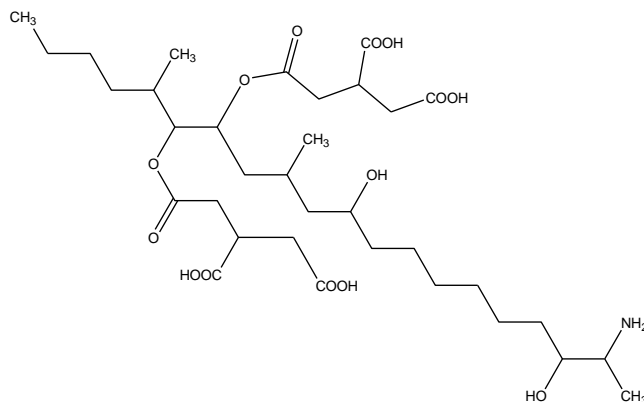


**Figure 2.1:** Chemical structures of (a) AFB<sub>1</sub> (b) AFB<sub>2</sub> (c) AFG<sub>1</sub> (d) AFG<sub>2</sub> (e) AFM<sub>1</sub> and (f) AFM<sub>2</sub> (Dhanasekaran *et al.*, 2011).

Aflatoxins are highly carcinogenic and equally recognized as being immunosuppressive. Among the AF group, AFB<sub>1</sub> is considered the most toxic. This one has been established as the most notorious naturally occurring carcinogen (IARC, 2002; D’Mello, 2003; Makun *et al.*, 2012). For that reason, it has been classified as a group 1 human carcinogen by the International Agency for Research on Cancer (IARC) (IARC, 2002; Park *et al.*, 2004a). Cereals such as maize are common crops that are contaminated by AFs. Additionally, crops such as oilseeds, including peanuts, different kinds of spices, figs and other dried fruit, are also familiar but most susceptible substrates. Aflatoxins are also very stable chemical compounds and notoriously difficult to eradicate in food commodities (Bullerman *et al.*, 1984; Turner *et al.*, 2009). They are chemically stable during processing and storage, even when heated at quite elevated temperatures such as those achieved during the production of breakfast cereals or baking of bread (Kabak, 2009; Turner *et al.*, 2009). This necessitates the avoidance of conditions that favor their production, which is not always feasible in practice (Turner *et al.*, 2009; Fernández-Cruz *et al.*, 2010).







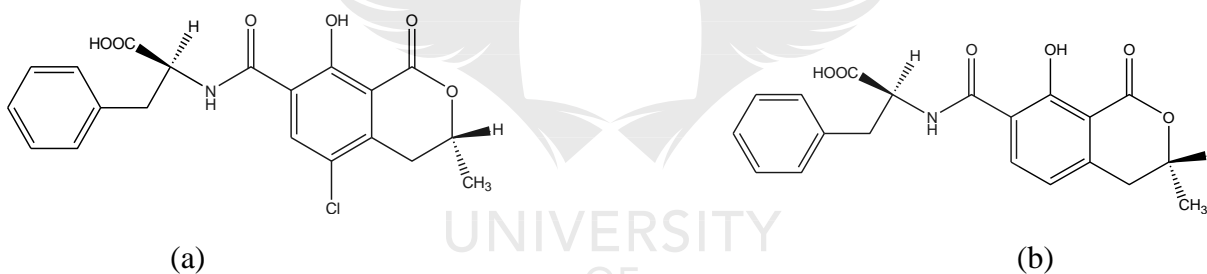
(c)

**Figure 2.2:** Molecular structures of (a) FB<sub>1</sub> (b) FB<sub>2</sub> and (c) FB<sub>3</sub> (Hussein and Brasel, 2001).

Fumonisinins are generally thermolabile and have shown significant losses in most heat-based food processing operations (Castelo *et al.*, 2001; Kabak, 2009; Patel *et al.*, 2011). Jackson *et al.* (1996) investigated the effects of temperature and time on the stability of FB<sub>1</sub> in aqueous model systems (*i.e.* aqueous solutions at pH 4, 7, and 10). It was observed that the rate of FB<sub>1</sub> decomposition increased in proportion to increasing temperature. Thermal processing at  $\leq 125$  °C for 60 min resulted in a 27% loss of FB<sub>1</sub>, after 60 min at 150 °C up to 18 to 90% of FB<sub>1</sub> was lost, depending on the pH buffer. Fumonisin B<sub>1</sub> was more thermally stable at neutral pH (*i.e.* pH 7), while the pH of 4 and 10 resulted in higher decomposition. The thermal processing condition of  $\geq 175$  °C for 60 min resulted in at least 90% decomposition regardless of the pH buffer. It has been shown that bound and hydrolysed forms of FBs are often formed during thermal processing of foods (Seefelder *et al.*, 2003; Humpf & Voss, 2004; Park *et al.*, 2004b). However, the occurrence of bound FBs is not limited to thermally processed food products (Patel *et al.*, 2011). Seefelder *et al.* (2001) reported the formation of hydrolyzed FB<sub>1</sub> when samples containing FB<sub>1</sub> and sucrose were thermally processed. These forms of FBs are usually elusive to conventional analytical methodologies (Park *et al.*, 2004b), as such, there is limited and inconsistent toxicological information about these compounds (Patel *et al.*, 2011; Braun & Wink, 2018). Nonetheless, a few reports have indicated that some hydrolysed forms of FBs are less toxic compared to the parent compound (Humpf & Voss, 2004; Voss *et al.*, 2017; Braun & Wink, 2018).

### 2.2.3 Ochratoxins

The ochratoxins are isocoumarin derivatives, occurring as ochratoxin A (OTA), B (OTB), C (OTC), D (OTD) and their methyl and ethyl esters (Haschek *et al.*, 2002). This group of mycotoxins are produced by some *Aspergillus* species (mainly *A. ochraceus* and *A. niger*) and some *Penicillium* species, particularly *P. carbonarius* and *P. verrucosum* (Bayman and Baker, 2006; Kočube *et al.*, 2013). Favored food substrates include cereals, coffee and grapes (Al-anati and Petzinger, 2006; El Khoury and Atoui, 2010). Similar to FB<sub>1</sub>, OTA is a prevalent toxin, classified as a group 2B carcinogen to human (IARC, 2002; Malir *et al.*, 2016). It accumulates in the organs and tissues of animals, including breast milk and human blood, thus, consumption of meat and meat products can constitute exposure to this toxin (Clark and Snedeker, 2006). In laboratory animals, OTA has been implicated for carcinogenicity (Mally and Dekant, 2009; Njobeh *et al.*, 2010). This toxin is also mutagenic and nephrotoxic (Palma *et al.*, 2007; Pfohl-Leszkowicz and Manderville, 2007). Figure 2.3 shows the chemical structure of OTA and OTB.

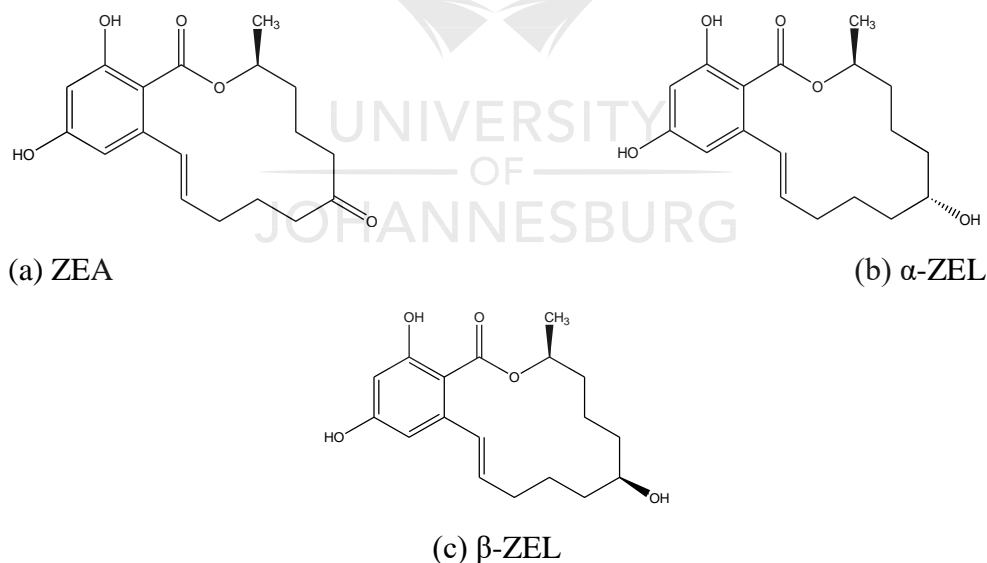


**Figure 2.3:** Molecular structures of (a) OTA, and (b) OTB (El Khoury & Atoui, 2010).

Ochratoxins are very stable to heat treatment (Raters & Matissek, 2008; Vidal *et al.*, 2015). This coupled to their widespread occurrence makes them very difficult to eradicate from the food chain (Kőszegi & Poór, 2016). Boudra *et al.* (1995) examined the stability of OTA under different moisture and temperature conditions. They observed that a temperature condition of 200 °C for 12 min could result in a 50% decomposition of OTA in dry wheat, while a temperature of 200 °C for 19 min was needed to achieve similar results when the wheat was heated under wet conditions. However, it was not possible to completely degrade OTA within the heating limits of the study i.e. conditions of 100-200 °C. This strongly indicates a high likelihood of detecting OTA in thermally processed food products, as such, it is recommended to adopt preventive measures in order to limit exposure to this mycotoxin.

### 2.2.4 Zearalenone

Zearalenone (ZEA) is a macrocyclic  $\beta$ -resorcyclic acid lactone metabolite (Figure 2.4) produced by certain *Fusarium* and *Gibberella* species, such as *F. culmorum*, *F. graminearum*, *F. roseum* and others (Atoui *et al.*, 2012; Hueza *et al.*, 2014). It has two major hydroxylated derivatives  $\alpha$ - and  $\beta$ - zearalenol ( $\alpha$ -ZEL and  $\beta$ -ZEL) (Figure 2.4), which are also lactone derivatives commonly found in food commodities (Gratz, 2017). However, many other derivatives and modified forms of ZEA occur in different agricultural commodities. Gromadzka *et al.* (2008) provides a detailed description and review of the ZEA and its metabolites, their occurrence, toxicity and detection in different food commodities. For the purpose of this review, emphasis will be placed only on ZEA,  $\alpha$ -ZEL and  $\beta$ -ZEL due to their toxicological significance and widespread occurrence in cereals from Africa. Food contamination with ZEA, and  $\alpha$ - and  $\beta$ -ZEL (ZEAs) has been reported worldwide and common food crop substrates include maize, millet, wheat, sorghum and rice (Atoui *et al.*, 2012; Hewitt *et al.*, 2012; Chilaka *et al.*, 2016). It has been reported that ZEAs usually co-occurs with one or more of the trichothecenes (THs), because of the ability of its producing fungi to synthesize more than one mycotoxin (Grenier & Oswald, 2011).



**Figure 2.4:** Molecular structures of (a) ZEA (b)  $\alpha$ -ZEL (c)  $\beta$ -ZEL (Hussein and Brasel, 2001).

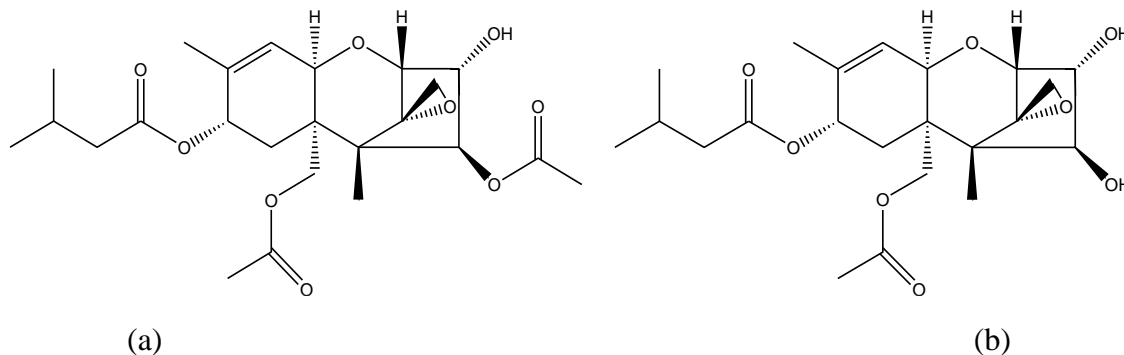
Zearalenone is soluble in alcohols, acetonitrile, benzene, chloroform, alkaline solutions but insoluble in water (Gromadzka *et al.*, 2008). Zearalenone,  $\alpha$ -ZEL and  $\beta$ -ZEL are chemically stable during oven heating, roasting a rotary gas-fired roaster, cooking, extrusion, milling and storage,

which may rationalize their quantification in processed food products such as beers, bread and processed animal feed (Yumbe-Guevara *et al.*, 2003; Gromadzka *et al.*, 2008; Hueza *et al.*, 2014). Numanoglu *et al.* (2013) modelled the thermal degradation of ZEA in bread made from naturally contaminated maize during baking at temperatures ranging from 100 to 250 °C. The authors reported no degradation of ZEA at 100 °C. Maximum degradation of ZEA was 28% which was achieved at 250 °C (for 15 min). However, statistical analysis of the results revealed that none of the degradations at the studied temperature conditions was statistically significant ( $p > 0.05$ ). Foods contaminated with ZEAs have been linked to female reproductive changes due to their potent estrogenic activity, which exceeds that of many naturally occurring non-steroidal estrogens (Bennett and Klich, 2003). Exposure to high concentrations of ZEA in cattle feed have been linked with enlargement of the mammary gland, infertility, reduced milk production, vaginal secretions and vaginitis particularly in young dairy heifers (Zinedine *et al.*, 2007). In swine, effects of ZEA include enlargement of the uterus, vaginal prolapse, swelling of the vulva, infertility, reduced litter size and embryonic death (Agag, 2004). These server effects of ZEAs in animals make its exposure a concern for human health.

### **2.2.5 T2-toxin and HT-2-toxin**

T2-toxin (T-2) is a type A trichothecene mycotoxin, and consists of a tetracyclic sesquiterpenoid 12,13-epoxytrichothene ring system (Mbundi *et al.*, 2014; Adhikari *et al.*, 2017). Together with its analogue HT-2 toxin (HT-2), these toxins (Figure 2.5) are reported to be produced by *F. poae*, *F. sporotrichioides*, *F. acuminatum* and *F. equiseti*, which are the predominant pathogens of rice, wheat, maize and other cereal grains including their processed products (D’Mello, 2003; Galbenu-Morvay *et al.*, 2011). T2-toxin and HT-2 have been reported to have different derivatives which exist in various modified forms such as glucosides (McCormick *et al.*, 2015; Bryła *et al.*, 2018; Schmidt *et al.*, 2018). It has been suggested that wheat and oat may metabolize T-2 and HT-2 to T-2 3-O-glucoside (T-2Glc) and to HT-2-O-3-glucoside (HT-2Glc) (Busman *et al.*, 2011). Several studies have reported the natural occurrence of glucosides of T-2 and HT-2 in maize, wheat, barley and oat grain (Veprikova *et al.*, 2012; Nakagawa *et al.*, 2013; Lattanzio *et al.*, 2015). Lattanzio *et al.* (2015) performed the first quantitative analysis of T-2 and HT-2 glucosides. The ratio between the free toxins (i.e. sum of T-2 and HT-2) and their corresponding glucosylated forms (i.e. sum of T-2 and HT-2 glucosides) was found to range from 2 to 283%. The authors reported levels up to

163  $\mu\text{g}/\text{kg}$  in 17 of the 18 analysed unprocessed barley grains for the glucosyl derivative of HT-2, whereas, much lower levels (and in fewer samples) were reported for the monoglucosyl derivative of T-2.



**Figure 2.5:** Molecular structures of (a) T-2 and (b) HT-2 (Adhikari *et al.*, 2017).

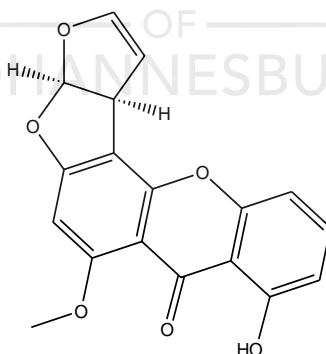
There is limited information in literature on the thermal stability of T-2 and HT-2. However, it is known that T-2 is non-volatile and relatively stable to adverse photo and thermal degradation conditions, as well as, during milling, storage, autoclaving, cooking, and other food processing conditions, though easily deactivated by strongly alkaline or acidic conditions (Marin *et al.*, 2013; Adhikari *et al.*, 2017). Schmidt *et al.* (2017) systematically investigated the degradation of T-2 and HT-2 in naturally and artificially contaminated oats during industrial and laboratory extrusion cooking. There was a higher degradation in artificially contaminated oats compared to the naturally contaminated oats. The laboratory cooking conditions for fortified oats resulted in 35 and 22% degradation of H2 and HT-2, respectively. Generally, higher degradation was observed in T-2 as compared to HT-2. In another study, Kuchenbuch *et al.* (2018) investigated the heat stability of T-2 and HT-2 during the baking and roasting process for biscuit, crunchy muesli and toasted oat flakes-production. Again, the authors reported higher thermal instability for T-2 as compared to HT-2; up to 45 and 20% of T-2 and HT-2, respectively, were thermally degraded during the biscuit-making process.

Though insoluble in water, T-2 is soluble in ethanol, methanol, acetone, ethyl acetate, chloroform and propylene glycol (Adhikari *et al.*, 2017). Its epoxide ring and several hydroxyl and acetyl functional groups on the side chains are responsible for its potent toxicity and biological activity (Vanhoutte *et al.*, 2016). T2-toxin is known to be genotoxic (Horvatovich *et al.*, 2013) and has been reported to induce apoptosis (Fang *et al.*, 2012). In China, consumption of mouldy rice

contaminated with *Fusarium* and T-2 have been implicated in human mycotoxicosis (Wang *et al.*, 1993).

### 2.2.6 Sterigmatocystin

Sterigmatocystin (STEG) is an AF-related substance produced during the biosynthesis of AFB<sub>1</sub> as an intermediate molecule (Nieto *et al.*, 2018). Its chemical structure (Figure 2.6) consists of a bifuran structure to which a xanthone nucleus is attached (Chen *et al.*, 2010). Sterigmatocystin is mainly produced by *A. versicolor* and *A. nidulans* (Nieto *et al.*, 2018), and has been reported as a contaminant of a variety of poor-quality cereal crops and other food/feed products such as maize, wheat, animal feed, pecan nuts and hard cheese (Ferrante *et al.*, 2012). There are indications that the toxicity of STEG is much similar to that of AFB<sub>1</sub>, as such, it is considered a potent mutagen, carcinogen and teratogen (Veršilovskis & De Saeger, 2010; Huang *et al.*, 2014b; Nieto *et al.*, 2018). However, literature reports on the occurrence and prevalence of this mycotoxin is scarce. This lack of information may be due to limitations in analytical methods, and may be the reason for lack of specific regulatory limits for this toxin in food and feed (Stroka *et al.*, 2004). Nonetheless, some European (EU) countries such as Czech republic and Slovakia have regulations for STEG ranging from 5-20 µg/kg depending on the food commodity (Stroka *et al.*, 2004). There is currently no information in literature on the thermal stability of STEG.



**Figure 2.6:** Molecular formula of sterigmatocystin (Nieto *et al.*, 2018).

### 2.2.7 Alternaria toxins

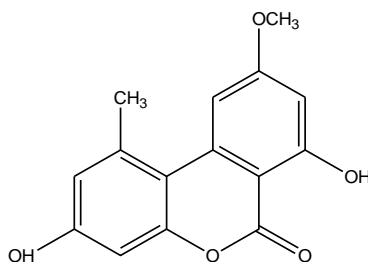
Alternaria toxins are a group of possible health-endangering secondary metabolites produced mainly by the *Alternaria* fungal species (Escrivá *et al.*, 2017; Hickert *et al.*, 2017). In terms of



their chemical structure, these mycotoxins are related to FBs and are reported to contaminate mainly fruits and vegetables, however, they are equally found in other crops, especially cereals (Ostry, 2008; Escrivá *et al.*, 2017). *Alternaria alternata* is the most important mycotoxin-producing species of the *Alternaria* species, and frequently contaminates a number of economically important crops (Li *et al.*, 2001; Meena *et al.*, 2017). Many important *Alternaria* toxins are known to naturally contaminate *Alternaria*-infected crops, some of which include alternariol, tenuazonic acid, altenuene, alternariol monomethyl ether (AME), and altertoxin I, however, for the purpose of this review, the focus would be on AME, due to its economic and health significance in various cereal crops from Africa.

The *Alternaria* toxin, AME, is a benzopyrone secondary metabolite, structurally elucidated as 3,7-dihydroxy-9-methoxy-1-methyl-6H-dibenzo[b,d]pyran-6-one (Figure 2.7) which is produced mainly by *Alternaria alternata* (Scott *et al.*, 2012), though other *Alternaria* species (Ostry, 2008; Logrieco *et al.*, 2009), and other fungi genera such as *Phomopsis strains* (Abreu *et al.*, 2012) and *Stagonospora nodorum* (Tan *et al.*, 2009) are reported to produce this mycotoxin as well. Alternariol monomethyl ether is a mycotoxin that is prevalent in the temperate regions of the world (Juan *et al.*, 2016; Escrivá *et al.*, 2017), however, recent reports show its increasing presence in more tropical countries, particularly in Africa (Van de Perre *et al.*, 2015; Abass *et al.*, 2017; Hickert *et al.*, 2017). Favored food substrates include rice, maize, barley, sorghum, bread and other bakery products, fruits, vegetables and beverages (Asam *et al.*, 2011; Escrivá *et al.*, 2017). Despite being identified and characterized over 65 years ago (Raistrick *et al.*, 1953), there are still limited studies on the toxicity of this compound. Alternariol monomethyl ether is reported to be mutagenic *in vitro* (Schrader *et al.*, 2001; Yekeler *et al.*, 2001; Scott *et al.*, 2012). Podlech and Marko (Podlech & Marko, 2009) observed that AME and alternariol (AOH) induced breaks in DNA strands in cell cultures (Podlech & Marko, 2009). There is limited information in literature on the thermal stability of AME, however, it has been shown to be thermally stable during wet baking conditions (Siegel *et al.*, 2010).





**Figure 2.7:** Molecular structure of alternariol monomethyl ether (Ostry, 2008)

### 2.2.8 Other mycotoxins

Aside from the afore-mentioned mycotoxins, many other mycotoxins exist which are equally of health and economic significance, such as citrinin (CIT), nivalenol (NIV), deoxynivalenol (DON), patulin (PAT), moniliformin (MON), ergot alkaloids (EAs), Fusarenon-X (FUS-X), penicillic acid (PA), including emerging mycotoxins such beauvericin (BEA), 3-acetyldeoxynivalenol (3-ADON), 15-acetyldeoxynivalenol (15-ADON), and the enniatins (ENNs). Nivalenol and FUS-X usually co-occur in nature and are some of the best known THs (Omurtag, 2008; Saengtienchai *et al.*, 2014). Diacetoxyscirpenol (DAS) is prevalent in mixed feed samples and various cereal crops such as barley, maize and other grains around the world. The co-occurrence of T-2 and DAS in food and feed constitutes poses a concern to human and animal health in some parts of the world (Omurtag, 2008; Rodrigues *et al.*, 2011). The fungal genera *Balarisia*, *Acremonium*, *Aspergillus* and *Claviceps* are responsible for the production of EAs (Panaccione *et al.*, 2006; Schardl *et al.*, 2006), which have been linked with a number of outbreaks of mycotoxicosis around the world (Schneider *et al.*, 1996; De Costa, 2002; Naude *et al.*, 2005). The prevalence of these mycotoxins in food crops have been reviewed extensively in literature (Cardwell, 2000; Darwish *et al.*, 2014; Magoha *et al.*, 2014; Misihairabgwi *et al.*, 2017), and can be strongly associated with a number of socio-economic impacts (Gbashi *et al.*, 2018).

Another important group of mycotoxins that are gaining increased popularity recently are the modified mycotoxins. Modified mycotoxins refer to any alteration of the basic chemical structure of the mycotoxin enabled by matrix-association, biological (plant, animal or fungi) or chemical (thermal or non-thermal processing) modifications (Rychlik *et al.*, 2014). These modified forms of the mycotoxins are usually undetected during conventional analysis of mycotoxins (Chilaka *et al.*, 2017; Freire & Sant'Ana, 2018). A case in point which stimulated interest in the study of

modified mycotoxins was reported by Gareis *et al.* (1990) where mycotoxicosis symptoms were observed in animals fed with feed containing relatively low levels of mycotoxins. The unexpected elevated toxicity which could not be correlated with the levels of the mycotoxins in the feed was credited to hidden (conjugated) forms of mycotoxins present in the animal feed. After ingestion, these modified mycotoxins are “unmasked” *i.e.* converted into free mycotoxins in the digestive system of the animals (Gareis *et al.*, 1990). As a result of this finding and other subsequent corroborating reports in the literature (Ajandouz *et al.*, 2016; Gratz *et al.*, 2017), there has been growing interest in the prevalence and toxicity of modified mycotoxins (Galaverna *et al.*, 2009; Freire & Sant’Ana, 2018). Advances in analytical methodologies such as the use of high-resolution mass spectrometry (HR-MS) coupled with ultra-high performance liquid chromatography (UPHLC) have enabled easier and more efficient study of these mycotoxin and the discovery of newer ones (Cirlini *et al.*, 2012; Rychlik *et al.*, 2014).

The occurrence of various modified mycotoxins have been reported in African commodities (Shephard *et al.*, 1994; Chilaka *et al.*, 2016, 2017). Zearalenone-4-sulfate (ZEN-4S) has been reported in Cameroonian maize beer in the range of 0.01 to 0.6 µg/kg (Abia *et al.*, 2013). Deoxynivalenol-3-glucoside (DON-3G) and Hydrolysed FB<sub>1</sub> (HYD FB<sub>1</sub>) have been reported in stored maize from Nigeria (Adetunji *et al.*, 2014). Seventy-seven animal feed samples from Egypt were screened for the presence of multiple mycotoxins by Abdallah *et al.* (2017). All samples were contaminated with at least four toxins, the presence of modified mycotoxins such as deoxynivalenol-3-glucoside and other emerging mycotoxins such as beauvericin and fusaproliferin were established.

## **2.3 EXPOSURE TO MYCOTOXINS AND THE SOCIO-ECONOMIC IMPACT**

The presence of mycotoxins in the food and feed supply chain is of much concern because it results in serious socio-economic problems.

### **2.3.1 Exposure to mycotoxins**

Common route of exposure to mycotoxins include oral ingestion of mycotoxin-contaminated food and feed, however, dermal, inhalation (respiratory) and parental (placental and breastfeeding) exposure have also been reported (Boonen *et al.*, 2012; Gbashi *et al.*, 2017c). After assimilation

into the body, mycotoxins enter the blood stream and lymphatic system, and their actions are usually mediated in important body organs and systems such as the kidney, liver, lungs, immune system, endocrine and nervous systems (Bennett & Klich, 2003; CAST, 2003; Atanda *et al.*, 2013). Exposure to mycotoxins can be chronic or acute, and the symptoms and severity of the resulting illness is dependent on the type of and concentration of the mycotoxin, as well as, the duration of exposure, age, sex, species and health status of the victim (Bennett & Klich, 2003).

The illness that results from consumption of mycotoxin-contaminated foods is termed mycotoxicosis (Richard, 2007). If there are evident symptoms within a period of seven days of exposure, it is termed “acute mycotoxicosis” and the victim may die if no proper medical attention is given. However, “chronic mycotoxicosis” has a longer window period of over seven days and the victim may survive though with protracted illnesses (Atanda *et al.*, 2013). Mycotoxicosis resulting from AF poisoning is referred to as “aflatoxicosis” (Dhanasekaran *et al.*, 2011), that resulting from poisoning by OTs is termed “ochratoxicosis” (Ibrahim *et al.*, 2013), whereas mycotoxicosis resulting from exposure to ergot alkaloids is termed “ergotism” (Naude *et al.*, 2005). A major public health concern of exposure to mycotoxins is that outbreaks of mycotoxicosis often remain unrecognized by health workers for an extended period of time, except when a large number of people are affected (Gbashi *et al.*, 2017c).

Numerous cases of mycotoxicosis have been reported in literature. The most recently reported instance of mycotoxicosis was the 2016 outbreak of acute aflatoxicosis in the central part of Tanzania which resulted in 68 cases, 50% of which were below the age of 15 years (Kamala *et al.*, 2018). Up to 30% of the cases ended in mortality. Highly contaminated home-grown maize (10 to 51,100 µg/kg) was implicated as the cause for the outbreak. In Ibadan, Nigeria, the death of some children who consumed mold-infested *kulikuli* was linked with aflatoxicosis (Atanda *et al.*, 2013). An outbreak of hepatitis in 1974 in India that killed 100 people and caused ailment in hundreds of others was as a result of exposure to AFs from heavily contaminated maize (Montville and Matthews, 2008). Fumonisin have been reported to be the cause of hepatotoxicity, carcinogenicity and nephrotoxicity in numerous animals (Howard *et al.*, 2001; Voss *et al.*, 2007; Stockmann-Juvala & Savolainen, 2008). One of the most epic episodes of mycotoxicosis reported in human history occurred in rural Kenya, of which 125 deaths and 317 cases of illnesses were reported (Lewis *et al.*, 2005). The cause of this outbreak was deciphered to be consumption of maize

products contaminated with AFs (above the Kenyan regulatory limit of 20 µg/kg). Examples of well-known cases of mycotoxicosis and details on several other known mycotoxin related diseases in animals have also been provided by Pettersson (2004), Richard (2007) and Peraica *et al.* (2014).

### **2.3.2 Socio-economic impact of mycotoxins**

Mycotoxin contamination has contributed significantly to the elusive sustainable development in many parts of the world. The socio-economic significance of mycotoxin prevalence has reached global proportions, with both the developed and developing nations incurring severe consequences, though the developing nations are the most affected.

#### **2.3.2.1 Impact on health**

The most significant impact of mycotoxin contamination has been demonstrated to be on human and animal health. Some of the significant health problems of mycotoxins have previously been described in Section 2.3.1, where different incidences of mycotoxicosis around the world, including those of aflatoxicosis in Nigeria, Kenya, India and Tanzania have been described. The 1993 World Bank report highlighted the various health problems modulated by exposure to mycotoxins accounting for up to 40% of lost disability-adjusted life years (DALYs) (Marechera & Ndwiga, 2014). In sub-Saharan Africa, about 250,000 deaths are caused by hepatocellular carcinoma annually and this can be linked to risk factors such as AFs and high prevalence of hepatitis B (Zain, 2011). AF contamination in groundnuts and maize in Nigeria contributed to 7,761 liver cancer cases, which results in a total burden of 100,965 DALYs (Atanda *et al.*, 2015). In 2014, due to AF contamination, about 3,334 cases of hepatocellular carcinoma were reported in Tanzania, 95% of which ended as deaths resulting to a loss of 96,686 DALYs (Kimanya *et al.*, 2012).

Based on several studies in Southern Africa, mycotoxin contamination has been strongly linked to child undernutrition, increased mortality and morbidity due to their negative effects on micronutrient absorption and immune function (Katerere *et al.*, 2008). With immune disruption by AFs, it may aggravate health impacts of principal diseases plaguing Africa such as malaria, kwashiorkor and HIV/AIDS (Gnonlonfin *et al.*, 2013). In Nigeria, posthumous autopsy of infants who suffered from kwashiorkor showed significant levels of AFs in their brains after consumption of AF-contaminated maize-based gruel (Oyelami *et al.*, 1997). According to Jolly *et al.* (2007),

high levels of AFB<sub>1</sub> and acute aflatoxicosis symptoms were found within the Ghanaian population that also had abnormal liver function and high level of hepatitis B virus (HBV) infections. Turner *et al.* (2003) reported decreased levels of secretory immunoglobulin A (IgA) in Gambian children exposed to AFs. In Kenya, the mean birthweight of the children of women exposed to AFs prenatally was lesser than that of those who had not been similarly exposed (Hendrickse, 1999).

In the Gambia, maternal dietary intake was indicated to be an important factor in carcinogenic-induced damage in the unborn baby, due to a highly significant correlation between AF-albumin adduct levels in the mothers' venous and respective cord sera (Wild *et al.*, 1991). In the same country, children with reduced levels of salivary Secretory Immunoglobulin A (sIgA) have been linked with exposure to AFs (Turner *et al.*, 2003). The consumption of heavily FB-contaminated maize has been correlated to increased incidence of oesophageal cancer in some parts of South Africa (Wagacha & Muthomi, 2008) and Malawi (Ferlay *et al.*, 2013). According to Ferlay *et al.* (2013), Malawi has the highest prevalence rate (24.2 per 100,000 persons) of oesophageal cancer in the world. Zearalenone as a naturally occurring endocrine-disrupting chemical, has been implicated in the manifestations of gynecomastia with testicular atrophy in rural males in Southern Africa (Shephard, 2008). Between 1977 and 1978, an outbreak of ergotism occurred in Wollo, Ethiopia wherein, 140 persons were affected, 4 children lost both or at least one leg and mortality as high as 34% (King, 1979).

In North Africa, particularly Tunisia and Egypt, cases of human nephropathies have been strongly associated with elevated exposure to OTA and cases of ochratoxicosis, *i.e.*, illness due to OTA exposure (Maaroufi *et al.*, 1995; Wafa *et al.*, 1998; Zaied *et al.*, 2011). Alpha-ZEA has been implicated as a potential risk factor for breast cancer in Tunisia (Belhassen *et al.*, 2015). Likewise, high levels of OTA in Moroccan foods and other agricultural commodities have been linked to some chronic illnesses (Filali *et al.*, 2002; Zinedine & Mañes, 2009). Table 2.1 shows some other mycotoxins and the toxic effects they provoke in humans. On the Asian continent, consumption of mouldy rice contaminated with *Fusarium* and T-2 was associated with the first human mycotoxicosis case in China, with an incidence rate of 59% and a latent period of only 10-30 min (Wang *et al.*, 1993). Further studies are required to establish the association between other poorly investigated diseases and dietary exposure to mycotoxins (emerging, modified and multiple mycotoxins).

**Table 2.1:** Mycotoxins and their toxic effects on human health. Adapted from Capriotti *et al.* (2012).

Mycotoxins	Toxic effects	Reference
EAs	Ergotism: central nervous system disorder, gastrointestinal symptoms, & gangrene	Capriotti <i>et al.</i> (2012)
CIT	Hepatonephrotoxic	Capriotti <i>et al.</i> (2012)
PAT	Genotoxic, teratogenic, carcinogenic, & acute toxicity to kidney	Capriotti <i>et al.</i> (2012)
STEG	Carcinogenic, & hepatotoxic	Capriotti <i>et al.</i> (2012)
MON	Acutely toxic, & cardiac impairment	Capriotti <i>et al.</i> (2012)
AFs	Carcinogenic, & immunosuppressive	Gbashi <i>et al.</i> (2017)
OTs	Mutagenic, carcinogenic, & nephrotoxic	Clark & Snedeker, (2006); Palma <i>et al.</i> (2007); Pfohl-Leszkowicz & Manderville, (2007); Malir <i>et al.</i> (2016)
FBs	Carcinogenic, nephrotoxic, hepatotoxic, immunosuppressive, atherogenic, & embryotoxic	Nair, (1998); Soriano & Dragacci, (2004)
DON	Immunosuppressive, immunostimulative, & causes fertility problems	Bondy & Pestka, (2000); Pinton <i>et al.</i> , (2010); Becker <i>et al.</i> , (2011); Awad <i>et al.</i> , (2013)
ZEAs	Infertility, reduced milk production, vaginal secretions, & vaginitis	Agag, (2004); Zinedine <i>et al.</i> (2007)
T-2	Cardiovascular defects, gastroenteritis, & alimentary toxic aleukia	Semple <i>et al.</i> (1989); Yuan <i>et al.</i> (2014)

**Key:** EAs – ergot alkaloids. CIT – citrinin. PAT – patulin. STEG – sterigmatocystin. MON – moniliform. AFs – aflatoxins. OTs – ochratoxins. FBs – fumonisins. DON – deoxynivalenol. ZEAs – zearalenone,  $\alpha$ -zearalanol and  $\beta$ -zearalanol. T-2 – T-2 toxin.

Though tremendously difficult to estimate, the net monetarized impact of mycotoxins on human health in Africa [including physical pain, death (in severe cases), temporary or permanent impairment, loss of productivity, costs of diagnosis, treatment, hospitalization and health care (morbidity), cost of anxiety, misdiagnosis, suffering and reduced life quality, etc] could be enormous and demanding on national budget. A case in point is a study conducted in Gambia that observed diseases consistent with mycotoxin exposure (in particular, Hepatitis B and its associated medical complications) that resulted in a total monetized DALY worth over 94 million US\$ of gross domestic product (GDP), which equals 9.4 % of the nation's GDP (ECOACAP, 2014). This



is a huge loss to the health of the populace and country's economy. Similarly, in Senegal, the cumulative cost in terms of health due to AFs is estimated at no less than 92 million US\$ of the nation's GDP (ECOACAP, 2014). In 2014 in Tanzania, the economic impact (in monetary terms) of AFs was estimated between 6 million and 264 million US\$ due to the resultant health impact (Kimanya *et al.*, 2012).

For animals, very little work has been done on health impact of mycotoxins even though the term 'mycotoxins' was first coined in 1960 following the discovery that 'Turkey X' disease in which about 100,000 turkey poults died was caused by consumption of poultry feed which was contaminated by secondary metabolites of fungi origin (specifically AFs from *A. flavus*) (Bennett & Klich, 2003). This is understandable as the health effects and losses in animals (such as feeding efficiency, infertility, meat, milk and egg quality losses, susceptibility to diseases etc) are subtler to decipher. Moreover, in Africa, people have limited resources and may prioritize the care of humans above the 'waste of resources' on animals. To this effect, when mouldy cereals are too bad to be consumed, they are usually not disposed, but blended with non-mouldy ones and used as animal feed, or in some cases fed directly to the animals. However, monogastric farm animals such as poultry, swine and dogs are particularly at high risk, because their basal diet (feed) is made up of cereals (Bhat *et al.*, 2010). Additionally, these animals also lack reservoir that harbours microorganisms that can break down secondary metabolites of fungi before they are absorbed into the blood stream.

In South Africa, there has been two episodes of aflatoxicosis among dogs through the consumption of contaminated dog food. The first occurred in 1987 where 10 cases of fatality were reported, and histopathological evaluation revealed chronic symptoms of necrosis, bile duct proliferation, hepatocellular fatty degeneration, fibroplasia, etc. were observed (Bastianello *et al.*, 1987). The second episode occurred in 2011 wherein, over 220 dogs died, and several others were affected in the Gauteng province (Arnot *et al.*, 2012). Subsequent clinical examinations revealed that the dogs were exposed to highly contaminated feed (with levels of AFs as high as 4,946 µg/kg), which is several folds above regulatory limits. In addition to AFs, other mycotoxins such as FB<sub>1</sub>, ZEA, and OTA were all later implicated in this outbreak (Mwanza *et al.*, 2013). Mwanza *et al.* (2007) evaluated the productivity and general health of domesticated animals in Limpopo Province of South Africa in relation to fungal and mycotoxin contamination, the results revealed that these

animals were at risk to mycotoxin contamination, which possibly plays an important role in abortion, low productivity, chronic and acute diseases, as well as reduced immunity in these animals. All these effects of mycotoxins reviewed herein, seriously impact negatively on food security, agricultural trade and the economy of any nation.

### **2.3.2.2 Impact on food security, agricultural trade and the economy**

Mycotoxins have also been implicated as a major cause of food insecurity particularly in the developing nations. It has been estimated that at least 25% of global food and feed commodities is contaminated by mycotoxins; consequent food losses have been calculated at about 1 billion metric tons annually (Rahmani *et al.*, 2009; Schmale & Munkvold, 2009; Rajani *et al.*, 2012; Wilson *et al.*, 2017). Such huge losses undoubtedly strain economic fortunes and stability. For example, losses linked with AF contamination of maize in the United States is estimated at around 1.68 billion USD annually (Schmale & Munkvold, 2009; Mitchell *et al.*, 2016). Due to high levels of AF contamination, about 2.3 million bags of maize worth over Ksh 3.2 billion *i.e.*, roughly 30 million USD were declared unfit for human consumption by the Kenyan Ministry of Public Health and Sanitation in 2010 (Marechera & Ndwiga, 2014).

Globalization of trade has added to the cost and complexity of the situation. In Kitui, Kenya in 2009, it was reported that maize prices dropped by half from 1,800 to 900 Kenyan shillings due to concerns over possible contamination by AFs (Marechera, 2015). The enforcement of regulatory standards primarily by developed nations which are the main destinations of African agricultural export commodities have resulted in a more critical situation for the African agricultural trade (Wu, 2004; Gbashi *et al.*, 2017c). It was estimated that adopting the EU standard limit of 4 µg/kg for AFs in peanuts would cost about 450 million USD in annual losses on exports (Wilson & Otsuki, 2001; Schmale & Munkvold, 2009). Between 2000 and 2014, the cumulative economic loss on domestic and international trade in Gambia was about 23 million USD, which amounts to a yearly loss of about 1.52 million USD (ECOACAP, 2014). The International Institute of Tropical Agriculture (IITA) reported an annual global loss of 1.2 billion USD due to AF contamination, with 38% of this loss (450 million USD) incurred by African nations (Lamb *et al.*, 2015).

In 2014, the Economic Community for West African States (ECOWAS) in collaboration with the African Union's Partnership for Aflatoxin Control in Africa (PACA) and other stakeholders



developed the “ECOWAS Aflatoxin Control Action Plan (ECOACAP)” which identified key actionable strategic interventions in order to combat the prevalence of AFs across ECOWAS member States. Policy 4.3 SO3 of this plan recommended that ECOWAS member states increase budgetary allocations and investments to at least 1% of national GDP for the development and enforcement of AFs control efforts (ECOACAP, 2014). An annual cost of 7.5 million USD was calculated by member states of the African Groundnut Council (Mali, Nigeria, Gambia, Sudan, Niger and Senegal) for the implementation of an AF contamination reduction program (Atanda *et al.*, 2013). The Maize Trust, an initiative principally funded by the government of South Africa, spends over 4 million USD per annum on funding projects directly targeted at improving the South African maize industry, and one of the outlined key objectives is to combat mycotoxins in South African maize (Du Plessis, 2014).

### 2.3.2.3 Commitment to research and the cost implications

Mycotoxicological research is an important component of mycotoxin management and provides insight on the toxicity, level of exposure, and public health significance of mycotoxins. Such knowledge is critical for adoption of appropriate mitigation strategies and regulatory limits for the toxins. The lack of regulation in the developing countries may be due to limited data on the prevalence of mycotoxins in these countries, poverty and inadequate research infrastructure (Darwish *et al.*, 2014). Two mycotoxin intervention initiatives, Aflasafe™ and Aflastop projects, were implemented to combat the prevalence of AFs in foods (particularly maize and peanuts). The former (*i.e.* Aflasafe™) being implemented in the West African countries of Nigeria, Ghana, Tanzania, Burkina Faso, Senegal, Kenya, Mali, and Zambia, whereas, the latter (*i.e.* Aflastop) was adopted in the East African countries of Kenya, Tanzania and Rwanda. The Aflasafe™ and Aflastop projects together with other mycotoxin projects described by Bowman *et al.* (2012) and CIMMYT (2013) costed about 15-20 million USD in 2014 and 2-5 million USD in 2010, sponsored by the US Government under the Feed the Future (FTF) - USAID Bureau for Food Security (Bowman *et al.*, 2012; CIMMYT, 2013).

A study conducted in West Africa estimated annual costs averaging 466 million USD from testing, regulatory enforcement, to other quality control measures (CAST, 2003). In 2000, the United States Department of Agriculture (USDA) Agricultural Research Service (ARS) instituted a

mycotoxin research program worth 17.7 million USD primarily geared towards prevention of fungal contamination and toxin production in crops (Robens & Cardwell, 2003). On average, total value of commercially available test kits for AFs on the market is approximately 10 million USD annually, whereas the cost for analysis of AFs alone is placed at 30 to 50 million USD on annual basis (Robens & Cardwell, 2003).

## **2.4 ANALYSIS OF MYCOTOXINS**

Due to the severe effects that mycotoxins elicit in humans and animals, and with the globalization of trade, several countries and economic unions have placed high priority on the safety of agricultural commodities marketed and consumed within their jurisdiction (FAO, 2004b; Van Egmond *et al.*, 2007; Gbashi *et al.*, 2017c). However, it is apparent that the complete elimination of mycotoxins from foods is unrealistic (Bennett & Klich, 2003). This has led to various interventions put in place to control and minimize exposure to them (Lopez-Garcia *et al.*, 1999; Aldred *et al.*, 2004). Adequate risk management has been identified as a critical frontline defense in the overall control of mycotoxins in food and feed (FAO/IAEA, 2001; Aldred *et al.*, 2004; Toregeani-Mendes *et al.*, 2011; Atanda *et al.*, 2013; Gil *et al.*, 2016).

Any good food safety management programme for naturally occurring toxicants such as Hazard Analysis of Critical Control Points (HACCP) assumes a holistic and multifaceted approach, such as determination of exposure levels, establishment of analytical capabilities, setting and ensuring compliance to regulatory limits, and establishment of surveillance programmes (Atanda *et al.*, 2013; Gil *et al.*, 2016). This positions analysis at the epicenter of mycotoxin management and risk control which is a global priority (Patel, 2004; Krska *et al.*, 2008). Bearing in mind that decisions relating to regulatory issues or commercial arbitration need to be based on well-defined methods of analysis (Gil *et al.*, 2016), it is thus vital to ensure that methods for mycotoxin analysis are sensitive, efficient and validated against standard guidelines (Pittet, 2005; Arroyo-Manzanares *et al.*, 2014).

### **2.4.1 Sampling**

Sampling is an important part of a good and accurate mycotoxin analytical method. This is because mycotoxins are often not evenly distributed in agricultural commodities (Krska *et al.*, 2008; Rahmani *et al.*, 2009), as such, if the sample fraction is not selected correctly, it can lead to large

errors when the result obtained for the selected sample is used to extrapolate for the larger population. It has been estimated that up to 76% of the total uncertainty in an analytical procedure is due to sampling error (Biomin, 2018). It is thus the main objective of sampling to obtain a sample fraction that is as representative as possible to the overall sample population.

The importance of sampling in mycotoxin analysis has been recognized by various international regulatory bodies, and various guidelines have been established in this regard (FAO, 2004b; Commission Regulation, 2006a, 2014; FDA, 2018). The general approach is to obtain a large number of small incremental samples from different locations distributed throughout the entire sampling population which helps to get a more representative sample (FSA, 2015). For example, for sampling of cereals and cereal products from lots < 50 tonnes, the EC Commission Regulation 401/2006 as amended by Commission Regulation 519/2014 requires that 10 to 100 small incremental samples be obtained, depending on the weight of the entire sample lot, resulting in a combined sample of 1 to 10 kg. If however the sample lot is very small i.e.  $\leq 0,5$  tonnes, then a lower number of small incremental samples may be obtained, notwithstanding, the combined sample should be at least 1 kg (Commission Regulation, 2006a, 2014).

#### **2.4.2 Extraction of mycotoxins**

The extraction and sample preparation part of an analytical process is often the most critical and difficult, both in terms of difficulty in extracting the desired analyte(s) from the matrix and the time involved, in addition to the fact that each sample matrix has its own unique challenges (Vaghela *et al.*, 2016). In fact, it has been estimated that up to 70% and perhaps even more of the effort and time that goes into sample analysis comprises the extraction and sample preparation process (Rezaee *et al.*, 2015). Many efforts have been geared towards developing suitable methods to quantitatively extract and detect mycotoxins in agricultural commodities. For any bioanalytical scientist, the goal is to develop methods with improved sensitivity and selectivity, while at the same time maintaining the credibility of the results, as well as reduce cost and time (Augusto *et al.*, 2013).

A number of studies have aimed at designing methods for mycotoxin analysis that avoid a clean-up step, however, such easy-to-use methods often demonstrate lack of sensitivity or are too expensive (Rahmani *et al.*, 2009). An efficient combination of these two characteristics (efficacy

and low-cost) in one method is rare and highly desirable. Proper design of the extraction process facilitates rapid, efficient and quality analytical results (Rezaee *et al.*, 2015). In the succeeding section, a description of some widely referenced conventional methods of mycotoxin extraction will be provided.

#### **2.4.2.1 Conventional methods of mycotoxin extraction**

##### ***Solvent extraction***

Of the available methods for mycotoxin extraction, solvent extraction is one of the oldest but still most frequently used method (Patterson & Roberts, 1979; Cigić & Prosen, 2009). Solvent extraction separates analytes based on their solubilities and mass transfers in organic solvent(s), often by adding the solvent to the sample containing the analyte of interest and shaking rigorously (Patterson & Roberts, 1979; Monbaliu *et al.*, 2010; Kovalsky *et al.*, 2016). The enriched solvent is called the extract. Common solvents used for solvent extraction include methanol, acetonitrile, chloroform, ethyl acetate, isooctane, ethanol and dichloromethane (Zabe *et al.*, 2008; Cigić & Prosen, 2009; Chilaka *et al.*, 2012). One of the earliest and frequently used solvent extraction method for mycotoxin analysis is the multi-mycotoxin extraction method of Patterson and Roberts, (1979). This method utilizes different organic solvents and reagents such as acetonitrile, isooctane, potassium chloride, dichloromethane and sulphuric acid. It has been widely favored because, it selectively extracts several mycotoxins in a single extraction. However, the application of this solvent extraction method, and perhaps other solvent-based extraction methods has been greatly limited because of the consumption of large quantities of organic solvents, which pose hazards to public health and the environment (Santana *et al.*, 2009; Tabaraki & Nateghi, 2011).

These solvents are often toxic to humans, chlorinated, and reasonably contribute to greenhouse effects and other detrimental environmental impacts (Ismail & Hameed, 2013; Gbashi *et al.*, 2017d). On the other hand, green solvents, are innocuous, biodegradable and generally derived from sustainable and renewable resources often naturally occurring (Sherman *et al.*, 1998; Prat *et al.*, 2013). Aside the development of harmless and effective procedures, efforts are made in adopting greener solvents, particularly in earliest stages of the design of the extraction processes (Bradley *et al.*, 2015). For example, in the United States, the Pollution Prevention Act passed in 1990 encouraged the reduction or prevention of pollution at the source, hence limiting consequent

environmental issues before they happen (Sherman *et al.*, 1998). The California Green Chemistry Initiative launched in 2008 approved two legislations encouraging green chemistry, one of which required California's Department of Toxic Substances Control (DTSC) to develop new regulations to ensure prioritization of “chemicals of concern” and promote the use of safer alternatives, the resulting regulations which took effect in 2013, initiating the DTSC's Safer Consumer Products Program (Cowan *et al.*, 2014).

Another disadvantage of solvent-based extraction methods is that they often involve long extraction times and laborious procedures with the process extending up to 24 h or more (Patterson & Roberts, 1979; Chilaka *et al.*, 2012). Moreover, solvents of the required purity tend to be expensive and there are often additional costs with proper disposal of wastes after use (Sapkale *et al.*, 2010; Tabaraki & Nateghi, 2011).

### ***Solid-phase extraction***

Solid phase extraction (SPE) is another very commonly used extraction method for mycotoxins (Mata *et al.*, 2015; Wang *et al.*, 2016). It involves the separation of analytes between a liquid mobile phase and a stationary phase contained in a cartridge. Typical materials used as the solid adsorbent include ethyl (C2), octyl (C8), octadecyl (C18), cyanopropyl (CN), aminopropyl (NH<sub>2</sub>), and an ion exchange phase (Limsuwan, 2011). Non-specific SPE materials are commonly still employed in mycotoxin analysis, which is often used for the extraction of more than one mycotoxin (Cigić & Prosen, 2009). The use of more analyte specific stationary phases such as molecularly imprinted polymers (Pakade *et al.*, 2013), magnetic solid-phase extraction (Ibarra *et al.*, 2015), and immuno-affinity (IA) materials that contain specific antibodies that bind to the analyte of interest are also gaining much attention (Gam *et al.*, 2003; Uchigashima *et al.*, 2012; Arroyo-Manzanares *et al.*, 2014). Although SPE techniques are relatively simple, have higher specificity and require little quantities of solvents, they are also very expensive, and the antibodies are not available for some mycotoxins and products.

### ***Microwave-assisted extraction***

Microwave-assisted extraction (MAE) involves the use of microwave energy to increase the thermal energy of solvents in contact with sample matrices in order to enhance the mass transfer of analytes from the sample matrix into the solvent (Devgun *et al.*, 2009). In recent times, there

has been an increased popularity in the use of MAE techniques in bioanalytical sciences (Devgun *et al.*, 2009; Sibiya *et al.*, 2013), possibly because of the obligation to reduce the quantity of organic solvents being used for extraction. Pallaroni *et al.* (2002) reported the use of MAE for the recovery of ZEA from maize, while Chen and Zhang, (2013) described a microwave-assisted extraction method for the analysis of AFs in grains and grain products. The fundamental difference between MAE and conventional solvent extraction is that MAE uses electromagnetic waves to alter the cellular structures of the sample matrices hence enabling partitioning of analytes from the matrix into the extraction solvent (Veggi *et al.*, 2013). Microwaves heat up microscopic traces of residual moisture in matrix tissues, resulting in expansion and pressure on the cell walls, and eventual rupture of the walls thus releasing analytes trapped in the cellular structures (Tatke and Jaiswal, 2011).

In contrast to other traditional extraction techniques, MAE requires less extraction time and reduced solvent consumption (Doughari, 2012; Veggi *et al.*, 2013). A typical MAE procedure takes between 15–30 min, and uses a little amount of solvent (10 to 30 mL) which is about 10 times less than volumes required for conventional solvent extraction techniques (Eskilsson & Björklund, 2000). However, there are some disadvantages of this method. It is known that microwaves are ionizing electromagnetic waves that can catalyze or perhaps initiate irreversible chemical reactions or changes in some of the target analytes (Ghani *et al.*, 2008; Zhang *et al.*, 2011). The quantity of sample to be extracted is limited to 1 g, which is inadequate for a reasonable homogenous analysis (Shu *et al.*, 2000). Moreover, after extraction, there is need to remove the abundant solid residues of the matrix from the extracts via another sample preparatory step (Wang, 2010; Veggi *et al.*, 2013).

### ***Supercritical fluid extraction***

Supercritical fluid extraction (SFE) is an extraction technique that employs high diffusion of CO<sub>2</sub> under supercritical conditions for the extraction of analytes from sample matrices (Co, 2010; Sapkale *et al.*, 2010). A number of studies have described SFE methods for mycotoxin extraction (Josephs *et al.*, 1998; Ambrosino *et al.*, 2004; Zougagh & Rios, 2008). Under supercritical conditions, there are no distinct liquid or gaseous phases for the extraction fluid (Sharma, 2015), as such, the fluids have zero surface tension and can diffuse through solid sample matrices like gases while dissolving the analytes like solvents (Co, 2010; Attawood & Florence, 2012; Sofi *et*



*et al.*, 2013). Extraction by means of SFE takes between 10 to 60 min, is automatable and completely eliminates the use of toxic organic solvents, while leaving no trace of the extraction fluid in the extracts (Sapkale *et al.*, 2010; Ayre *et al.*, 2013). Despite the advantages, extraction using this method has some major setbacks. For example, the cost of the SFE equipment is very high, it is energy-intensive (CO<sub>2</sub> heating and compression) and handling the equipment requires technical expertise as well as rigorous precautions (Bulgariu and Bulgariu, 2015; Shine *et al.*, 2015). Only analytes that are soluble in CO<sub>2</sub> can be extracted (Co, 2010).

### ***Other methods for mycotoxin extraction***

Several other methods exist for mycotoxin extraction aside from the ones discussed above, some of which include ultrasonic extraction (Kong *et al.*, 2013), accelerated solvent extraction (Royer *et al.*, 2004), aqueous two-phase (Pimentel *et al.*, 2013), liquid-phase microextraction (González-Peñas *et al.*, 2004), and many others reviewed in the literature (Cigić & Prosen, 2009; Rahmani *et al.*, 2009; Anfossi *et al.*, 2010; Arroyo-Manzanares *et al.*, 2014; Turner *et al.*, 2015). However, these methods have shortcomings, fundamentally being limited by cost, long and laborious procedures, issues of low recovery efficiency, and use of large volumes of organic solvents usage, some of which are well known for to be toxic and considered as environmental hazards (Henderson *et al.*, 2011; Augusto *et al.*, 2013; Sharma, 2015). Moreover, the emergence of novel mycotoxins and advancements in spectrometric analysis are pushing the limits of some of these conventional extraction techniques (Zhang *et al.*, 2012; Augusto *et al.*, 2013).

Based on the above described reasons, there is an eminent need for a greener approach that is cheap, fast and efficient in the extraction and analysis of mycotoxins (Augusto *et al.*, 2013; Susanti *et al.*, 2015). A green extraction method is one that is focused on limiting energy and solvent consumption, permits the use of safer alternative solvents from renewable sources, while ensuring high quality of the end product (Chemat *et al.*, 2012). It is in line with this that we propose the adoption of pressurized hot water extraction (PHWE) as an alternative to conventional extraction methods. Pressurized hot water extraction has been in the spotlight as an efficacious and highly promising alternative to traditional techniques of extraction, whose successful applications in the biochemical, pharmaceutical and chemical engineering fields have been well documented in the literature (Wilson *et al.*, 1993; Ibañez *et al.*, 2003; Ozel *et al.*, 2003; Gupta *et al.*, 2012; Liang &

Fan, 2013; Shaddel *et al.*, 2014; Gbashi *et al.*, 2016, 2017d). A brief description of this method of extraction is presented in the succeeding section of this chapter.

## 2.5 PRESSURIZED HOT WATER EXTRACTION (PHWE)

Pressurized hot water extraction is a green, cheap and easy-to-adopt extraction technique that utilizes water at its subcritical state as the extraction solvent (Gbashi *et al.*, 2017d). This method of extraction has often been represented under different names such as subcritical water extraction (SWE) (Liang & Fan, 2013), hot water extraction (HWE) (Paredes *et al.*, 2008), hot liquid water extraction (HLWE) (Wan and Li, 2011) and pressurized low polarity water extraction (PLPWE) (Cacace and Mazza, 2006; Guclu-Ustundag and Mazza, 2009). The use of pressurized hot water (PHW) as an extraction solvent was first reported by Hawthorne *et al.* (1994), when it was observed that sub- and supercritical water can be used for the recovery of organic pollutants from soil samples. Since then, numerous scientific researches have been carried out towards exploiting this novel technology.

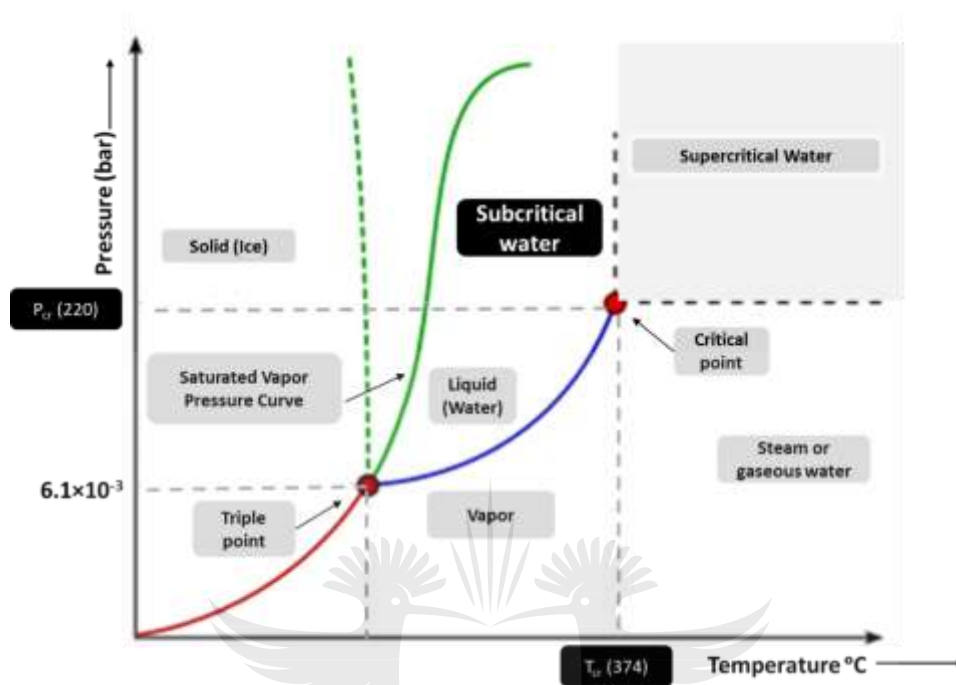
### 2.5.1 Concept and principle of PHWE

The term pressurized hot water or subcritical water refers to liquid water between the boiling point temperature and critical point temperature of water (100 – 374 °C) (Figure 2.8) (Gbashi *et al.*, 2017d). Pressure is applied to keep the water in liquid state. The phenomenon behind the extractability of PHW is based on the fact that when the temperature of water is raised and the pressure kept sufficient to maintain it in its liquid state (e.g. 250 °C and 50 bar), the dielectric constant of water decreases and the hydrogen bond and other intermolecular forces of water weakens, which greatly enhances its extractability (Table 2.1) (Alupului *et al.*, 2012; Gbashi *et al.*, 2017d).

At atmospheric temperature and pressure (25 °C at 1 bar), water has one of the highest dielectric constants amongst non-metallic liquids ( $\epsilon=80$ ) (Cabane & Vuilleumier, 2005). However, when the temperature and pressure of water is raised to 250 °C and 50 bar respectively, the dielectric constant falls ( $\epsilon=27$ ), which is around the range of non-polar solvents such as methanol ( $\epsilon=33$ ), acetone ( $\epsilon=20.7$ ), ethanol ( $\epsilon=24$ ), and acetonitrile ( $\epsilon=37$ ) (Teo *et al.*, 2010; Alupului *et al.*, 2012). As a result of the drop in dielectric constant of subcritical water, its surface tension and viscosity decreases, while its diffusivity increases (Teo *et al.*, 2010; Gbashi *et al.*, 2017d). As such, water



behaves like an organic solvent, dissolving a wide range of low and medium polarity analytes (Gbashi *et al.*, 2017d).



**Figure 2.8:** Phase diagram of water as a function of temperature and pressure (Gbashi *et al.*, 2017c).

Interestingly, the extractability and selectivity of subcritical water can be easily maneuvered to extract a range of analytes by simply varying the temperature conditions of the water (Liang & Fan, 2013). Another theoretical explanation on the extractability of subcritical water bases this ability on the fact that, as the temperature of water increases, the average kinetic energy of the molecules of the mixture also increases. This thus disrupts the bonds that exist within and between the molecules, as such, increasing extraction rate.

**Table 2.2:** Important electro- and physicochemical properties of water that changes with increase in temperature and pressure (Gbashi *et al.*, 2017c)

S/No	Property	Status	Reference
1.	Adhesion and cohesion	Decreases	Chaplin (2008)
2.	Collision frequencies	Increases	Buhler <i>et al.</i> (2002); Kruse and Dinjus (2007)
3.	Compressibility	Increases	Kruse and Dinjus (2007); Chaplin (2008)

S/No	Property	Status	Reference
4.	Density	Decreases	Kruse and Dinjus (2007); Chaplin (2008)
5.	Dielectric constant	Decreases	Kruse and Dinjus (2007); Chaplin (2008)
6.	Diffusivity	Increases	Kruse and Dinjus (2007); Teo <i>et al.</i> (2010)
7.	Electrical conductivity	Increases	(Hawthorne, 2000)
8.	Extraction rates	Increases	Teo <i>et al.</i> (2010); Gupta <i>et al.</i> (2012)
9.	Hydrogen bonding	Decreases	Yamaguchi (1998); Chaplin (2008)
10.	Miscibility	Increases	(Weingartner and Franck, 2005)
11.	Solubility	Increases	(Miller <i>et al.</i> , 1998)
12.	Surface tension	Decreases	(Chaplin, 2008)
13.	Viscosity	Decreases	(Kruse and Dinjus (2007); Teo <i>et al.</i> , (2010)

Key: S/No.: serial number

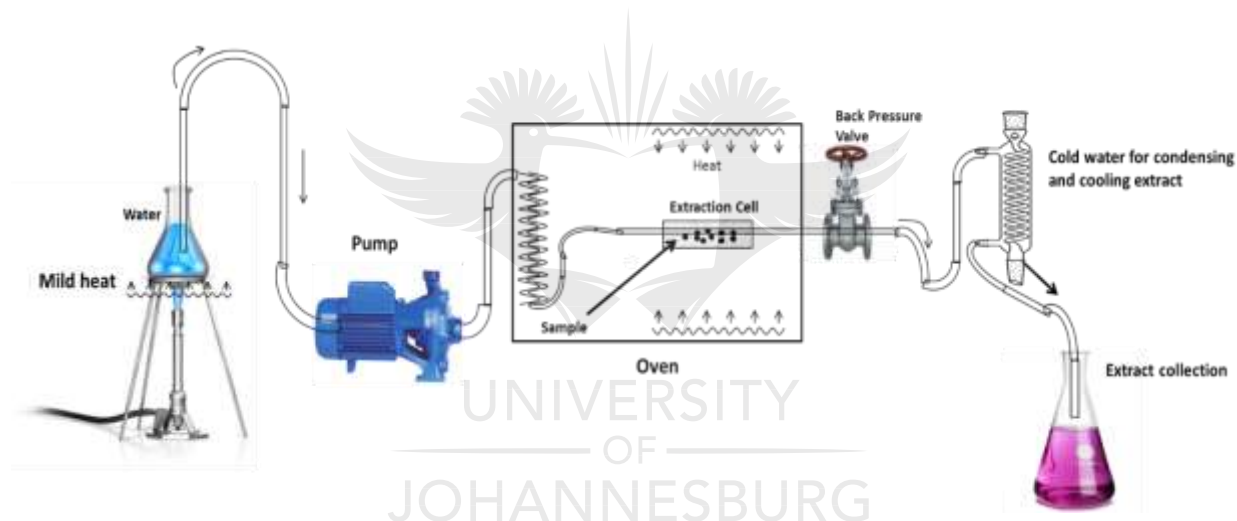
### 2.5.2 Instrumentation and mechanism of PHWE

A typical setup of a laboratory scale PHWE unit comprises a source of water, temperature retention coil, a solvent pump, an oven and extraction cell, a backpressure valve and a condenser connected to the outlet (Figure 2.9). The grounded sample to be extracted is placed inside the extraction cell which is located inside the oven. The oven which usually has an automatic thermostat mechanism is set to the desired temperature, the backpressure valve is partially locked to maintain the desired pressure and water is pumped at a preset flow rate through the retention coil into the extraction cell. The extraction takes place in the extraction cell as the pressurized hot water flows through it and mixes with the sample. The hot water extract flows through the condenser and is collected at the outlet (Gbashi *et al.*, 2017d). The extraction mechanism of PHWE involves the processes of heat convection, rapid fluid flow into matrix pores, analyte partition into solvent via diffusion and elution of analytes through bulk flowing of fluid (Asl & Khajenoori, 2013; Gbashi *et al.*, 2017d). In addition, the high pressures enhance extraction by forcing the fluid into matrix cellular structures where low pressure water may not normally reach (Gbashi *et al.*, 2017d).

### 2.5.3 Operational modes of PHWE

Extraction with PHW is performed in two common modes, static mode or flow-through (dynamic) mode. Extraction in the static mode involves retaining the sample in the extraction cell with subcritical water for short periods after which the fluid is allowed to flow out purging the extraction

cell and extract collected. It is important to optimize the retention periods to allow for an equilibrium to be reached between the solvent and analyte. The disadvantage of operating in this mode is that within a short time the analyte-fluid equilibrium is reached, hence no further extraction of the analyte occurs no matter how long the samples are retained in the extraction. On the other hand, extraction in the dynamic mode allows for a continuous flow of fresh fluid through the extraction cell which reduces or eliminates analyte-fluid equilibrium in a single operation when properly optimized. As such, recovery efficiency is higher in the dynamic mode, although, fluid consumption could be more, resulting in lower energy efficiency compared to the static mode (Teo *et al.*, 2010; Gbashi *et al.*, 2017d). In a study by Yang and Wyman, (2004), it was observed that extraction in dynamic mode resulted in higher recovery of lignin and hemicelluloses from maize stover cellulose than in the static mode.



**Figure 2.9:** Simple laboratory setup of a PHWE unit (Gbashi *et al.*, 2016)

## 2.5.4 Factors affecting PHWE

A number of factors such as temperature, flow rate, pressure, particle size, co-solvents and surfactants affect the performance of PHWE. Some of these factors are further described below.

### 2.5.4.1 Temperature

The extraction efficiency of PHWE is strongly affected by changes in temperature (Asl & Khajenoori, 2013). Generally, extraction efficiency increases with increase in temperature. A higher recovery of total antioxidants was achieved from grape pomace by increasing the extraction temperature (Vergara-Salinas *et al.*, 2013). Despite the increase in efficiency by increase in

temperature, excess temperatures can result in degradation of thermolabile analytes, hence the need for optimization (Asl & Khajenoori, 2013; Khoza *et al.*, 2015). The recovery of carvacrol and thymol from *Zataria multiflora* between 100 and 175 °C indicated that recoveries increased steadily with increase in temperature up until 150 °C, then a degradation phenomenon followed with a noticeable burning smell (Khajenoori *et al.*, 2009).

#### 2.5.4.2 Pressure

The effect of pressure on the extraction efficiency of PHWE has been described as insignificant (Hawthorne *et al.*, 1994; Deng *et al.*, 2004). In a study by Shalmashi *et al.* (Shalmashi *et al.*, 2010), changes in pressure *i.e.*, 20, 30 and 40 bar during PHWE did not show any significant effect on the recovery of caffeine from tea waste. This is because water is fairly incompressible at temperatures below 300 °C, which implies that pressure has very little influence on the physicochemical properties of water, as long as it can maintain in a liquid state (Ramos *et al.*, 2002; Carr *et al.*, 2011). Nevertheless, increased pressure can compromise matrix tissue membranes and force the extraction fluid deep into matrix pores where water at lower pressure may not normally reach (Ong *et al.*, 2006).

#### 2.5.4.3 Co-solvents and modifiers

Co-solvents and solvent modifiers are often used to enhance the extractability of PHWE. Co-solvents are secondary solvents (usually organic solvents) that are added to subcritical water to enhance its solvation power (Williams *et al.*, 2013; Gbashi *et al.*, 2016). The incorporation of methanol during PHWE was observed to significantly ( $p < 0.05$ ) increase yield of flavonoids and di-acylated cinnamic acids from *Bidens pilosa* (Gbashi *et al.*, 2016, 2017a). Solvent modifiers such as salts and other reagents can alter important physicochemical properties of water such as polarity, surface tension, and hydrogen bonding strength which results in an enhanced extractability (Curren & King, 2001b; Teo *et al.*, 2010). Modifiers can also interact directly with the sample matrix, reducing the activation energy required for analyte desorption and diffusion (Plaza & Turner, 2015; Gbashi *et al.*, 2017d). Curren and King (2001a) observed that the solubility of atrazine can be doubled when urea was added to subcritical water, and when ethanol was used, the solubility increased by over 10-folds.

In addition to the above described factors, other factors that influence the extractability of PHWE include solvent flow rate, physicochemical and functional characteristics of the sample matrix and analyte, matrix particle size and geometry of the extraction cell (Teo *et al.*, 2010; Shitu *et al.*, 2015; Gbashi *et al.*, 2017d).

## **2.5.5 Advantages and disadvantages of PHWE**

### **2.5.5.1 Advantages of PHWE**

The major advantage of PHWE is that it is a green (*i.e.*, environmentally friendly) extraction method. The extractant is water, which is non-toxic, non-flammable and renewable. Moreover, water is readily available and cheap, and extraction with it does not generate harmful by-products (Chemat *et al.*, 2012; Liang & Fan, 2013). In comparison with traditional extraction methods, PHWE is less time-consuming and much easier to perform with very few extraction steps, as such, human errors are greatly minimized. When put side-by-side with supercritical fluid extraction (SFE), PHWE edges on the basis of being a simple technology, hence, requiring much lower maintenance and engineering cost for equipment (Bart, 2005; Gbashi *et al.*, 2017d). During extraction with PHW, the fluid can be maneuvered to selectively extract a range of analytes with different polarities by mere adjusting the temperature of the water, whereas SFE extracts only non-polar or light-weight compounds (Curren & King, 2001b; Liang & Fan, 2013). Further to this, PHWE is very compatible with various analytical instrumentations because water is colorless and may not interfere with sorts of photodetection such as ultraviolet (UV) detection or flame ionization detection (FID) (Khoza *et al.*, 2016; Gbashi *et al.*, 2017d).

### **2.5.5.2 Disadvantages of PHWE**

A major setback of PHWE is the thermal degradation of some thermolabile analytes at elevated temperatures (Moreno *et al.*, 2007; Khoza *et al.*, 2014). When the temperature and pressure of water are extremely high (*i.e.*, above 374 °C and 221 bar), there is also the risk that water can become very reactive and could oxidize or catalyze hydrolysis of some compounds (Teo *et al.*, 2010). However, optimization by means of the adoption of a co-solvent or modifier could ameliorate or eliminate these issues (Gbashi *et al.*, 2016).

### 2.5.6 Applications of PHWE

In the last decade, PHWE has been widely investigated for the extraction of various nutritional constituents, organic pollutants, and pharmacologically active compounds from vegetal tissues, food products, soil residues and other ecological biomasses (Teo *et al.*, 2010; Asl & Khajenoori, 2013; Duy *et al.*, 2015; Gbashi *et al.*, 2017d). Free fatty acids and other oils were extracted from spent bleaching earth using PHWE (Fattah *et al.*, 2014). Likewise, it was possible to recover important metabolites from *Moringa oleifera* leaves using PHWE (Khoza *et al.*, 2014). A similar extraction method was used for the recovery of proteins, carbohydrates and lignans from flaxseed meal (Ho *et al.*, 2007), catechins and proanthocyanidins from grape seeds (García-Marino *et al.*, 2006), flavonoids from aspen knotwood (Hartonen *et al.*, 2007) and antioxidants from microalga *Spirulina platensis* (Herrero *et al.*, 2004). The use of PHWE in various applications in different scientific disciplines has been reviewed (Ramos *et al.*, 2002; Asl & Khajenoori, 2013; Liang & Fan, 2013).

### 2.5.7 Prospects of PHWE of mycotoxins

In a preliminary study, Gbashi *et al.* (2017b) developed and validated a PHWE method for the extraction of AFB<sub>1</sub> from maize followed by analysis on high performance liquid chromatography coupled to a Photodiode array detector (HPLC-PDA). Results obtained from that study revealed that PHWE could be suitable for the effective extraction of AFs from maize, with a recorded recovery rate of 115%. It has been stated earlier in Section 2.4 that more countries are enforcing stringent regulations limiting mycotoxins in food and feed, which is increasing the demand for their analysis. The speed, efficiency, simplicity, safety and low-cost implications of using PHWE are very attractive and compelling in this regard.

It is known that mycotoxins occur in a diverse manner and can be found deeply deposited inside the food matrices, and as such, their extraction usually requires a process that allows the solvent to penetrate all areas of the matrix to reach hidden toxins trapped in matrix pores (Scudamore, 2008). The high pressures involved in PHWE seem very suitable in meeting this requirement. Although issues with thermal degradation of some analytes have been a major limiting factor of PHWE, it is interesting to know that mycotoxins and most other mycotoxins are relatively thermally stable (Bullerman & Bianchini, 2007; Turner *et al.*, 2009). Moreover, optimization using

co-solvents has been found effective in ameliorating this setback (Curren & King, 2001a; Gbashi *et al.*, 2016). Based on these observations and other consulted literature reports, it is evident that PHWE is a viable alternative to conventional extraction methods for mycotoxins (Ong *et al.*, 2006; Teo *et al.*, 2010; Plaza & Turner, 2015; Gbashi *et al.*, 2017d, 2017b). In the next section, a discussion on approaches used for the detection and quantification of mycotoxins after effective extraction will be presented.

## **2.6 CHROMATOGRAPHIC SEPARATION, DETECTION AND QUANTIFICATION OF MYCOTOXINS**

After extraction of mycotoxins the next step is the detection (identification) of the specific mycotoxin and quantification of the amount of the mycotoxin present in the extracts. For this purpose, chromatographic equipment coupled with different types of detectors is being employed. Many of the official validated methods for mycotoxin detection and quantitation approved by regulatory authorities such as the Food and drug administration of the US (FDA), European Commission (EC) and The Association of Official Analytical Chemists (AOAC) are based on high-performance liquid chromatography (HPLC) coupled to an UV detector, fluorescence detector (FLD), or mass spectrometer (MS). Other detection and quantitation methods utilized for mycotoxins involve thin layer chromatography (TLC) followed by UV detection and gas chromatography linked to an MS (GC-MS) (Shephard, 2008a; Monbaliu *et al.*, 2009).

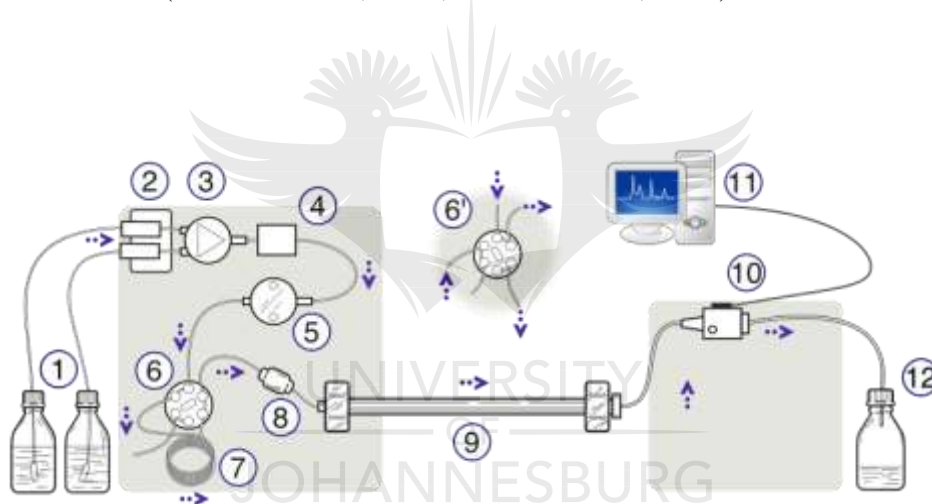
### **2.6.1 Chromatographic separation of mycotoxins**

Amongst chromatographic techniques employed for the analysis of mycotoxins in agricultural commodities, HPLC (Figure 2.10) is the most popular (Rahmani *et al.*, 2009; Turner *et al.*, 2015; Zhang *et al.*, 2018). HPLC essentially relies on high-pressure pumps to convey the liquid mobile phase containing the sample extract or analyte(s) through a narrow column filled with a solid adsorbent material. The components present in the sample then interact with the adsorbent material in a slightly different manner depending on a number of factors such as polarity, chemical structure, size of molecule, functional groups present etc., causing different rates of flow for each component. This results in a partitioning of the components which then elutes from the column at a specific retention time (Kumar *et al.*, 2013). The size of the sorbent particles packed into the



column directly affects partitioning of the analytes and their retention times; as the particle size decreases, the resolution and efficiency of the partitioning increases (Narwate *et al.*, 2014).

The ultra-high performance liquid chromatography (UHPLC) is a superior evolution of the HPLC which preserves the basic principles of HPLC while increasing the overall combined elements of speed, sensitivity, and resolution (Wu & Engen, 2006). It uses finer particles (smaller than 2  $\mu\text{m}$  in diameter), saves time and reduces solvent consumption compared to traditional HPLC (Wu & Engen, 2006; Srivastava *et al.*, 2010). Some benefits of HPLC include low detection limits, small sample requirement and the ability to accommodate a vast range of analytes with various physicochemical characteristics. HPLC has numerous applications in mycotoxin analysis depending on the choice of analytical column, mobile phase, design of the gradient program and type of detector utilized (Rahmani *et al.*, 2009; Roseanu *et al.*, 2010).



**Figure 2.10:** Schematic representation of a typical HPLC unit (Haider & Asif, 2011). (1) Mobile phase tanks, (2) Mobile phase degasser, (3) Gradient valve, (4) Vessel for mixing and delivery of the mobile phase(s), (5) Pressure pump, (6) Inject-positioned switching valve, (6') Load-positioned switching valve, (7) Injection loop, (8) Guard column (pre-column), (9) Chromatographic analytical column, (10) Detector (11) Data acquisition and processing, (12) Waste disposal or fraction collector.

The two broad categories of analytical columns utilized with HPLC are the normal-phase and the reversed-phase columns (Roseanu *et al.*, 2010). Normal-phase columns contain a polar sorbent (*i.e.* stationary phase) such as silica or alumina resins which separate analytes based on their ability



to engage in polar interactions such as hydrogen bonding, ionic, dipole-induced dipole, or dipole-dipole type interactions with the stationary phase. Normal phase columns are employed for the separation of analytes that are readily soluble in non-aqueous, non-polar mobile phases such as chloroform (Yang *et al.*, 2013; Wierucka & Biziuk, 2014). Reversed-phased columns on the other hand involves the use of a hydrophobic stationary phase which is essentially the reverse of normal-phase columns (which uses hydrophilic sorbents), hence the term ‘reversed-phased’ columns. Generally, alkyl chains such as C<sub>18</sub>H<sub>37</sub> or C<sub>8</sub>H<sub>17</sub> covalently bonded to the sorbent particles create a hydrophobic environment in reversed-phased columns, hence less affinity for hydrophobic compounds and stronger interactions with hydrophylic compounds. An aqueous (polar) or moderately polar mobile is employed for the separation of analytes on the reversed-phase column (Jandera, 2002; Yang *et al.*, 2013; Wierucka & Biziuk, 2014). The reversed-phase columns are the most commonly used in mycotoxin analysis. In the past decade, almost all mycotoxins have been partitioned, detected and quantified by HPLC when coupled to a suitable detector (Arranz *et al.*, 2004; Berthiller *et al.*, 2007; Rahmani *et al.*, 2009; Turner *et al.*, 2009, 2015; Varga *et al.*, 2013; Zhang *et al.*, 2018).

### **2.6.2 Detection and quantification of mycotoxins**

Detection and quantification is the final step in the analysis of mycotoxins aside data analysis and result interpretation. Detection is a qualitative process which confirms the presence of an analyte or group of analytes while quantification determines the amount of the analyte available in the sample extract. Detection and quantification are achieved by means of detectors that are linked to a chromatograph. The detectors convert the physical or chemical attributes of an analyte into measurable signals corresponding to elution time, identity and quantity of the analyte (Scott, 1996; Snyder *et al.*, 2010).

There are many different detectors that have been effectively combined with HPLC instruments for the detection and quantitation of mycotoxins, which include FLD (Wen *et al.*, 2014; Ali *et al.*, 2015), UV detectors (Klinglmayr *et al.*, 2010; Ramni *et al.*, 2011), photo-diode array detector (PDA) (Maragos *et al.*, 2008; Pascale *et al.*, 2012), flame ionization detectors (FID) (Eke *et al.*, 2004; Wu & Smith, 2007) and mass spectrometric detectors (MS) (Sulyok *et al.*, 2006; Geary *et al.*, 2016). A number of published literature have reviewed the principles and applications of the

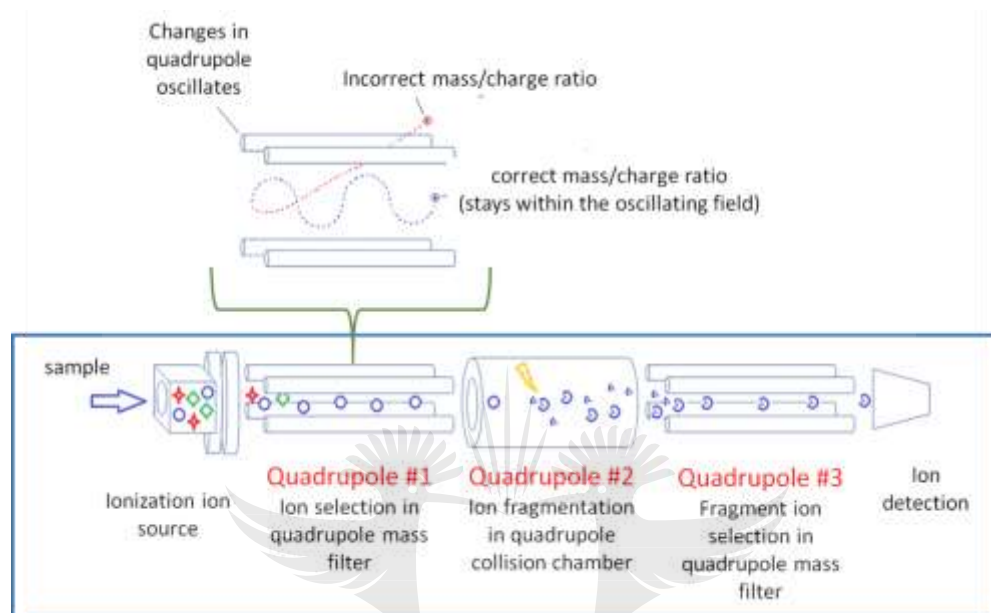
different kinds of detectors utilized in chromatography and mycotoxin analysis (Scott, 1996; Swartz, 2010; Ramni *et al.*, 2011; Sriveena *et al.*, 2015). For the purpose of this thesis, only the MS detectors are discussed.

### 2.6.2.1 Mass spectrometry (MS)

Mass spectrometry is an analytical technique that relies on ionization of chemical species, fragmentation and sorting the ions based on their mass-to-charge ratios (Siuzdak, 2004; Sriveena *et al.*, 2015). Achieving better accuracy, sensitivity and selectivity, MS is considered the standard method for detection and quantitation of mycotoxins (Cigić and Prosen, 2009; Rahmani *et al.*, 2009; Turner *et al.*, 2009). Key features of MS include the capacity to determine the (accurate) molecular mass, and generate information on elemental composition and structure of unknown substances (Siuzdak, 2004; Sriveena *et al.*, 2015). MS is also used for verification of the identity and purity of known compounds, providing data on isotopic signature of a sample and quantification of the concentration of the analyte(s). Analysis by means of MS does not depend on the UV absorbance or fluorescence characteristics of the analyte, as such, the need for derivatization prior to detection may be eliminated (Rahmani *et al.*, 2009; Sriveena *et al.*, 2015). Additionally, MS has the ability to accommodate a wide range of analytes of various molecular masses and polarities, in addition to small sample amount requirements. MS also achieves lower detection limits and good repeatability even for complex sample matrices (Lattanzio *et al.*, 2007, 2011; Ediage *et al.*, 2011; Njobeh *et al.*, 2012; Arroyo-Manzanares *et al.*, 2018).

There are many variants of MS detectors such as ion trap (IT), quadrupole (Quad), time-of-flight (TOF) and Fourier transform-ion cyclotron resonance (FT-ICR), however, the Quad is the most widely utilized for mycotoxin analysis (Rahmani *et al.*, 2009; O'Mahony *et al.*, 2013; Adekoya *et al.*, 2018). In a typical (triple) quadrupole MS system (Figure 2.11), the sample to be analyzed is conveyed into the source where it is ionized either positively or negatively depending on the nature of the analyte. Two kinds of ionization sources are typically used for mycotoxin ionization in MS, the atmospheric-pressure ionization (API) (Zöllner & Mayer-Helm, 2006) and the electron-spray ionization (ESI) (Ho *et al.*, 2003). The ESI is however the most favored for mycotoxin analysis because it is suited for medium to high polar and medium to high molecular mass analytes (Rahmani *et al.*, 2009). After ionization, the molecules acquire a charge and their masses are

measured with respect to their charge, *i.e.*,  $m/z$ . The ionized species are then absorbed via a strong vacuum into the first quadrupole which functions as an ion filter, where the ions are filtered according to their  $m/z$  allowing only the desired ions (precursors) to pass into the second quadrupole (Siuzdak, 2004; Sriveena *et al.*, 2015).



**Figure 2.11:** Schematic representation of a typical triplequad MS instrument (Adapted from Emerypharma, 2019)

In the second quadrupole also referred to as the collision cell, the precursor ions which are already structurally unstable by reason of bearing a charge are bombarded with a collision gas, typically argon gas. This causes the species to disintegrate into a number of charged fragments. The fragments are then accelerated into the third quadrupole where they are filtered, allowing only the pre-specified product fragments to pass onto the detector for identification and quantitation (Rahmani *et al.*, 2009; Sriveena *et al.*, 2015). The results from the MS detector are then translated into signals and displayed as mass chromatograms and spectrums. The identity of an analyte present in a sample is confirmed by observing the precursor  $m/z$  and its fragmentation pattern (*i.e.*, product ions) (Siuzdak, 2004), whereas the concentration is confirmed by correlating the abundance of the ions of a specific analyte to those of pure standards by means of a calibration curve.

### 2.6.3 Application of LC-MS/MS for mycotoxin analysis

Using a solvent extraction method followed by analysis on a triple quad MS detector, Chilaka *et al.* (2016) determined the incidence rates and levels of 16 *Fusarium* mycotoxins including FBs and hidden FBs, DON, ZEA and their metabolites, T-2, HT-2, FUS-X, NIV, neosolaniol (NEO) and DAS in 363 samples of maize, sorghum, millet and *ogi* from Nigeria. Ochratoxin A, AFM<sub>1</sub>, ZEA and  $\alpha$ -ZEL in milk have been determined based on a method using LC-MS/MS (Huang *et al.*, 2014a). In a study by Varga *et al.* (2013), 191 mycotoxins and other fungal metabolites from hazelnuts, pistachios, peanuts and almonds were analyzed using a semi-quantitative method based on an LC-MS/MS. Elsewhere, 295 fungal and bacteria metabolites were simultaneously quantitatively analyzed using an optimized solvent extraction method followed by LC-MS/MS (Malachová *et al.*, 2014).

Having described different methods for mycotoxin extraction, detection and quantification, in the next section, a discussion on the process of method development for mycotoxin analysis is presented. Also, the process of validating a newly developed analytical method is described.

## 2.7 DEVELOPMENT AND VALIDATION OF METHODS FOR MYCOTOXINS ANALYSIS

Development and validation of analytical methods play important role in the study of mycotoxins, particularly with regards to monitoring, policy and regulatory purposes.

### 2.7.1 Method development

Method development constitutes the process of designing an analytical procedure to enable the extraction, identification and/or quantification of an analyte of interest in a sample matrix (Arora & Gangadharappa, 2016). A number of reasons exists for developing new methods, some of which include (Arora & Gangadharappa, 2016); (1) lack of a suitable method for the analyte(s) of interest in a specific sample matrix; (2) existing methods may be inefficient and unreliable; (3) existing methods may be too expensive, tedious, energy intensive or time-consuming; (4) existing methods may not be compatible with analytical equipment, or may not provide adequate analyte selectivity, sensitivity and accuracy in samples of interest; (5) existing methods may be deficient in terms of human and environmental safety and sustainability; (6) an alternative method may be needed for

confirmation of data originally acquired using existing methods, for scientific or legal reasons. Literature evidence shows that safety considerations (human and environmental), cost, as well as, sample throughput are critical areas of interest in the development of new analytical methods for mycotoxin analysis (Zheng *et al.*, 2006; Cigić & Prosen, 2009; Razzazi-Fazeli & Reiter, 2011; Arroyo-Manzanares *et al.*, 2013, 2014).

When developing new methods that involve simultaneous extraction of more than one analyte, particularly those with diverse physicochemical characteristics, it is common practice to use a combination of solvents, as well as, manipulate different extraction conditions (such as temperature, pH etc.) in order to achieve the best extraction efficiency. This task can be very daunting, involving several experimental trials. An effective way to overcome this challenge is the adoption of chemometric optimization models which help in the selection of optimal sample preparation conditions (Díez *et al.*, 2011; Khazaeli *et al.*, 2016; Bhusnure *et al.*, 2017). Examples of some of these chemometric models and their applications in the development and optimization of sample preparation procedures will be discussed in a subsequent section (Section 2.8) of this chapter. In the meantime, the process of determining the suitability of a newly developed analytical method (*i.e.*, method validation) will be discussed in the succeeding section.

### **2.7.2 Validation of analytical methods**

Subsequent to method development is the validation of the developed method. Method validation is important in order to be confident in the reliability of the testing procedure. It is also a recommended process of any official and standard analytical procedure (Pittet, 2005; Hussain, 2011; Arora & Gangadharappa, 2016). The objective of the validation exercise is to demonstrate that the analytical procedure being employed for a specific analyte in a specific matrix is suitable, in terms of quality, consistency and reliability for its intended use (Anklam *et al.*, 2002; Trombete *et al.*, 2014; Arora & Gangadharappa, 2016). The validated method should also correspond to standard pre-established method performance criteria (Gilbert & Anklam, 2002; Arora & Gangadharappa, 2016).

A full method validation is expected when developing or implementing an analytical method for the first time, whereas a partial validation is required when minor modifications are made to an already validated method (Arora & Gangadharappa, 2016). Such minor modifications can include

changes in the extraction solvent, clean-up material, sample matrices, concentration ranges, analytical instrumentation, transfer of analytical methods between laboratories or amongst analysts. A partial method validation can range from a simple recovery or precision assay to an almost full validation performance (Arora & Gangadharappa, 2016). A cross-validation on the other hand implies a comparative assessment of the validation parameters of two or more methods that are used to generate data in a study or across different studies (Arora & Gangadharappa, 2016). For example, a cross-validation would be applicable where an original validated method is used as a control reference against a revised form of the original method or a newly developed method (Arora & Gangadharappa, 2016). Typical method validation parameters to be evaluated include, accuracy, linearity, sensitivity, selectivity, intra-day precision, inter-day precision, robustness and matrix effect (Anklam *et al.*, 2002; Arora & Gangadharappa, 2016). The details about these validation parameters are described in the succeeding sub-sections of this chapter.

### 2.7.2.1 Accuracy

Accuracy, also referred to as recovery efficiency or trueness is arguably the most important validation parameter. It estimates the closeness of agreement between experimentally observed values and the accepted reference value (Huber, 2010). Accurate quantification of mycotoxins in food and feed commodities is essential in order to assess the compliance of the contamination levels of the toxin in the sample with respect to the legal limits (Anklam *et al.*, 2002). The FDA recommends recovery values between 80 to 110% for concentrations ranging from 100 to 10,000 µg/kg (FDA, 2015). The EC recommends values between 60 and 130% (Commission Regulation, 2006a), the AOAC recommends 70 to 125% in foodstuff contaminated with 10 to 1,000 µg/kg of mycotoxins (AOAC, 2009), whereas, *Codex Alimentarius* (CODEX) recommends 80 to 110% for accuracy in agricultural commodities contaminated with mycotoxins depending on the type of mycotoxins and level of contamination (CODEX, 2015).

### 2.7.2.2 Specificity

Specificity or selectivity measures the ability of a method to differentiate and quantify an analyte of interest in the presence of other components in the sample (Anklam *et al.*, 2002; Arora & Gangadharappa, 2016). This implies that no endogenous peaks should be present within 10% window of the retention time of the target analyte and an internal standard. In the event there is a



peak within this range of the retention time, its response should not be greater than 20% of the response of an extracted lower limit of quantification (LLOQ), and if any peak is present within the retention time of the internal standard, the response of such a peak should not exceed 5% of the extracted internal standard at a concentration of interest in the study (Anklam *et al.*, 2002; Arora & Gangadharappa, 2016). Furthermore, the signal-to-noise ratio (S/N) should be  $\geq 3$ . In case there is no noise, then a signal should be obtained in at least 5 subsequent scans. Target analyte peaks in the extracted ion chromatograms should overlap fully. Ion ratio should be within  $\pm 30\%$  relative of average of the calibration standards from the sequence (EC, 2016).

### 2.7.2.3 Sensitivity

Sensitivity measures the ability of a method to demonstrate that two samples containing different amounts of an analyte of interest has indeed different amounts of the analyte. Sensitivity is essentially determined in terms of the limit of detection (LOD) and the limit of quantification (LOQ). The LOD estimates the minimum level from which an analyte of interest in a sample can be detected with a given certainty (e.g. 95%). The LOQ estimates the smallest amount of an analyte in a sample that can be accurately quantified by a method (Anklam *et al.*, 2002). Usually the LOD and LOQ values are expected to be less than the maximum limits of the mycotoxin stipulated by regulatory agencies.

### 2.7.2.4 Linearity and range

Linearity measures the ability of an analytical method to, within a given range, provide instrumental responses that are proportional to the analyte concentration in the sample (Huber, 2010). The EC and the International Conference on Harmonization (ICH) recommends that coefficients of determination for linearity should be  $\geq 0.95$  (Shabir, 2005). The ICH further recommends a maximum of 2% for the y-intercept of the target concentration response (Shabir, 2005). Range on the other hand refers to the concentration interval of an analyte over which a validated method is considered to perform in a linear manner. The criteria for the linear range can be different. Generally, the linear range should cover 25 to 200% of the target (expected) analyte concentration.

### 2.7.2.5 Intra- and inter-day precision

Intra-day precision (RSD<sub>r</sub>) also referred to as repeatability or within-day precision expresses the closeness of results obtained under the same working conditions over a short interval of time, usually within the period of 24 h (Huber, 2010). The EC recommends RSD<sub>r</sub> values not exceeding the computed values of the Horwitz equation (Equation 2.1). Usually, for a mass fraction of  $\geq 10$   $\mu\text{g/kg}$  to 100  $\mu\text{g/kg}$ , this value should not exceed 20% (Rodríguez-Carrasco *et al.*, 2016; Meerpoel *et al.*, 2018). In the cases where the concentrations are lower than 100  $\mu\text{g/kg}$ , care must be taken when calculating the Horwitz values as this could be too high (*i.e.*,  $>20\%$ ). In such situations, the RSD<sub>r</sub> values should be as low as possible (EC, 2002; Meerpoel *et al.*, 2018). It should be noted that specific RSD<sub>r</sub> values have been established for some well-known mycotoxins: the AOAC recommends an RSD<sub>r</sub> of  $< 25\%$  for each mycotoxin (AOAC, 2009), the EC recommends  $\leq 20\%$  for OTA,  $\leq 25$  for ZEA,  $\leq 20\%$  for FBs,  $\leq 30$  for T-2 (Commission Regulation, 2006a).

$$\text{RSD}_r = \frac{2}{3} \left( 2^{[1-0.5 \log C]} \right) \quad \text{Equation 2.1}$$

Where C is the mass fraction expressed as a power of 10 (EC, 2002).

Inter-day precision also referred to as between-day (intermediate) precision (RSD<sub>R</sub>), though similar to the RSD<sub>r</sub>, measures the relative standard deviation of repeated measurements for experiments conducted within a longer interval of time (usually over 24 h). The recommended values for the RSD<sub>R</sub> values are similar to those of the RSD<sub>r</sub>, however, the Horwitz equation for calculation of RSD<sub>R</sub> (Equation 2.2) is a little bit different than that of RSD<sub>r</sub> (EC, 2002; Meerpoel *et al.*, 2018).

$$\text{RSD}_R = 2^{[1-0.5 \log C]} \quad \text{Equation 2.2}$$

### 2.7.2.6 Robustness

Robustness measures the capacity of an analytical method to produce consistent results despite relatively small, but deliberate perturbations in analytical parameters (Shabir, 2005). In other words, robustness measures the stability of a method during little but deliberate variations in the analytical parameters. There are no specific criteria for robustness.



Further details on various other requirements for validation of methods for mycotoxin analysis as outlined by the EC, CODEX, AOAC, FDA, ICH can be found in the following literature (Anklam *et al.*, 2002; Gilbert & Anklam, 2002; Shabir, 2005; Commission Regulation, 2006a; AOAC, 2009; CODEX, 2015; FDA, 2015). The next section of the chapter describes the importance of chemometric models in the development and validation of analytical methods. It also gives examples of some of these models and their applicability in the development of extraction methods.

## **2.8 CHEMOMETRIC APPROACHES FOR OPTIMIZATION OF EXTRACTION METHODOLOGIES IN SAMPLE PREPARATION**

Chemometrics involves the use of mathematical and statistical tools for modelling of patterns, extraction of meaning information and interpretation of chemical and biochemical datasets (Bu, 2007; El-Gindy & Hadad, 2012; Ab Ghani *et al.*, 2014). The application of chemometric tools in the design and optimization of sample preparation methodologies is gaining increasing popularity and leading to the development of more efficient analytical procedures (Ab Ghani *et al.*, 2014; Li *et al.*, 2017). Development and optimization of efficient sample extraction methods is often a very difficult task as very often the extraction efficiency is influenced by more than one analytical parameter. Achieving the best possible outcome usually requires repeated experimental trials under different conditions in order to select the best. For each experimental trial, there is a corresponding decision challenge to make as to whether the outcome is a feasible and optimal solution to the objective variable. When more than one objective variable is involved, the number of experimental trials required to make a logical inference on the optimal solution increases exponentially. The decision on the solution becomes very complex and often cannot be addressed using conventional statistical tools.

Chemometric optimization models such as the response surface methodology (RSM) are ideal for tackling such challenges of enhancing the performance of analytical procedures, typically an improved quantitative analytical response, and yielding maximum information (Gbashi *et al.*, 2016; Adebo *et al.*, 2018b). In terms of cross-validation of extraction methods or interpretation of multivariate datasets, the principal component analysis (PCA) and orthogonal projections to latent structures discriminate analysis (OPLS-DA) have found applicability (Yamamoto *et al.*, 2009; Song *et al.*, 2013; Bro & Smilde, 2014; Khoza *et al.*, 2014). The application of chemometric tools

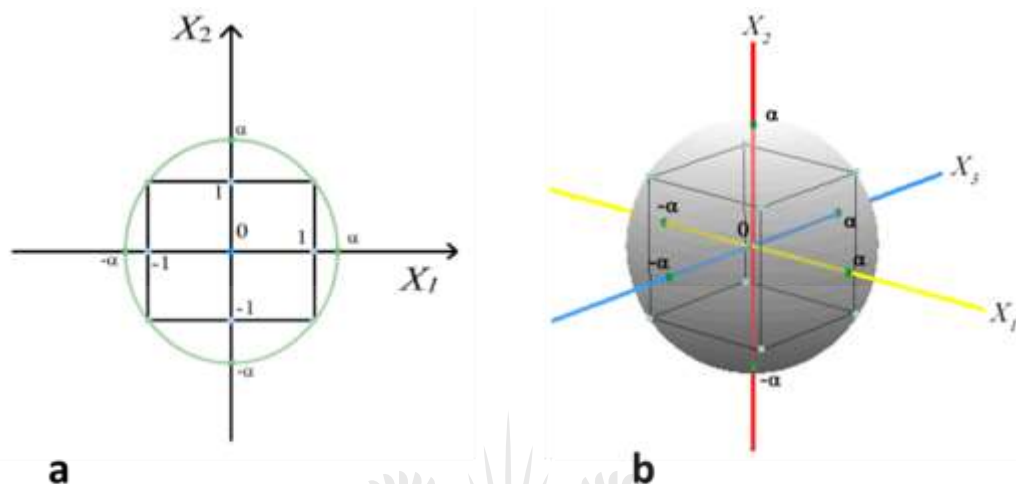
in the design and optimization of sample preparation methodologies is gaining increasing popularity and leading to the development of more efficient analytical procedures (Ab Ghani *et al.*, 2014; Li *et al.*, 2017). By proper use of the proposed mathematical models during method development and validation, a more efficient, robust and goal-specific method is possible. In the succeeding sub-sections of this chapter, a brief description of RSM, PCA and OPLS-DA will be presented.

### 2.8.1 Response surface methodology (RSM)

RSM employs mathematical algorithms in establishing approximate functional relationships between an objective variable(s) and a set of control variables by means of a series of pre-designed experiments, and then computing the value of the objective function using probabilistic analysis (Uma *et al.*, 2010; Morshedi & Akbarian, 2014). When more than one responses exist, it becomes critical to find the compromise or global optimum that takes into consideration all the response variables (Adebo *et al.*, 2018b). Examples of the commonly adopted approaches of RSM include the fractional and full factorial designs (Gunst & Mason, 2009; Rakić *et al.*, 2014), Box-Behnken design (Maran *et al.*, 2013), Plackett–Burman design (Robert *et al.*, 2006), Doehlet design (Adebo *et al.*, 2018b) and the Box-Wilson central composite design (CCD) (Mirzajani *et al.*, 2010). Amidst these approaches, the CCD is the most widely used RSM technique. Bas and Boyaci, (2007), Bezerra *et al.* (2008) and Azami *et al.* (2012) have described in detail the mathematical principles behind these different approaches of RSM.

The CCD has been widely used for optimization of various sample preparatory methodologies (Nazari *et al.*, 2007; Mirzajani *et al.*, 2010; Shi *et al.*, 2012). This model enables approximate estimation of second-degree polynomial models, with a reduced number of experimental runs (Goncalves *et al.*, 2006; Tamhane, 2014). Typically, a set of experiments are statistically designed and conducted. The experiments consist of (1) levels of a factorial or fractional factorial design, (2) a set of replicated center points which represent median values for each factor used in the factorial section of the design. The number of center points depends on the specific characteristics desired by the design, (3) a set of star or axial points which are similar to the center points except that one of the factors takes values of  $\alpha$  which are both above and below the median of the factorial levels (typically outside of the factorial range) which allows for the estimation of curvature. The

exact value of  $\alpha$  depends on specific properties desired for the experimental design and the number of independent factors involved. In any case, a more common choice of  $\alpha$  is  $\alpha = \sqrt{k}$  which yields a spherical design (Figure 2.12), where  $k$  is the number of independent factors (STAT503, 2018).



**Figure 2.12:** The central composite design of the response surface model for (a)  $\alpha = \sqrt{k}$ , where  $k=2$ , and (b)  $\alpha = \sqrt{k}$ , where  $k=3$ .  $X_1$ =independent factor 1,  $X_2$ = independent factor 2 and  $X_3$ = independent factor 3.

After the design, experiments are performed based on the design and a linear regression approach is used for fitting the optimization model to the experimental data. The resultant quadratic models give the best approximate description of the patterns and behavior of the dataset, and thus can be maneuvered to obtain the best system performance *i.e.*, the optimal value of the response variable or to obtain a specific target value of the response variable (Bezerra *et al.*, 2008). The quadratic models usually take the form of Equation 2.3.

$$Z = \beta_0 + \sum_{i=1}^k \beta_i x_i + \sum_{i=1}^k \beta_{ii} x_i^2 + \sum_{i=1}^k \sum_{j=1}^k \beta_{ij} x_i x_j \quad \text{Equation 2.3}$$

Where  $z$  is the response variable,  $x_i$  and  $x_j$  are the factors or independent variables,  $\beta_0$  is the model constant,  $\beta_i$ ,  $\beta_{ii}$  and  $\beta_{ij}$  are the coefficients for the linear, quadratic and interaction terms, respectively (Adebo *et al.*, 2018b).

Further to this, the model-fit can be used to study the linear, quadratic and interaction effects of the control variable on the response variable (Uma *et al.*, 2010). In more complex optimization

problems where more than one response exists, there is the possibility that the optimal value for one of the responses may not yield an optimal response for the other response(s). In this case, a global optimization approach is adopted which reduces variability in one or more of the responses while simultaneously optimizing or targeting a specific value for the other response(s).

### **2.8.2 Principal component analysis (PCA) and orthogonal projections to latent structures discriminate analysis (OPLS-DA)**

The PCA (Bro and Smilde, 2014) and OPLS-DA (Song *et al.*, 2013) are amongst the most widely utilized chemometric models for multivariate data interpretation in analytical and bioanalytical sciences (Daszykowski *et al.*, 2003; Cordella, 2012; Worley & Powers, 2013). The PCA uses advanced mathematical algorithms based on a vector-space orthogonal (*i.e.*, uncorrelated) transformation to reduce the dimensionality of large datasets into a fewer number of latent variables also called principal components (PCs) while preserving as much of the variation in the data as possible (Daszykowski *et al.*, 2007; Cordella, 2012; Worley & Powers, 2013). Examination of the compressed data allows for an easier and quicker determination of outliers and observation of the trends, patterns and overall structure of the dataset (Daszykowski *et al.*, 2007; Worley & Powers, 2013).

An important feature of the PCA is that the PCs are chosen in order of magnitude in a manner that maximizes the variance of the projected points (Aliferis *et al.*, 2010). The first PC explains as much of the total variation in the dataset as possible, and each other subsequent PC is chosen under the constraint that it is orthogonal to the previous PCs while explaining as much of the remaining variation in the data as possible (Panigrahi, 2014). Generally, the first few PCs are sufficient to describe the overall data structure and make inferential interpretations (Daszykowski *et al.*, 2007). PCA is essentially an unsupervised model *i.e.*, it interrogates the dataset for patterns without making reference to the sample class labels in the dataset. As such, the PCA is helpful in exploring patterns in high-dimensional datasets when there is no specific information of class labels. However, the separation between data groups is not maximized nor is information provided on why the data groups are different.

The OPLS-DA on the other hand is somewhat similar to the PCA, however, it is a linear discriminant model which adopts a supervised approach (*i.e.*, makes reference to data class labels)

to minimize within-class variance and maximize the between-class variance in the data groups (Ballabio & Todeschini, 2009). OPLS-DA is particularly useful when there are two classification labels associated with the dataset, such as a control (*i.e.*, independent or predictor) group and a response (dependent) group. The objective is to predict a set of response variables (say  $X_1, \dots, X_n$ ) from a set of control variables ( $Y$ ) by extracting a set of orthogonal latent variables (or PCs) which have the best predictive power. These PCs can then be used to create visual displays such as the score, loadings and variable importance plot (VIP) similar to those obtained by the PCA model (Abdi, 2010).

The score plot is a scatter plot that projects the data onto a two-dimensional subspace, emphasizing the variations in the data by highlighting similarities or differences between the various subsets by way of clusters. The loadings plot describes the relationship between original variables and subspace dimensions, showing the contribution of separate variables to a given PC. Whereas, the VIP shows the most important variables ranked in terms of significance in descending order by a mean decrease in Gini. Gini is a statistical measure of the degree of variation (or inequality) represented in a set of values of a frequency distribution. The top variables have higher predictive power and contribute more to the overall model. These dynamic and visually interpretable tools make PCA and OPLS-DA very attractive for multi-dimensional data analysis (Brereton, 2003; Daszykowski *et al.*, 2003, 2007; Yamamoto *et al.*, 2009; Tugizimana, 2012).

For both the PCA and OPLS-DA analysis, a data scaling and a data clustering approach is usually required. A number of data scaling approaches exists such as centering, unit variance, range, and Pareto scaling amongst others (Worley & Powers, 2013). The Pareto scaling is one of the most frequently utilized amongst the scaling methods because it aims to minimize the relative importance of large values while partially preserving the data structure. It stays closer to the original measurement than the unit variance scaling approach (Worley & Powers, 2013). In terms of data clustering methods, the Ward's method and the K-means are favorites, however, the Ward's method is regarded as being superior for data amalgamation because it adopts an analysis of variance (ANOVA) approach to evaluate the distances between the different data clusters. This approach is more efficient when the distance between clusters is estimated using the squared Euclidean method which is essentially robust to outliers or the addition of new objects to the analysis (Sima *et al.*, 2017).

PCA and OPLS-DA have a wide range of applications in bioanalytical sciences. Some common applications include; data compression, de-noising signals, blind source separation, and cross-validation or authentication of data from different sources. PCA and OPLS-DA have been utilized for authentication, quality control and discrimination of different extraction methods (Tambellini *et al.*, 2013; Cubero-Leon *et al.*, 2014, 2018; Liu *et al.*, 2016). Tambellini *et al.* (2013) demonstrated the use of PCA and OPLS-DA for the comparison of three different solvent extraction methods for the ability to simultaneously extract polar and non-polar yeast metabolites. It was shown that such an approach was a quicker and cheaper way to comparatively discriminate between extraction methods, and to identify the most efficient and reproducible method from the three methods.

## 2.9 CONCLUDING REMARKS FROM THE LITERATURE REVIEWED

From the various literature consulted and reviewed herein, it has been established that mycotoxins are potent natural toxins of fungi origin that constitute a significant nuisance to human and animal health as well as the economy. One way to adequately combat the prevalence of these toxic substances is by frequent monitoring of their prevalence along the food supply chain, in order to ensure conformity to established regulatory limits. This makes analysis as a critical element in mycotoxin management and control. Extraction being an important step during mycotoxin analysis hence requires constant improvement, as such, a priority in mycotoxicological research. At present, most of methods for mycotoxin analysis present a number of challenges such as being laborious, largely chemical-dependent and expensive, which are yet to be fully addressed. There is thus a continual quest for newer extraction methods that are fast, cheap, efficient and involve complete or partial replacement of organic solvents. Pressurized hot water extraction seems very promising in addressing all these requirements, if well exploited. Harnessing of PHWE using chemometric tools could yield a very efficient method for routine analysis of mycotoxins and other important fungal metabolites in foods and feeds.

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## CHAPTER THREE<sup>#</sup>

### NUMERICAL OPTIMIZATION OF TEMPERATURE-TIME DEGRADATION OF MULTIPLE MYCOTOXINS

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#### Abstract

Mycotoxins are potent food contaminants that exert significant deleterious effects on human and animal health, yet, there is limited and often conflicting data on their thermal stability. The present study systematically investigated the thermal degradation patterns of multiple mycotoxins as a function of temperature and time, in pure form and spiked into a food matrix (maize flour), using a numerical modelling approach. Mycotoxins under investigation included aflatoxins (AFs), fumonisins (FBs), zearalenone and its analogue  $\alpha$  and  $\beta$  epimers (ZEAs), ochratoxins (OTs), T-2 toxin (T-2), alternariol monomethyl ether (AME) and sterigmatocystin (STEG). A set of statistically-designed experiments were conducted, and a second-order optimization function fitted to the experimental data. The resultant models were well fit with  $R^2$  values ranging from 0.87 to 0.99 and 0.89 to 0.99, for pure mycotoxin standards and spiked maize flour, respectively. It was also possible to statistically determine the optimum degradation conditions which were 217 °C/63.28 min and 211 °C/54.71 min for pure mycotoxins and spiked into maize flour, respectively. Our observations herein could be critical for food safety applications targeted at reducing or at best eliminating completely multi-mycotoxins in food using heat processing while limiting the destruction of food quality factors.

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## Highlights

- Mycotoxins are unwanted poisonous secondary metabolites produced by fungi that contaminate a wide range of food commodities globally.
- Thermal treatment is commonly employed in food processing to ensure safety *via* degradation of toxic components present in food.
- The effectiveness of this process is proportional to the amount of thermal energy supplied and exposure time.
- Numerical modelling is useful for optimization of thermal degradation patterns of multiple mycotoxins as a function of temperature and time.

**Key words:** Mycotoxins; numerical modeling; optimization; thermal degradation; thermal stability

### 3.1 Introduction

Mycotoxins are poisonous biochemical compounds of fungal origin that contaminate various food and feed commodities on a global scale. They have been implicated as major environmental hazards due to their perpetual proliferation in food and feed products, and subsequent possible lethal effects on humans and animals (Njobeh *et al.*, 2010a; Zain, 2011; Makun *et al.*, 2012; Enyiukwu *et al.*, 2014; Gbashi *et al.*, 2017c). One of the mycotoxins, aflatoxin B<sub>1</sub> (AFB<sub>1</sub>), has been classified as the most noxious naturally-occurring carcinogen known to man (FAO, 2004a). Although mycotoxins have been estimated in a wide range of food and feed commodities (Mircea *et al.*, 2008; Yang *et al.*, 2014; Chilaka *et al.*, 2016), maize in particular is a favored food substrate for incessant contamination (often at levels above regulatory limits) due to its susceptibility to attack by mycotoxigenic fungal species (Makun *et al.*, 2012; Njobeh *et al.*, 2010; Njobeh *et al.*, 2012). This is of great concern because maize and maize-based products are staple foods for billions of people, and as well often constitute a major component of animal feed (du Plessis, 2003; Ranum *et al.*, 2014). In South Africa for instance, daily consumption of maize and maize-based meals can reach up to 328 g/person (du Plessis, 2003; Ranum *et al.*, 2014). Because of that, maize is an ideal reference matrix for investigating various mitigation approaches in mycotoxicology (Brown, 1999; Lauren & Smith, 2001; Raters & Matissek, 2008).



Different approaches have been investigated for the degradation of mycotoxins, some of which include gamma irradiation (Hooshmand & Klopfenstein, 1995), UV irradiation (Murata *et al.*, 2008), thermal processing (Bretz *et al.*, 2006; Raters & Matissek, 2008; Kabak, 2009), microbial and enzyme degradation (Ji *et al.*, 2016; Adebo *et al.*, 2017), plasma-based degradation (ten Bosch *et al.*, 2017), microwave-induced argon plasma degradation (Park *et al.*, 2007), oxidative degradation using ozone (McKenzie *et al.*, 1997), and many others (Doyle *et al.*, 1982; Juodeikiene *et al.*, 2012). Amongst these, heat treatment remains a cheap, simple and sustainable approach for mitigating the prevalence of mycotoxins, and has had a good track record of effectively reducing other contaminants present in food (Yazdanpanah *et al.*, 2005; Kabak, 2009; Méndez-Albores *et al.*, 2013; Wu *et al.*, 2017). However, because of its unsophisticatedness and everyday use, a critical understanding of the goal-specific applications of thermal processing is often unintentionally neglected (Sindelar & King, 2013). This perhaps could be the reason for the limited and conflicting studies on thermal stability of many mycotoxins (Raters & Matissek, 2008; Kabak, 2009; Turner *et al.*, 2009).

The efficacy of a thermal processing system is known to be in proportion to the amount of heat energy supplied and time of exposure. Higher temperatures and longer heating times are known to result in greater degradation of mycotoxins (Kabak, 2009; Gbashi *et al.*, 2017e). However, due to the detrimental effects higher temperatures have on important food quality factors, it is important to optimize these parameters in order to achieve maximum degradation of these toxins at the lowest possible temperature and time conditions. Moreover, the notoriously incessant prevalence of mycotoxins even in heat-processed foods (Stoloff & Trucksess, 1981), has necessitated the systematic re-investigation of their response to heat treatment.

In this regard, numerical modelling is a useful optimization approach that has found wide applicability in thermal processes in biological systems (Sendín *et al.*, 2010; Abakarov & Nuñez, 2013). Amidst various approaches, central composite design (CCD) is one of the most commonly used numerical optimization techniques in food processing. This is because it offers the advantage of a reduced number of experimental runs, and provides a function and empirical relationship between the objective function (response variable) and the various control variables, as well as provides details on the effects of different control variables on a response variable (Goncalves *et al.*, 2006; Khuri & Mukhopadhyay, 2010; Uma *et al.*, 2010; Gbashi *et al.*, 2016). The present study



adopts a CCD numerical modelling approach to systematically investigate, and optimize the temperature-time degradation patterns of multiple mycotoxins in pure and spiked form (maize flour).

## 3.2 Materials and methods

### 3.2.1 Materials

Mycotoxin reference standards, AFB<sub>1</sub>, aflatoxin B<sub>2</sub> (AFB<sub>2</sub>), aflatoxin G<sub>1</sub> (AFG<sub>1</sub>), aflatoxin G<sub>2</sub> (AFG<sub>2</sub>), ochratoxin A (OTA), ochratoxin B (OTB), fumonisin B<sub>1</sub> (FB<sub>1</sub>), fumonisin B<sub>2</sub> (FB<sub>2</sub>), fumonisin B<sub>3</sub> (FB<sub>3</sub>), zearalenone (ZEA),  $\alpha$ -zearalenol ( $\alpha$ -ZEL),  $\beta$ -zearalenol ( $\beta$ -ZEL), T2-toxin (T-2), AME, and STEG were purchased from the Council for Scientific and Industrial Research (CSIR). Solvents used included LC-MS grade acetonitrile, methanol and formic acid which were purchased from Sigma, Aldrich (South Africa). Ultrapure water was obtained from a Milli-Q Gradient A10 dispensing system (Millipore, Billerica, MA, USA). Maize flour was purchased from a Shoprite grocery store in Johannesburg (South Africa).

### 3.2.2 Methods

#### 3.2.2.1 Experimental design

A set of experiments was statistically designed based on the response surface methodology (RSM) using Statistica version 7 statistical software (StatSoft, USA). Specifically, the central composite design (CCD) (Hossain *et al.*, 2015) approach was adopted because it permits building second-order optimization models without the need for a complete three-level factorial experimental design (Goncalves *et al.*, 2006; Tamhane, 2014). Accordingly, a 2-factor, 1 block experimental design was achieved, which consisted of 10 experimental levels (Table 3.1); 2 levels of fractional factorial design for each of the factors studied, a replicated center-point to improve the precision of the model, and a set of axial points (*i.e.*,  $\alpha$  and  $-\alpha$ ) that permits rotatability of the model and ensures estimation of response curvature. Rotatability of the model is desirable because it allows for equal variance of prediction for all points equal-distance from the center point irrespective of the direction. The experimental region was selected based on preliminary laboratory trials (Gbashi *et al.*, 2017e).

**Table 3.1:** Two-factor, 1 block standard order CCD experimental design for temperature-time degradation of mycotoxins

S/No	Temperature (°C)	Time (min)	RSM Codes	Comment
1	120	15.00	-1, -1	Factorial level
2	120	55.00	-1, +1	Factorial level
3	200	15.00	+1, -1	Factorial level
4	200	55.00	+1, +1	Factorial level
5	103	35.00	- $\alpha$ , 0	Axial point
6	217	35.00	+ $\alpha$ , 0	Axial point
7	160	6.72	0, - $\alpha$	Axial point
8	160	63.28	0, + $\alpha$	Axial point
9	160	35.00	+1, +1	Center point
10	160	35.00	+1, +1	Center point

**Key:** S/No.: serial number. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol. RSM – response surface methodology

After conducting the experiments, a second-order optimization model described by Equation 3.1 (Adebo *et al.*, 2018b) was fitted to the experimental data using the method of least squares (MLS) which generates the lowest possible residuals (Bas & Boyaci, 2007).

$$Z = \beta_0 + \sum_{i=1}^k \beta_i x_i + \sum_{i=1}^k \beta_{ii} x_i^2 + \sum_{i=1}^k \sum_{j=1}^k \beta_{ij} x_i x_j \quad \text{Equation 3.1}$$

Where  $z$  is the response variable *i.e.*, degradation (%),  $x_i$  and  $x_j$  are the factors, temperature (°C) and time (min), respectively,  $\beta_0$  is the model constant,  $\beta_i$ ,  $\beta_{ii}$  and  $\beta_{ij}$  are the coefficients for the linear, quadratic and interaction terms (Adebo *et al.*, 2018b).

The model fitness and adequacy were determined by evaluating the coefficient of determination ( $R^2$ ), adjusted  $R^2$ , Pearson's correlation coefficient ( $r$ ), average absolute deviation (AAD), accuracy factor ( $A_f$ ) and the bias factor ( $B_f$ ). Model parameters and significance were determined at a probability level of 95% (*i.e.*,  $p < 0.05$ ). The various mathematical functions used to compute these parameters are presented in the Equations 3.2 to 3.7 (Morshedi & Akbarian, 2014; Adebo *et al.*, 2018b).

$$R^2 = \frac{\sum_{i=1}^n (\hat{y}_i - \bar{y})^2}{\sum_{i=1}^n (y_i - \bar{y})^2} \quad \text{Equation 3.2}$$

Where  $R^2$  is the coefficient of determination,  $n$  is the sample size,  $\bar{y}$  is estimated mean value,  $y_i$  and  $\hat{y}$  are the experimental and predicted values, respectively.

$$R^2_{adj} = 1 - \frac{k-1}{k-p}(1 - R^2) \quad \text{Equation 3.3}$$

Where  $R^2_{adj}$  is the adjusted coefficient of determination,  $R^2$  is the coefficient of determination,  $p$  is number of regression coefficients and  $k$  is total number of observations.

$$r = \frac{\sum_{i=1}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^n (x_i - \bar{x})^2} \sqrt{\sum_{i=1}^n (y_i - \bar{y})^2}} \quad \text{Equation 3.4}$$

Where  $r$  is the Pearson's correlation coefficient,  $n$  is the sample size,  $x_i$  and  $y_i$  are single measurements indexed with  $i$  for predicted and experimental values, respectively, and  $\bar{x}$  and  $\bar{y}$  are the means for the predicted and experimental variables, respectively.

$$AAD = \frac{\left[ \sum_{i=1}^n \left( \frac{y_{i \text{ exp}} - y_{i \text{ cal}}}{y_{i \text{ exp}}} \right) \right]}{n} \quad \text{Equation 3.5}$$

Where  $AAD$  is the average absolute deviation,  $n$  is the sample size, and  $y_{i \text{ exp}}$  and  $y_{i \text{ cal}}$  are the individual experimental and predicted values indexed with  $i$ , respectively.

$$B_f = 10^{\frac{1}{n}} \sum_{i=1}^n \log \left( \frac{y_{i \text{ cal}}}{y_{i \text{ exp}}} \right) \quad \text{Equation 3.6}$$

Where  $B_f$  is the bias factor,  $n$  is the sample size, and  $y_{i \text{ exp}}$  and  $y_{i \text{ cal}}$  are the individual experimental and predicted values indexed with  $i$ , respectively.

$$A_f = 10^{\frac{1}{n}} \sum_{i=1}^n \left[ \log \left( \frac{y_{i \text{ cal}}}{y_{i \text{ exp}}} \right) \right] \quad \text{Equation 3.7}$$

Where  $A_f$  is the accuracy factor,  $n$  the sample size, and  $y_{i \text{ exp}}$  and  $y_{i \text{ cal}}$  are the individual experimental and predicted values indexed with  $i$ , respectively.

After the model-fit and validation of the model adequacy, the resultant quadratic optimization models were used for optimization and computation of the globally optimal conditions for the degradation of real samples *i.e.*, pure mycotoxin standards and spiked maize flour, using the Minitab 17 global optimization function. The 3-D surface plots and Pareto charts were used to examine the degradation patterns of the analytes, with and without matrix interference.

### 3.2.2.2 Sample preparation

Spiking of maize matrix was performed as described by Sameni *et al.* (2014) with little modifications. To obtain a spiked maize concentration of 2 µg/g, exactly 2 mL of multi-mycotoxin standards stock solution (1 µg/mL) was added to 1 g of blank maize flour (previously tested on UHPLC-MS/MS) contained in a 16 mL glass vial (25×50 mm). The spiked sample was thoroughly mixed and left overnight in the dark in a fume hood to allow for slow evaporation of the solvent at ambient conditions and for the mycotoxins to be absorbed into the matrix. For the pure standards, 2 mL of the multi-mycotoxin stock solution (1 µg/mL) was transferred into a 16 mL glass vial and dried under similar conditions.

### 3.2.2.3 Thermal treatment

Thermal treatment of samples was achieved using a GC 600 Vega Series 2 oven (Carlo Erba Instruments, Italy) with an automatic temperature control unit ( $\pm 1$  °C). The oven was allowed to equilibrate at a desired temperature for 5 min before samples were introduced. Samples were placed inside the oven which was maintained at the preset temperature. After heating for the desired time, samples were retrieved immediately and allowed to cool under ambient conditions. The vials containing pure mycotoxin standards were then reconstituted in 1 mL of methanol, thoroughly vortexed for 3 min, allowed to stand and vortexed again for 2 min, filtered through a 0.22 µm syringe filter into a 1.5 mL clear HPLC vial for subsequent analysis on UHPLC-MS/MS. The thermally-treated spiked maize samples were extracted using the method of Bertuzzi *et al.* (2011) with slight modifications. To a 1 g of maize flour, 2 mL of methanol/acetonitrile (50:50, v/v) was added, and placed on a bench shaker (LABCON GmbH, Heppenheim, Germany) for 1 h. After which samples were centrifuged at 4,000 RPM, and the supernatant was filtered through a 0.22 µm syringe filter into a 1.5 mL HPLC vial for subsequent analysis on UHPLC-MS/MS.

### 3.2.2.4 Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS)

Chromatographic separation followed by quantification of multi-mycotoxins was accomplished using a Shimadzu UHPLC-MS/MS 8030 equipment (Shimadzu Corporation, Tokyo, Japan), which consists of an LC-30AD Nexera chromatograph connected to a SIL-30 AC Nexera autosampler and a CTO-20 AC Prominence Column Oven. Analytes were separated on a Raptor™

ARC-18 column (2.7  $\mu\text{m}$ , 2.1 mm  $\times$  100 mm) (Restek Corporation, Pennsylvania USA), thermostated at 40 °C. The mobile phases used consisted of (A) 0.1% formic acid (FA) in deionized water, and (B) 0.1% FA in methanol/acetonitrile (50:50 v/v), and was delivered at a constant flow rate of 0.2 mL/min. The gradient elution program began with 10% B for 0.1 min, ramped to 95% B in 8.4 min, kept constant for 3 min, and the initial condition (10% B) was re-instated for 1 min, after which, the column was allowed to re-equilibrate for 4.5 min for the next run, bringing these to a total run time of 17 min.

Following chromatographic separation, analytes were detected and quantified on a Shimadzu triple-quadrupole MS model 8030 (Shimadzu Corporation, Kyoto, Japan) operated in positive ionization mode with an electron spray ionization (ESI<sup>+</sup>) source. The interface nebulizing gas flow rate was 3 L/min, desolvation line (DL) temperature was 250 °C, heat block temperature was 400 °C, and drying gas flow rate was 15 L/min. Data acquisition was by means of a multiple reaction monitoring (MRM) method operated using optimized MS conditions for the analytes (Table 3.2). The Shimadzu LabSolutions software was used for subsequent processing and visualization of the data.

**Table 3.2:** MRM transitions, optimized MS conditions and retention times of multi-mycotoxins; Ret. time – retention time; Q1 – quadrupole 1; Q3 – quadrupole 3; CE – collision energy.

S/No	Mycotoxin	Recovery (%) <sup>*</sup>	Ret. time (min)	Precursor (mz)	Products (mz)	Q1 Pre Bias (V)	CE (eV)	Q3 Pre Bias (V)
1.	AFB <sub>1</sub>	110	8.55	313.00	241.00*	-22.00	-41.00	-23.00
					285.10	-22.00	-24.00	-29.00
2.	AFB <sub>2</sub>	102	8.30	315.00	259.10*	-22.00	-31.00	-25.00
					287.00	-23.00	-26.00	-30.00
3.	AFG <sub>1</sub>	101	8.08	329.00	243.00*	-12.00	-28.00	-23.00
					311.10	-16.00	-24.00	-14.00
4.	AFG <sub>2</sub>	96	7.83	331.00	245.10*	-12.00	-32.00	-24.00
					313.00	-12.00	-24.00	-20.00
5.	AME	100	10.32	273.00	128.10*	-10.00	-49.00	-21.00
					115.05	-18.00	-54.00	-19.00
6.	FB <sub>1</sub>	106	8.11	722.20	352.20*	-34.00	-42.00	-11.00
					334.30	-20.00	-42.00	-11.00
7.	FB <sub>2</sub>	109	9.17	706.10	336.30*	-20.00	-38.00	-22.00

S/No	Mycotoxin	Recovery (%) <sup>*</sup>	Ret. time (min)	Precursor (mz)	Products (mz)	Q1 Pre Bias (V)	CE (eV)	Q3 Pre Bias (V)
					318.30	-26.00	-41.00	-22.00
8.	FB <sub>3</sub>	94	8.85	706.30	336.30*	-40.00	-39.00	-11.00
					354.40	-20.00	-35.00	-24.00
9.	OTA	119	10.31	403.80	239.00*	-15.00	-27.00	-24.00
					221.00	-12.00	-38.00	-21.00
10.	OTB	109	9.56	370.10	205.00*	-13.00	-22.00	-21.00
					324.10	-13.00	-14.00	-22.00
11.	STEG	99	10.52	324.90	310.00*	-22.00	-24.00	-30.00
					281.10	-22.00	-40.00	-27.00
12.	T-2	120	10.03	467.20	245.10*	-13.00	-11.00	-16.00
					305.20	-22.00	-11.00	-20.00
13.	ZEA	119	10.26	319.10	185.00*	-12.00	-27.00	-30.00
					187.10	-15.00	-21.00	-19.00
14.	$\alpha$ -ZEA	128	8.80	323.10	277.20*	-17.00	-17.00	-18.00
					305.20	-24.00	-9.00	-20.00
15.	B-ZEA	135	8.39	323.10	277.20*	-16.00	-16.00	-18.00
					305.20	-16.00	-11.00	-20.00

**Key:** S/No.: serial number. \*Extraction recovery for mycotoxins spiked into the maize. Ret. Time: retention time. Q1 Pre bias: quadruple one pre-rod bias. Q3 Pre bias: quadruple three pre-rod bias. CE: collision energy. \* Quantitative product ion. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

### 3.3 Results and discussion

#### 3.3.1 Thermal degradation of mycotoxins

Results for the thermal stability of pure multi-mycotoxin standards as well as mycotoxins spiked into the maize matrix as a function of temperature and time are presented in Tables 3.3 and 3.4. Clearly, thermal degradation of all studied mycotoxins increased proportionately with increasing temperature and exposure time (Appendices 3.A & 3.B). For pure mycotoxin standards, OTB was the most thermally stable mycotoxin with an average degradation of 20%, followed by OTA (24%), AME (36%), AFG<sub>2</sub> (40%), AFB<sub>2</sub> (44%), T-2 (49%),  $\alpha$ -ZEL (50%), ZEA (51%),  $\beta$ -ZEL (52%), AFB<sub>1</sub> (53%), AFG<sub>1</sub> (55%), STEG (61%), FB<sub>1</sub> (63%), FB<sub>3</sub> and FB<sub>2</sub> (65% each). When

mycotoxins were spiked into the maize matrix, AME showed the highest resilience to heat treatment with an average percentage degradation of 33%, followed by AFG<sub>2</sub> and STEG (37% each), T-2 and  $\alpha$ -ZEL (37% each), OTB and  $\beta$ -ZEL (39% each), ZEA (42%), OTA (46%), AFG<sub>1</sub> and AFB<sub>1</sub> (47% each), AFB<sub>2</sub> (51%), FB<sub>2</sub> (77%), FB<sub>1</sub> (78%), and FB<sub>3</sub> (81%). It can be observed that mycotoxins that were relatively stable to heat treatment have a compact molecular structural configuration, *i.e.*, OTA, AME, and AFG<sub>2</sub>, whereas the more structurally spread-out mycotoxins were more thermolabile, *i.e.*, FB<sub>3</sub>, FB<sub>2</sub> and FB<sub>1</sub> (Lerda, 2011; De Souza *et al.*, 2013). A more compact structural configuration could possibly imply a more difficult thermal break down (Gibbs *et al.*, 1998; Cremer *et al.*, 2000). Generally, evaluation of the results presented in Tables 3.3 & 3.4 revealed that the temperature-time conditions that resulted in the most degradation of all classes of the mycotoxins was a temperature of 217 °C at a time of 35 min.

Although all mycotoxins showed a differential degradation pattern for pure mycotoxin standards compared with mycotoxins spiked into maize matrix, an independent-samples Student's t-test showed that only FB<sub>1</sub>, FB<sub>2</sub>, FB<sub>3</sub>, and AME had statistically significant ( $p \leq 0.05$ ) differences between pure standards and spiked maize matrix (Appendix 3.C). A temperature of 217 °C for 35 min was sufficient to completely eradicate all the aflatoxins (AFs) in the absence of matrix interference, except for AFB<sub>2</sub> which had over 86% degradation (Table 3.3). Whereas when spiked into maize matrix, all AFs were completely degraded at similar condition (217 °C for 35 min), except for AFG<sub>2</sub>, which had over 97% degradation (Table 3.4). Our results agree with Yazdanpanah *et al.* (2005), who reported that roasting nuts which contained AFs at 90 to 150 °C for 30 to 120 min resulted in reduced AF levels that ranged from 17 to 63%, depending on the temperature and exposure time (Yazdanpanah *et al.*, 2005). The *Fusarium* group of toxins, FBs, were the most thermolabile of all tested mycotoxins for both spiked and unspiked standards. Average degradation for FBs ranged from 79 to 82%, with FB<sub>3</sub> being the most susceptible analogue in this group. Scott and Lawrence (1987) made similar observations, where heating maize meal at 190 °C for 60 min degraded FBs by 60 to 80%, whereas, when the conditions were increased to 220 °C and 25 min, FBs were almost completely eliminated. Our observations also agree with reports by Castelo *et al.* (1998), who noted that roasting of artificially-contaminated maize meal at 218 °C for 15 min eliminated FB<sub>1</sub> from the food samples (Scott & Lawrence, 1987).



**Table 3.3:** Temperature-time degradation of pure multi-mycotoxin standards.

Mycotoxin	Percentage degradation of mycotoxins at different temperature-time conditions									Average
	120 °C/ 15 min (%)	120 °C/ 55 min (%)	200 °C/ 15 min (%)	200 °C/ 55 min (%)	103.43 °C/ 35 min (%)	217 °C/ 35 min (%)	160 °C/ 6.72 min (%)	160 °C/ 63.28 min (%)	160 °C/ 35 min (%)	
AFB <sub>1</sub>	17 <sup>a</sup> ±12	12 <sup>a</sup> ±3.3	93 <sup>d</sup> ±0.53	99 <sup>d</sup> ±0.2	3 <sup>a</sup> ±2.9	100 <sup>d</sup> ±0	49 <sup>bc</sup> ±1.3	66 <sup>c</sup> ±4.7	41 <sup>b</sup> ±2.4	53±3.1
AFB <sub>2</sub>	31 <sup>a</sup> ±17	19 <sup>a</sup> ±7.1	62 <sup>ab</sup> ±0.17	89 <sup>b</sup> ±3	23 <sup>a</sup> ±16	86 <sup>b</sup> ±5.6	31 <sup>a</sup> ±29	33 <sup>a</sup> ±13.8	22 <sup>a</sup> ±1.8	44±10
AFG <sub>1</sub>	12 <sup>a</sup> ±6.4	14 <sup>a</sup> ±4	97 <sup>e</sup> ±0.2	99 <sup>e</sup> ±0	6 <sup>a</sup> ±2.9	100 <sup>e</sup> ±0	39 <sup>b</sup> ±2.7	72 <sup>d</sup> ±1.3	52 <sup>c</sup> ±2.2	55±2.2
AFG <sub>2</sub>	17 <sup>ab</sup> ±2.1	7 <sup>a</sup> ±0.13	68 <sup>d</sup> ±0.06	89 <sup>d</sup> ±0.31	6 <sup>a</sup> ±0.25	100 <sup>d</sup> ±0	13 <sup>a</sup> ±8.5	30 <sup>c</sup> ±4.1	27 <sup>bc</sup> ±2.1	40±2
AME	7 <sup>ab</sup> ±8.8	2 <sup>a</sup> ±1.6	55 <sup>d</sup> ±1.8	89 <sup>e</sup> ±0.98	7 <sup>ab</sup> ±4.1	94 <sup>e</sup> ±0.4	18 <sup>bc</sup> ±4	30 <sup>c</sup> ±1.2	25 <sup>c</sup> ±1.5	36±2.7
FB <sub>1</sub>	10 <sup>a</sup> ±13.6	6 <sup>a</sup> ±8.4	100 <sup>c</sup> ±0	100 <sup>c</sup> ±0	18 <sup>a</sup> ±13	100 <sup>c</sup> ±0	88 <sup>c</sup> ±0.41	93 <sup>c</sup> ±0	52 <sup>b</sup> ±5.8	63±4.5
FB <sub>2</sub>	20 <sup>b</sup> ±2.8	24 <sup>b</sup> ±2.3	100 <sup>e</sup> ±0	100 <sup>e</sup> ±0	2 <sup>a</sup> ±0	100 <sup>e</sup> ±0	89 <sup>d</sup> ±1.1	95 <sup>e</sup> ±0.37	54 <sup>c</sup> ±1	65±0.84
FB <sub>3</sub>	20 <sup>a</sup> ±5.6	8 <sup>a</sup> ±4.8	99 <sup>c</sup> ±0.24	100 <sup>c</sup> ±0.06	15 <sup>a</sup> ±15	100 <sup>c</sup> ±0	84 <sup>c</sup> ±2.2	96 <sup>c</sup> ±0.35	60 <sup>b</sup> ±1.7	65±3.4
OTA	10 <sup>ab</sup> ±11	6 <sup>ab</sup> ±3.8	39 <sup>cd</sup> ±1.3	48 <sup>de</sup> ±0.75	5 <sup>a</sup> ±3.6	59 <sup>e</sup> ±0.63	12 <sup>ab</sup> ±8.7	24 <sup>bc</sup> ±0.25	16 <sup>a</sup> ±0.61	24±3.4
OTB	23 <sup>abc</sup> ±6.6	2 <sup>a</sup> ±0.54	29 <sup>bc</sup> ±0.27	39 <sup>cd</sup> ±3.9	10 <sup>ab</sup> ±1.8	51 <sup>d</sup> ±3	11 <sup>ab</sup> ±5.3	11 <sup>ab</sup> ±5.8	9 <sup>ab</sup> ±7.2	20±3.8
STEG	17 <sup>a</sup> ±5.8	30 <sup>b</sup> ±2.9	94 <sup>f</sup> ±0.44	99 <sup>f</sup> ±0.07	18 <sup>a</sup> ±0.51	100 <sup>f</sup> ±0	62 <sup>d</sup> ±2	79 <sup>e</sup> ±0.44	48 <sup>c</sup> ±3.2	61±1.7
T-2	13 <sup>ab</sup> ±13	5 <sup>a</sup> ±4	84 <sup>de</sup> ±1.9	96 <sup>e</sup> ±0.96	6 <sup>a</sup> ±6.3	98 <sup>e</sup> ±0.89	35 <sup>bc</sup> ±4.2	66 <sup>d</sup> ±1.9	40 <sup>c</sup> ±7.3	49±4.5
ZEA	14 <sup>a</sup> ±0.62	20 <sup>a</sup> ±3.5	84 <sup>d</sup> ±1.5	95 <sup>e</sup> ±0.27	19 <sup>a</sup> ±2.7	100 <sup>e</sup> ±0	34 <sup>b</sup> ±3	53 <sup>c</sup> ±1	39 <sup>b</sup> ±1.3	51±1.5
α-ZEL	12 <sup>a</sup> ±2.9	20 <sup>ab</sup> ±3.6	89 <sup>e</sup> ±0.77	95 <sup>e</sup> ±0.7	13 <sup>a</sup> ±4.3	100 <sup>e</sup> ±0	33 <sup>c</sup> ±4.3	53 <sup>d</sup> ±0.28	31 <sup>bc</sup> ±3.5	50±2.3
β-ZEL	16 <sup>a</sup> ±1.3	19 <sup>a</sup> ±0.85	88 <sup>d</sup> ±1.1	96 <sup>e</sup> ±0.28	23 <sup>a</sup> ±2.8	100 <sup>e</sup> ±0	32 <sup>b</sup> ±0.07	57 <sup>c</sup> ±4.2	34 <sup>b</sup> ±1.7	52±1.4

Key: Values represent means of duplicate determinations of the percentage degradations ± standard deviation of the means. Significant differences among the sample treatments as a function of time and temperature are indicated as superscripted alphabets on the means, and were compared using Tukey's pairwise multiple comparison test following a one-way ANOVA. Values in the same row followed by the same alphabet are not significantly different ( $p > 0.05$ ). AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.

**Table 3.4:** Temperature-time degradation of multi-mycotoxins spiked into maize matrix.

Mycotoxin	Percentage degradation of mycotoxins at different temperature-time conditions									Average
	120 °C/ 15 min (%)	120 °C/ 55 min (%)	200 °C/ 15 min (%)	200 °C/ 55 min (%)	103 °C/ 35 min (%)	217 °C/ 35 min (%)	160 °C/ 6.72 min (%)	160 °C/ 63.28 min (%)	160 °C/ 35 min (%)	
AFB <sub>1</sub>	2.8 <sup>a</sup> ±3.1	6 <sup>a</sup> ±2.3	86 <sup>e</sup> ±0	99 <sup>f</sup> ±0.13	6 <sup>a</sup> ±4.5	100 <sup>f</sup> ±0	18 <sup>b</sup> ±0.38	59 <sup>d</sup> ±1.5	46 <sup>c</sup> ±0.47	47±1.4
AFB <sub>2</sub>	19 <sup>a</sup> ±15	31 <sup>abc</sup> ±11	73 <sup>cd</sup> ±13	91 <sup>d</sup> ±0	14 <sup>a</sup> ±17	100 <sup>d</sup> ±0	24 <sup>ab</sup> ±4.7	62 <sup>bcd</sup> ±18	46 <sup>abc</sup> ±3.3	51±9.1
AFG <sub>1</sub>	4 <sup>a</sup> ±4.2	6 <sup>a</sup> ±4	91 <sup>c</sup> ±0	100 <sup>c</sup> ±0	1 <sup>a</sup> ±3.3	100 <sup>c</sup> ±0	12 <sup>a</sup> ±12	60 <sup>b</sup> ±1.9	45 <sup>b</sup> ±2.2	47±3.1
AFG <sub>2</sub>	3 <sup>a</sup> ±3.7	7 <sup>a</sup> ±2.4	68 <sup>c</sup> ±2.4	89 <sup>d</sup> ±0	4 <sup>a</sup> ±2.4	98 <sup>d</sup> ±0.22	14 <sup>ab</sup> ±6.3	27 <sup>b</sup> ±8.5	22 <sup>b</sup> ±0.42	37±2.9
AME	28 <sup>a</sup> ±2.6	23 <sup>a</sup> ±6.1	30 <sup>a</sup> ±1.8	51 <sup>b</sup> ±0.99	32 <sup>a</sup> ±7.6	63 <sup>b</sup> ±2.9	29 <sup>a</sup> ±2.6	26 <sup>a</sup> ±0.64	19 <sup>a</sup> ±3.2	33±3.2
FB <sub>1</sub>	53 <sup>ab</sup> ±1.3	52 <sup>ab</sup> ±11	100 <sup>c</sup> ±0	100 <sup>c</sup> ±0	42 <sup>a</sup> ±5	100 <sup>c</sup> ±0	65 <sup>b</sup> ±4.6	97 <sup>c</sup> ±0	97 <sup>c</sup> ±0	78±2.5
FB <sub>2</sub>	44 <sup>ab</sup> ±4.8	53 <sup>b</sup> ±5	100 <sup>d</sup> ±0	100 <sup>d</sup> ±0	42 <sup>a</sup> ±5.3	100 <sup>d</sup> ±0	65 <sup>c</sup> ±0.84	97 <sup>d</sup> ±0.26	95 <sup>d</sup> ±0.16	77±1.8
FB <sub>3</sub>	55 <sup>a</sup> ±7	59 <sup>ab</sup> ±3.1	100 <sup>c</sup> ±0	100 <sup>c</sup> ±0	50 <sup>a</sup> ±5.7	100 <sup>c</sup> ±0	70 <sup>b</sup> ±2	98 <sup>c</sup> ±0.38	96 <sup>c</sup> ±0.49	81±2.1
OTA	25 <sup>a</sup> ±2.4	34 <sup>a</sup> ±6	56 <sup>b</sup> ±1.6	85 <sup>c</sup> ±0.65	26 <sup>a</sup> ±2.9	94 <sup>c</sup> ±0.18	33 <sup>a</sup> ±6.2	32 <sup>a</sup> ±4.2	26 <sup>a</sup> ±1.2	46±2.8
OTB	17 <sup>ab</sup> ±15	21 <sup>ab</sup> ±3.1	46 <sup>b</sup> ±2.2	80 <sup>c</sup> ±0.78	16 <sup>a</sup> ±13	92 <sup>c</sup> ±0.13	22 <sup>ab</sup> ±7.5	21 <sup>ab</sup> ±9.4	30 <sup>ab</sup> ±0.85	39±5.8
STEG	5 <sup>a</sup> ±0.21	7 <sup>a</sup> ±0.36	56 <sup>c</sup> ±4.1	94 <sup>d</sup> ±0.21	9 <sup>a</sup> ±0.21	98 <sup>d</sup> ±0.14	12 <sup>a</sup> ±2.6	39 <sup>b</sup> ±2.4	15 <sup>a</sup> ±5.2	37±1.7
T-2	9 <sup>a</sup> ±6.3	7 <sup>a</sup> ±3.4	53 <sup>b</sup> ±15	85 <sup>c</sup> ±0.3	13 <sup>a</sup> ±9.3	96 <sup>c</sup> ±2.2	19 <sup>a</sup> ±13	29 <sup>ab</sup> ±6.2	26 <sup>ab</sup> ±3	37±6.5
ZEA	14 <sup>a</sup> ±0.12	17 <sup>a</sup> ±11	56 <sup>b</sup> ±1.6	85 <sup>c</sup> ±1.1	21 <sup>a</sup> ±4.2	93 <sup>c</sup> ±0.3	22 <sup>a</sup> ±2.4	44 <sup>b</sup> ±2	27 <sup>a</sup> ±2.2	42±2.8
α-ZEL	6 <sup>ab</sup> ±0	17 <sup>bc</sup> ±0.66	58 <sup>e</sup> ±0.66	88 <sup>f</sup> ±0.72	3 <sup>a</sup> ±2.9	97 <sup>f</sup> ±0.61	14 <sup>abc</sup> ±4.1	35 <sup>d</sup> ±7.7	19 <sup>c</sup> ±0.18	37±1.9
β-ZEL	3 <sup>b</sup> ±0	20 <sup>b</sup> ±2.9	58 <sup>d</sup> ±0.58	90 <sup>e</sup> ±0.05	9 <sup>a</sup> ±5.4	98 <sup>e</sup> ±0.37	20 <sup>b</sup> ±1	32 <sup>c</sup> ±1.7	19 <sup>b</sup> ±1.2	39±1.5

Key: Values represent means of duplicate determinations ± standard deviation of the means. Significant differences among the sample treatments as a function of time and temperature are indicated as superscripted alphabets on the means, and were compared using Tukey's pairwise multiple comparison test following a one-way ANOVA. Values in the same row followed by the same alphabet are not significantly different ( $P > 0.05$ ). AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.

In the food industry, particularly the coffee industry, the thermal stability of ochratoxins (OTs) is of particular interest, because OTs have been reported to be prevalent even in processed ready-to-eat coffee (Studer-Rohr *et al.*, 1995; FAO, 2001; Kabak, 2009; Vanesa & Ana, 2013). It has not been possible to conclusively establish the thermal stability of OTs based on available literature. Tsubouchi *et al.* (1987) considers OTA as relatively heat stable, because only 0 to 12% of OTA was degraded in beans when roasted at 200 °C for 10 to 20 min (Tsubouchi *et al.*, 1987). Whereas, other reports consider OTA as relatively thermolabile (Studer-Rohr *et al.*, 1995; Perez de Obanos *et al.*, 2005). Ultimately, our findings reveal that the thermal stability of OTs is strongly influenced by matrix interactions (Table 3.5). As pure standards, OTs were highly resilient to heat treatment, such that a temperature-time condition of 217 °C and 35 min (a condition at which almost all the other mycotoxins completely degrade) resulted in only about 50% degradation of the OTs. However, when OTs were spiked into maize matrix and subjected to similar conditions (*i.e.*, 217 °C and 35 min), there was at least 94 and 92% degradation for OTA and OTB respectively. The mechanism of thermal degradation of OTA at higher temperatures (>250 °C) has been described as partial isomerization on the molecules, which results in the formation of a less toxic diastereomer (Studer-Rohr *et al.*, 1995).

Based on our results, T-2 and ZEA and its analogues (ZEAs) can be regarded as mid-thermally stable mycotoxins. The average thermal degradation of ZEAs ranged from 48 to 50% for pure standards, and 36 to 41% for spiked maize. Likewise, T-2 had an average degradation of 48 and 32% for pure standards and spiked maize respectively, which agrees with the findings by Schmidt *et al.* (2017). The thermal stability of the relatively understudied, AME and STEG, were also investigated in the present study. Alternariol monomethyl ether demonstrated a significantly strong thermal stability. In fact, it had the highest thermal stability for spiked maize (32%), second only to the OTs for pure standards with an average degradation of 35%. Just like the OTs, the thermal stability of STEG is strongly matrix-influenced. When in pure form, STEG had an average degradation of 60%, however, when spiked into maize matrix it had an average degradation of 35%. To the best of our knowledge, this is the first report on the thermal degradation of AME and STEG.

### 3.3.2 Matrix effect on thermal stability of mycotoxins

The effect of matrix interference on the thermal stability of mycotoxins is indisputably substantial. Depending on the mycotoxin and thermal conditions, maize matrix either accelerated or suppressed the degradation of mycotoxins (Tables 3.3 & 3.4). The mycotoxins most susceptible to matrix-enhanced degradation included FBs, OTs and AFB<sub>2</sub>. Sterigmatocystin, T-2 and the other mycotoxins demonstrated less susceptibility, and perhaps some level of matrix-suppressed degradation (Appendix 3.C). This phenomenon can be more clearly visualized on the compound 3-D surface plots (Figure 3.1), which is discussed in greater detail in the succeeding sections of this work. Raters and Matissek (2008) also observed that the presence of matrix components (starch) led to increased degradation of AFB<sub>1</sub> in spiked maize matrix compared to pure-form AFB<sub>1</sub>. In fact, they noted that when AFB<sub>1</sub> was spiked into a proteinous matrix (*i.e.*, soybean), thermal degradation was much more increased compared to starch (Raters & Matissek, 2008). Other possible matrix constituents that may interfere with the thermal stability of mycotoxins are polyphenols and moisture (Boudra *et al.*, 1995; Howard *et al.*, 1998; Raters & Matissek, 2008).

Previous studies have shown that mycotoxin-matrix interactions during thermal degradation entails a number of physicochemical possibilities such as breakdown or modification the chemical structures of the analytes, or heat-assisted binding of the toxins to matrix components (Seefelder *et al.*, 2001; Nicolás-Vázquez *et al.*, 2010; Dhanasekaran *et al.*, 2011), which could render the toxin undetectable during routine analysis and perhaps less toxic to humans and animals. For example, during thermal processing of maize or maize-based foods, it is known that fumonisins can bind to various components within the food matrix or react with other ingredients within the food such as reducing sugars (Seefelder *et al.*, 2001; Kabak, 2009). Lu *et al.* (2002) showed that the incubation of FB<sub>1</sub> with D-glucose resulted in the formation of N-carboxymethyl-FB<sub>1</sub>, a reaction product of FB<sub>1</sub> and reducing sugars. The four primary products of the FB<sub>1</sub>-reducing sugars reaction have been characterized as N-methyl-FB<sub>1</sub>, N-carboxymethyl-FB<sub>1</sub>, N-(3-hydroxyacetyl)-FB<sub>1</sub> and N-(2-hydroxy, 2-carboxyethyl)-FB<sub>1</sub> using nuclear magnetic resonance and electrospray mass spectroscopy (Lu *et al.*, 2002).

In another study, Seefelder and co-authors (2001) reported the formation of hydrolyzed fumonisin B<sub>1</sub> when samples containing FB<sub>1</sub> and sucrose were thermally processed. The authors also observed that N-(carboxymethyl)fumonisin B<sub>1</sub>, which was formed via thermal processing of samples

containing FB<sub>1</sub> and d-glucose is less toxic compared to FB<sub>1</sub>, the parent toxin. This heat-accentuated binding of FBs to matrix components could be the reason for the herein observed thermolabile nature of FBs.

The presence of residual moisture in sample matrices is known to enhance the thermal degradation of mycotoxins via formation of a carboxylic acid terminal on the molecule (Kabak *et al.*, 2006). This terminal is formed by addition of a water molecule to the lactone ring of the molecules, which subsequently undergoes heat-induced decarboxylation (Kabak *et al.*, 2006). Boudra *et al.* (1995) showed that when OTA was present in wheat matrix and dry-heated at 100 °C for 40 to 160 min there was no observable degradation, however, wet-heating at the same temperature (100 °C) for only 120 min resulted in over 50% degradation of OTA. It has been advanced that availability of moisture during heating of AFs hydrolyses its lactone ring, which makes them highly-chemically unstable, as such, subsequent mild heating (>100 °C) allows for clipping of the lactone ring of the molecule (Samarajeewa *et al.*, 1990; Raters & Matissek, 2008).

### 3.3.3 Numerical modelling of the degradation of mycotoxins

#### 3.3.3.1 Model fitting to experimental data

In order to describe the empirical relationship between the studied objective variables, *i.e.*, mycotoxin degradation (%) and control variables of temperature (°C) and exposure time (min), the quadratic regression function (Equation 3.1) was fitted to the experimental data. The resultant second-order model coefficients for the objective variables are presented in Tables 3.5 and 3.6 (Columns 2-6). These models provide a strong approximation to the true relationship between our objective variables and the control variables.

**Table 3.5:** Regression model fit coefficients and validation indices for thermal degradation for pure mycotoxins standards

Myco	$z(x,y) = C_{00} + C_{10}x + C_{20}x^2 + C_{01}y + C_{02}y^2 + C_{11}xy$												
	$c_{00}$	$c_{10}$	$c_{20}$	$c_{01}$	$c_{02}$	$c_{11}$	$R^2$	$R^2 Adj$	Residual	$\rho$	AAD	$B_f$	$A_f$
AFB <sub>1</sub>	13.68	-0.22	0.00	-1.84	0.02	0.00	0.98	0.97	37.59	0.99	0.16	1.06	1.15
AFB <sub>2</sub>	297.85	-3.41	0.01	-3.01	0.02	0.01	0.87	0.82	139.67	0.93	0.33	1.06	1.31
AFG <sub>1</sub>	-92.07	0.79	0.00	-0.03	0.01	0.00	0.96	0.95	65.97	0.98	0.27	0.71	1.67
AFG <sub>2</sub>	177.89	-2.51	0.01	-1.19	0.00	0.01	0.98	0.98	27.99	0.99	0.25	1.02	1.24

Myco	$z(x, y) = C_{00} + C_{10}x + C_{20}x^2 + C_{01}y + C_{02}y^2 + C_{11}xy$												
	$c_{00}$	$c_{10}$	$c_{20}$	$c_{01}$	$c_{02}$	$c_{11}$	$R^2$	$R^2$ Adj	Residual	$\rho$	AAD	$B_f$	$A_f$
AME	163.93	-2.25	0.01	-1.63	0.00	0.01	0.99	0.99	14.46	0.99	0.51	1.05	1.30
FB <sub>1</sub>	-76.53	1.25	0.00	-2.64	0.04	0.00	0.95	0.84	245.39	0.94	0.47	1.17	1.26
FB <sub>2</sub>	-124.16	1.85	0.00	-2.53	0.04	0.00	0.98	0.97	37.25	0.99	0.60	1.05	1.08
FB <sub>3</sub>	-116.69	1.83	0.00	-2.48	0.03	0.00	0.91	0.88	170.19	0.95	0.54	1.18	1.24
OTA	97.40	-1.33	0.01	-0.81	0.00	0.00	0.96	0.95	18.86	0.98	0.38	1.10	1.32
OTB	199.85	-2.28	0.01	-1.84	0.00	0.01	0.92	0.89	28.28	0.96	0.51	0.97	1.58
STEG	-3.12	0.01	0.00	-1.14	0.03	0.00	0.98	0.97	28.41	0.99	0.09	0.96	1.10
T-2	20.96	-0.41	0.00	-1.5	0.01	0.01	0.95	0.94	80.65	0.98	0.58	1.16	1.23
ZEA	85.18	-1.36	0.01	-0.39	0.01	0.00	0.98	0.98	23.06	0.99	0.09	1.01	1.08
$\alpha$ -ZEL	118.92	-1.83	0.01	-0.83	0.02	0.00	0.98	0.97	30.04	0.99	0.11	1.00	1.12
$\beta$ -ZEL	146.69	-2.06	0.01	-1.00	0.01	0.00	0.97	0.96	43.93	0.98	0.13	1.01	1.13

**Key:** Myco: mycotoxin. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.  $c_{00}$  is a constant.  $c_{10}$  and  $c_{01}$  are the linear coefficients of  $x$  (temperature) and  $y$  (time), respectively.  $c_{20}$  and  $c_{02}$  are the quadratic coefficients of  $x$  and  $y$ , respectively.  $c_{11}$  is the interaction coefficient.

**Table 3.6:** Regression model fit coefficients and validation indices for thermal degradation for mycotoxin standards spiked into maize flour

Myco	$z(x, y) = C_{00} + C_{10}x + C_{20}x^2 + C_{01}y + C_{02}y^2 + C_{11}xy$												
	$c_{00}$	$c_{10}$	$c_{20}$	$c_{01}$	$c_{02}$	$c_{11}$	$R^2$	$R^2$ Adj	Residual	$\rho$	AAD	$B_f$	$A_f$
AFB <sub>1</sub>	-54.76	0.08	0.00	0.53	-0.01	0.00	0.96	0.95	69.52	0.98	0.36	1.10	1.32
AFB <sub>2</sub>	21.82	-0.63	0.00	0.34	0.00	0.00	0.92	0.89	98.83	0.96	0.49	1.09	1.33
AFG <sub>1</sub>	-56.35	0.02	0.00	0.64	-0.01	0.00	0.94	0.92	119.28	0.97	0.83	1.28	1.37
AFG <sub>2</sub>	154.33	-2.43	0.01	-0.72	0.00	0.01	0.99	0.98	25.17	0.99	2.52	1.19	1.48
AME	247.13	-2.70	0.01	-1.83	0.01	0.01	0.89	0.86	27.38	0.95	0.13	0.99	1.12
FB <sub>1</sub>	-227.76	3.09	-0.01	1.59	-0.02	0.00	0.93	0.9	54.12	0.96	0.07	1.00	1.07
FB <sub>2</sub>	-248.21	3.18	-0.01	2.08	-0.02	0.00	0.95	0.94	38.52	0.98	0.06	1.00	1.06
FB <sub>3</sub>	-189.89	2.68	-0.01	1.57	-0.02	0.00	0.94	0.92	34.64	0.97	0.06	1.00	1.06
OTA	264.86	-3.26	0.01	-1.53	0.01	0.01	0.95	0.93	42.44	0.98	0.11	1.00	1.12
OTB	177.39	-2.36	0.01	-0.69	-0.01	0.01	0.92	0.89	76.27	0.96	0.35	1.04	1.32
STEG	261.22	-3.51	0.01	-2.28	0.01	0.01	0.99	0.99	11.36	1.00	0.13	1.01	1.13
T-2	179.08	-2.45	0.01	-1.27	0.00	0.01	0.96	0.95	48.15	0.98	0.19	1.00	1.20
ZEA	189.42	-2.49	0.01	-1.29	0.01	0.01	0.99	0.98	14.12	0.99	0.11	1.01	1.10

Myco	$z(x,y) = C_{00} + C_{10}x + C_{20}x^2 + C_{01}y + C_{02}y^2 + C_{11}xy$												
	$c_{00}$	$c_{10}$	$c_{20}$	$c_{01}$	$c_{02}$	$c_{11}$	$R^2$	$R^2_{Adj}$	Residual	$\rho$	AAD	$B_f$	$A_f$
$\alpha$ -ZEL	189.15	-2.76	0.01	-1.22	0.01	0.01	0.99	0.98	18.02	0.99	0.47	1.05	1.28
$\beta$ -ZEL	210.15	-3.01	0.01	-1.18	0.01	0.01	0.98	0.98	23.59	0.99	0.23	1.05	1.22

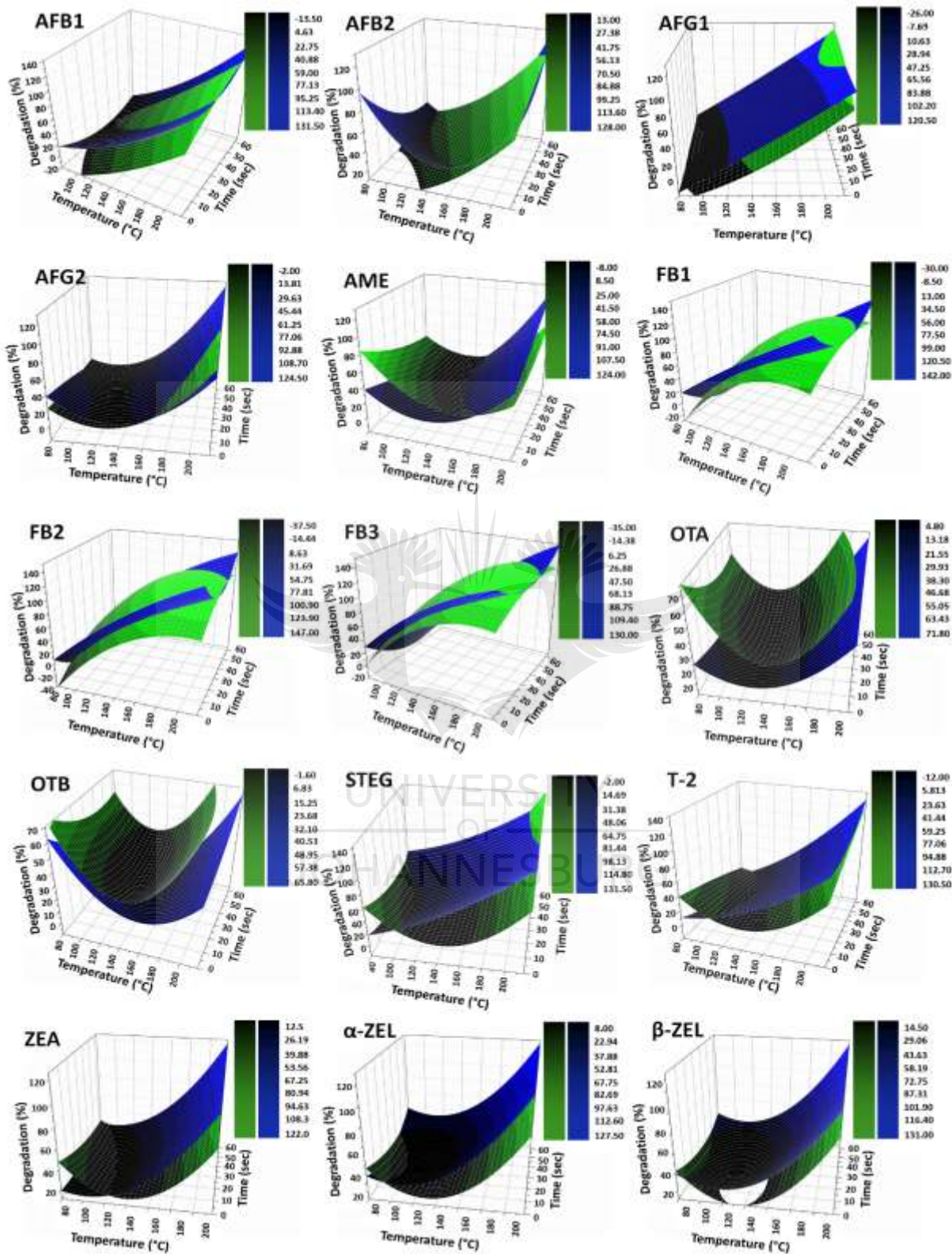
**Key:** Myco: mycotoxin. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.  $c_{00}$  is a constant,  $c_{10}$  and  $c_{01}$  are the linear coefficients of  $x$  (temperature) and  $y$  (time), respectively,  $c_{20}$  and  $c_{02}$  are the quadratic coefficients of  $x$  and  $y$ , respectively, and  $c_{11}$  is the interaction coefficient.

By means of these models, the compound 3-D surface plots (Figure 3.1) were generated using OriginPro 8.5 software (OriginLab, Massachusetts, US). These plots present a visual interpretation of the degradation patterns of each mycotoxin, as well allows the comparison of the degradation profile of pure mycotoxins and mycotoxins spiked into maize. Many of the degradation patterns in our data described by these plots are consistent with a first order reaction kinetics. On the plots, the blue surfaces represent the degradation profile of pure mycotoxin standards, while the green surfaces represent degradation profile of corresponding mycotoxin spiked into maize matrix. The color bands correspond to the value-ranges of the objective variable. Accordingly, lighter regions represent higher degradation, whereas, more intense (darker) regions corresponds to lower degradation.

### 3.3.3.2 Factor effects

In contrast to conventional optimization methods, RSM is able to make available details on the magnitude and significance of individual and pairwise factor effects on the objective variable(s) (Uma *et al.*, 2010; Gbashi *et al.*, 2016). Accordingly, our model fit gave the various factor effects for pure mycotoxin standards and mycotoxins spiked into maize matrix as shown in Figures 3.2a & b and Appendix 3.D. The Pareto charts of standardized factor effects (Figures 3.2a & b) graphically indicates the magnitude and importance of each effect. The red reference line indicated on the chart distinguishes between insignificant and significant effects at  $\alpha = 0.05$ . Any effect that is below this line is insignificant (Gbashi *et al.*, 2016).





**Figure 3.1:** Compound response surface plots for thermal degradation for pure mycotoxins and mycotoxins spiked into maize matrix. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin

G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

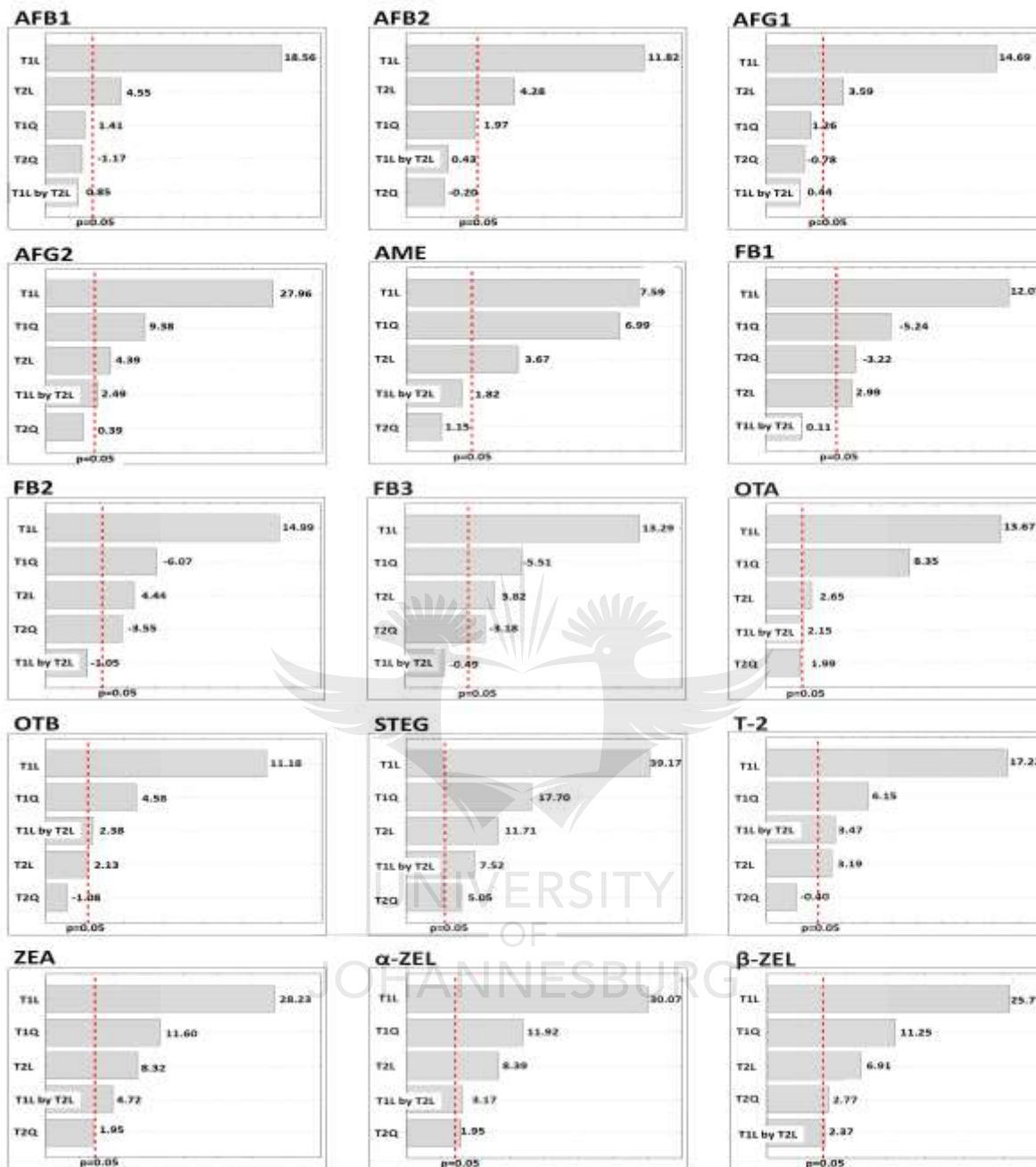
It can be seen that the linear effect of temperature (T1L) was significantly higher ( $p < 0.05$ ) across all response variables for pure mycotoxin standards and mycotoxins spiked into maize matrix, and ranged from 75.89 to 25.08, and 80.24 to 18.28 for pure mycotoxin standards and mycotoxins spiked into maize matrix (Appendix 3.D). This suggests that higher temperatures and shorter exposure times are more effective for mycotoxin degradation, compared to lower temperatures and longer exposure times. The other factor effects for pure mycotoxin standards and mycotoxins spiked into maize matrix, respectively, included quadratic effect of temperature (T1Q) that ranged from 35.76 to -10.49, and 39.46 to -25.5; Linear effect of time (T2L): ranged from 12.63 to -2.56, and 21.27 to 3.01; Quadratic effect of time (T2Q): ranged from 32.29 to -1.81, and 11.26 to -15.66; and interactive effect of temperature and time (T1L by T2L): ranged from 19.61 to -4.29, and 17.92 to -4.61.

### 3.3.3.3 Optimization of the thermal degradation of multi-mycotoxins

Using the response optimization function of the Minitab 17 statistical software (Pennsylvania, US), it was possible to derive the optimum conditions for the thermal degradation of individual mycotoxins, *i.e.*, the most efficient combination of temperature-time for the maximum degradation of individual mycotoxins (Appendix 3.E). An approximation of these solutions can also be visually extrapolated from the surface plots (Figure 3.1). For all mycotoxins, the optimum conditions varied from 178 °C/63.28 min to 217 °C/63.28 min for pure standard and 207 °C/24.43 min to 217 °C/63.28 for spiked maize matrix. Within the experimental range and model resources, it was not possible to achieve 100% degradation of pure-standard OTs due to their high thermal stability. A similar situation was observed for AME spiked into the maize matrix.



**Figure 3.2a:** Pareto charts of standardized factor effects for model fit of pure mycotoxin standards. T1L – Linear effect of temperature; T1Q – Quadratic effect of temperature; T2L – Linear effect of time; T2Q – Quadratic effect of time; and T1L by T2L – Interaction effect temperature and time. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.



**Figure 3.2b:** Pareto charts of standardized factor effects for model fit of mycotoxins spiked into maize matrix. T1L – Linear effect of temperature; T1Q – Quadratic effect of temperature; T2L – Linear effect of time; T2Q – Quadratic effect of time; and T1L by T2L – Interaction effect temperature and time. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.



As such, in order to at least have an idea of the region in which conditions for 100% degradation of these mycotoxins would fall, we interrogated the corresponding models beyond the available model resources, which gave values of 239 °C/63.28 for pure-standard OTs, and 230 °C/40.50 min for AME spiked into maize matrix. Although these values are not very far from the experimental range, it should be noted that because these values fall outside of the experimental range, their predictability may not be reliable, except confirmed by laboratory analysis. Essentially, the further away the solution is from the experimental range, the greater the variance and the less the precision (STAT503, 2018).

Beside optimization for individual objective variables, it is important to derive the global (synchronous) optimal solution for all the objective variables. This is critical because mycotoxins co-occur in nature in food commodities and exert synergistic effects (Serrano *et al.*, 2012; Smith *et al.*, 2016; Adekoya *et al.*, 2018). As such, a single compromise optimum that accounts for the maximum eradication of all mycotoxins present is a more meaningful solution for food safety and health applications. In this regard, using the global optimization function of the Minitab 17 statistical software, the compromise multi-objective optimum solution for our objective variables was 217 °C/63.28 min and 211 °C/54.71 min for pure mycotoxin standards and spiked maize matrix, respectively. The desirability factor (DF) in all cases was 1.00.

#### 3.3.3.4 Validation of model

To determine the adequacy of the models and ensure that they offer a good approximation of the true systems, we examined some important validation indices from the model fit which are presented in Tables 5 and 6 (columns 8-14). Significance was determined at a 95% probability level *i.e.*,  $\alpha=0.05$ . Computed values of the coefficients of multiple determination ( $R^2$ ) ranged from 0.87 to 0.99, and 0.89 to 0.99 for pure mycotoxin standards and mycotoxins spiked into maize matrix, respectively. This implies that our models describe between 87 to 99% of the variability in our data, reflective of its acceptability and significance (Adebo *et al.*, 2018b). Also, the adjusted  $R^2$  fell within less than  $\pm 0.05$  of the  $R^2$  values for all the models. The closeness of the  $R^2$  and adjusted  $R^2$  values, and their nearness to unity indicated that our empirical models were well fitted to the actual data (Babu & Srivastava, 2007; Morshedi & Akbarian, 2014; Adebo *et al.*, 2018b). The Pearson's correlation coefficient ( $r$ ) ranged from 0.91 to 0.99, and 0.95 to 1.00 for pure

mycotoxin standards and mycotoxins spiked into maize matrix, respectively, indicating a strong relationship between the predicted values and the experimental values.

The degree of variability in the dataset was estimated using the average absolute deviation (*AAD*), which ranged from 0.09 to 0.60, and 0.06 to 0.83 for pure mycotoxin standards and mycotoxins spiked into maize matrix, respectively. It should be noted that *AAD* values for AFG<sub>2</sub> in spiked maize matrix (2.25) was not included in the above ranges because it was considered as an outlier. Outliers were determined using the Q-Q plots in SPSS by a step of 1.5×IQR (interquartile range) (Marr, 2018). Average absolute deviation values closer to zero are desirable as it indicates agreements between the predicted and experimental values (Adebo *et al.*, 2018b). The bias factor (*B<sub>f</sub>*) and accuracy factor (*A<sub>f</sub>*) were also examined for our model fits. *A<sub>f</sub>* estimates the relative deviation of predicted values from the experimental values (Dominguez & Schaffner, 2007). Our *A<sub>f</sub>* values ranged from 1.08 to 1.68, and 1.06 to 1.48 for pure mycotoxin standards and mycotoxins spiked into maize matrix respectively. An *A<sub>f</sub>* value of 1.12 indicates an averagely 12% variation between observed and predicted values (Oscar, 2009). Similarly, the *B<sub>f</sub>* measures the relative deviation of predicted and experimental values (Dominguez & Schaffner, 2007). Our *B<sub>f</sub>* values ranged from 0.71 to 1.57, and 0.99 to 1.28 for 48 for pure mycotoxin standards and mycotoxins spiked into maize matrix, respectively. The closer the values of *A<sub>f</sub>* and *B<sub>f</sub>* to unity, the stronger the predictability of the associated models (Desobgo *et al.*, 2015; Adebo *et al.*, 2018b).

### 3.4 Conclusion

The present study profiled temperature-time degradation patterns of multiple mycotoxins with and without the effect of a matrix. Mycotoxins such as OTs, AFB<sub>2</sub>, ZEA and its analogues, STEG and the FBs showed a strongly enhanced degradation when spiked into maize matrix. Alternariol monomethyle ether demonstrated a very high thermal stability generally irrespective of matrix interference, while the FBs were the most thermolabile amongst the studied mycotoxins irrespective of the presence of a food matrix. Moreover, we have demonstrated for the first time the thermal stability of the mycotoxins, AME and STEG. In order to optimize the degradation of mycotoxins, the RSM optimization function was fitted to our experimental data, which yielded well-fit models that clearly define the empirical relationship between our control variables (temperature and time) and our objective variable (*i.e.*, mycotoxin degradation). The resultant

global optimum solution for multi-mycotoxin degradation was 217 °C/63.28 min and 211 °C/54.71 min for pure mycotoxin standards and spiked maize matrix, respectively. These values were the most efficient combinations of temperature and time to achieve maximum degradation of the analytes within the experimental range.

However, it was observed that these optimal conditions were not sufficient to completely eliminate OTs and AME for pure mycotoxins and in spiked maize, respectively, due to their high thermal stability, and because the optimal conditions are computed within the boundaries of the experimental range. As such, in order to obtain detectable levels (100% degradation) of the two mycotoxins in question, the optimization models were interrogated beyond the experimental ranges, which gave values of 239 °C/63.28 min for pure standard OTs, and 230 °C/40.50 min for AME in spiked maize. Besides optimization, our models can be useful in estimating any desired degradation outcome within the experimental domain. This could find applicability in food processing for goal-specific thermal processing of purportedly mycotoxin contaminated foods for food safety and optimum quality.

Further research however, is required to determine the effect of thermal treatment at the obtained optimal conditions on vital food quality factors. Also, other but more efficient thermal processing techniques such as micronisation (high intensity infrared heating) could be investigated as alternatives to conventional oven heating methods. It would also be interesting to investigate the effects of some specific matrix parameters such as pH and moisture, on the thermal degradation patterns of the mycotoxins. Furthermore, there is need to establish the identities of degradation products via high resolution mass spectrometry (HRMS). We do hope that our observations reported herein would positively contribute to the debate on thermal stability of some mycotoxins such as OTs and AFs.

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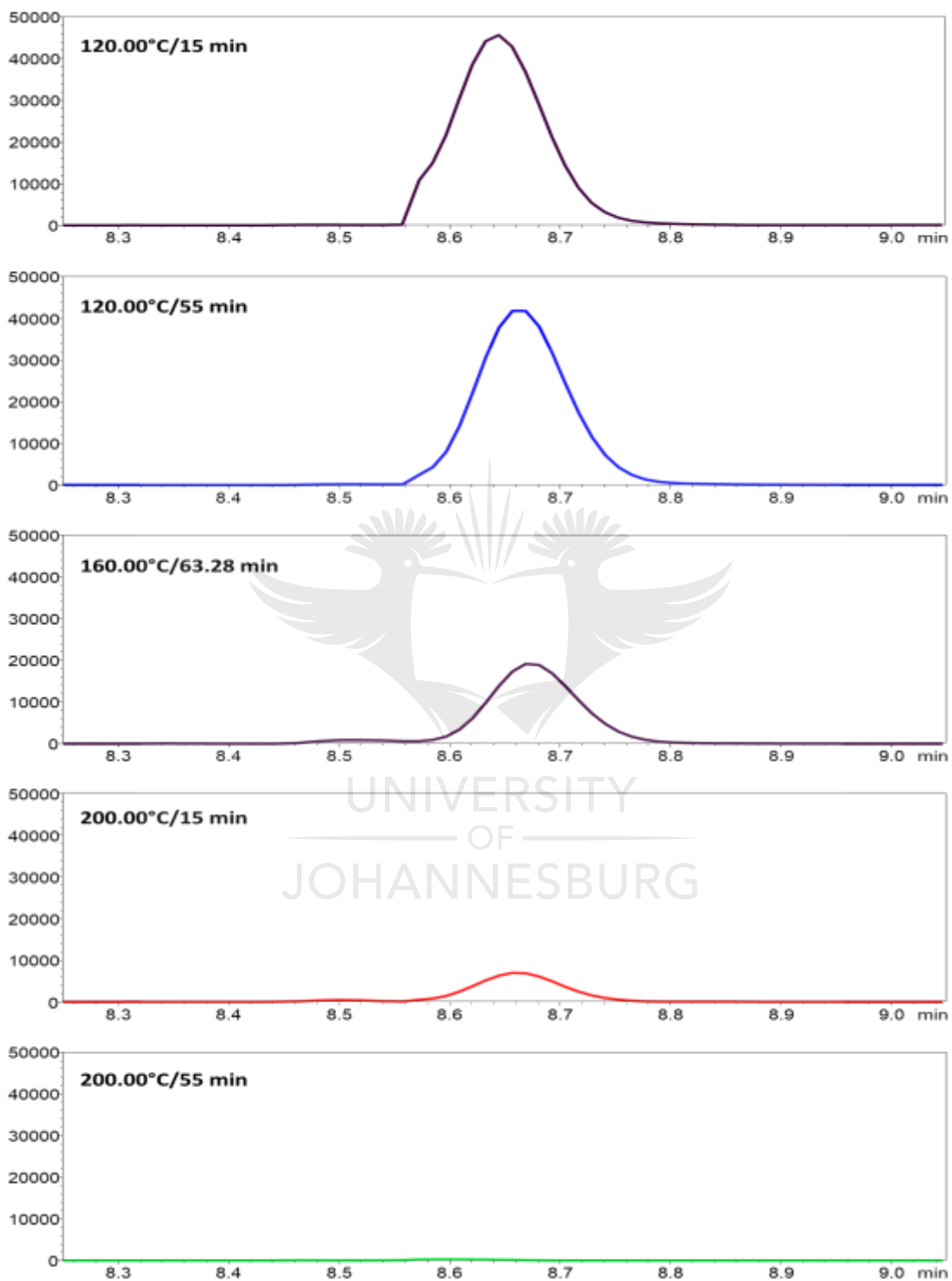
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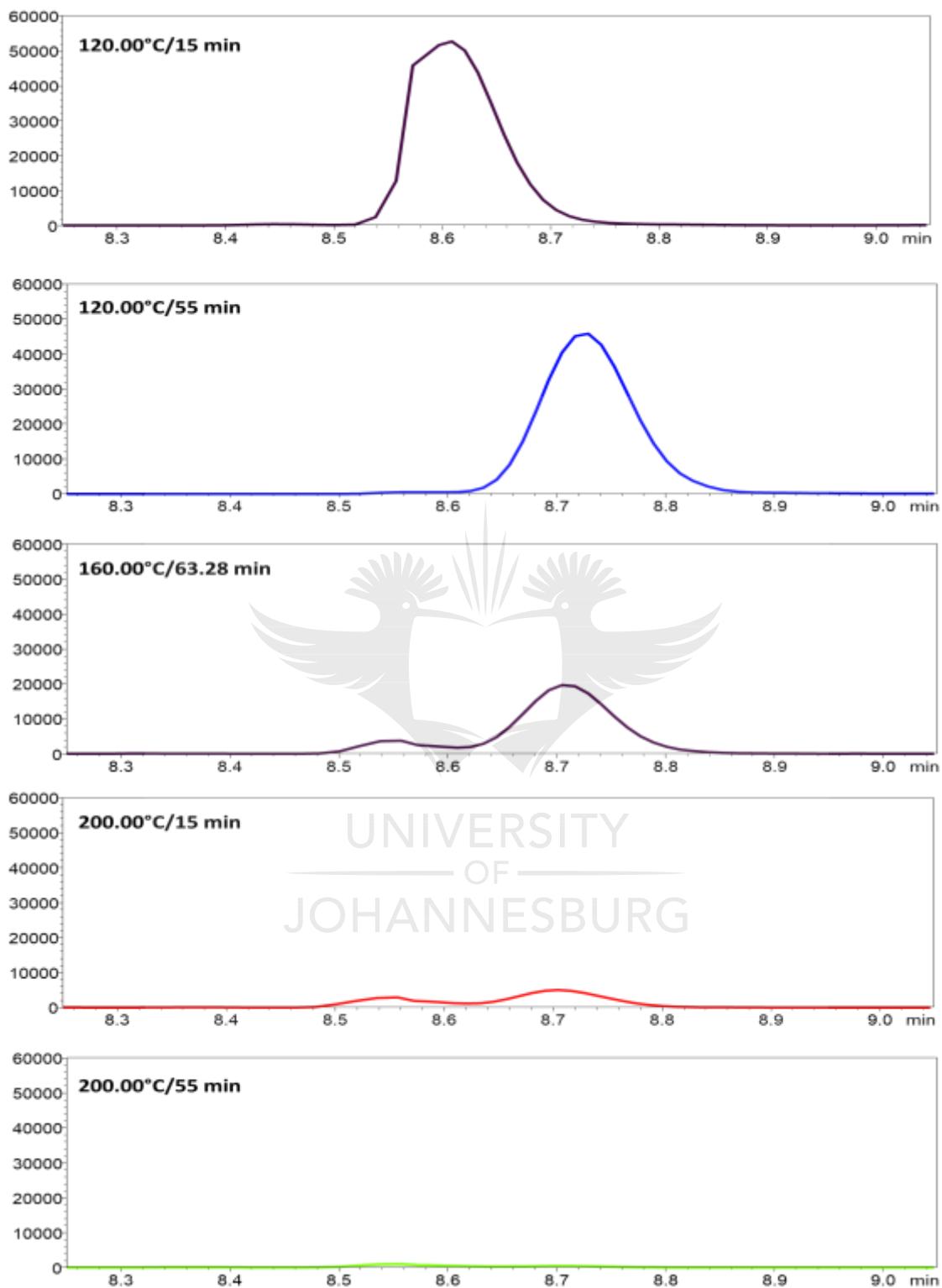
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## APPENDIX 3



**Appendix 3.A:** Single ion chromatogram of pure AFB<sub>1</sub> standard at different temperature-time conditions.



**Appendix 3.B:** Single ion chromatogram of AFB<sub>1</sub> spiked into maize matrix at different temperature-time conditions.

**Appendix 3.C:** Independent-samples t-test for average thermal degradation of pure mycotoxin and mycotoxins spiked into maize matrix.

Mycotoxin	Mycotoxin Standards	Mycotoxin spiked into maize matrix	F-value	p-value	Significance
AFB <sub>1</sub>	53±3.06	47±1.37	0.10	0.75	not sig.
AFB <sub>2</sub>	44±10.37	51±9.14	0.33	0.57	not sig.
AFG <sub>1</sub>	55±2.2	47±3.11	0.16	0.69	not sig.
AFG <sub>2</sub>	40±1.95	37±2.92	0.03	0.87	not sig.
AME	36±2.69	33±3.17	7.85	0.01	Sig.
FB <sub>1</sub>	63±4.53	78±2.46	7.65	0.01	Sig.
FB <sub>2</sub>	65±0.84	77±1.81	4.82	0.04	Sig.
FB <sub>3</sub>	65±3.38	81±2.07	7.12	0.02	Sig.
OTA	24±3.36	46±2.81	1.04	0.32	not sig.
OTB	20±3.82	39±5.76	2.93	0.11	not sig.
STEG	61±1.71	37±1.71	0.05	0.82	not sig.
T-2	50±4.51	37±6.52	0.58	0.46	not sig.
ZEA	51±1.54	42±2.81	0.36	0.56	not sig.
α-ZEL	50±2.26	37±1.94	0.06	0.81	not sig.
β-ZEL	52±1.37	39±1.47	0.03	0.87	not sig.

**Key:** AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol. Not sig.: not significant.

## Appendix 3.D: CCD regression model fit factor effects for thermal degradation of mycotoxins

Mycotoxins	Factor effects for pure mycotoxin standards					Factor effects for mycotoxins spiked into maize matrix				
	Temp. (L)	Temp. (Q)	Time (L)	Time (Q)	1L by 2L	Temp. (L)	Temp. (Q)	Time (L)	Time (Q)	1L by 2L
AFB <sub>1</sub>	74.99*	10.34*	6.20	16.21*	5.73	77.39*	7.80	18.96*	-6.43	5.01
AFB <sub>2</sub>	47.80*	35.76*	4.42	13.27	19.61*	58.77*	12.94	21.27*	-1.32	3.05
AFG <sub>1</sub>	75.89*	1.54	12.63*	3.73	0.14	80.24*	9.13	19.63*	-5.60	3.39
AFG <sub>2</sub>	66.72*	29.94*	8.82*	-1.81	15.76*	70.14*	31.12*	11.02*	1.31	8.83*
AME	64.52*	26.32*	11.49*	-0.37	19.51*	18.28*	26.29*	3.01	6.29	13.57*
FB <sub>1</sub>	74.85*	-3.49	0.79	28.32*	1.82	44.38*	-25.50*	11.03*	-15.66*	0.59
FB <sub>2</sub>	73.79*	-8.77*	3.42	32.29*	-2.08	46.52*	-24.94*	13.77*	-14.57*	-4.61
FB <sub>3</sub>	72.78*	-10.49	1.52	21.93*	5.99	39.13*	-21.45*	11.23*	-12.39*	-2.06
OTA	36.90*	16.34*	5.19*	2.53	7.23*	44.54*	35.98*	8.64*	8.62	9.90*
OTB	25.08*	22.68*	-2.56	3.18	15.01*	48.84*	26.48*	9.29	-6.24	14.68*
STEG	65.56*	9.08*	10.53*	20.88*	-4.29	66.00*	39.46*	19.73*	11.26*	17.92*
T-2	72.91*	11.04	11.93*	9.32	9.87	59.74*	28.22*	11.09*	-1.84	17.05*
ZEA	64.97*	21.32*	11.11*	5.27	2.03	53.05*	28.84*	15.64*	4.85	12.55*
$\alpha$ -ZEL	68.68*	27.13*	10.73*	13.87*	-1.14	63.82*	33.46*	17.83*	8.13*	9.50*
$\beta$ -ZEL	64.84*	28.15*	11.64*	11.62*	2.75	62.60*	36.16*	16.78*	8.90*	8.16*

**Key:** \*Statistically significant ( $p \leq 0.05$ ) factors. Temp. (L) – linear effect of temperature, Temp. (Q) – quadratic effect of temperature, Time (L) – linear effect of time, Time (Q) – quadratic effect of time, 1L by 2L – interaction effect temperature and time. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

**Appendix 3.E:** Individually optimized experimental conditions for pure mycotoxins and mycotoxins spiked into maize matrix

Mycotoxin	Mycotoxin standards			Spiked maize		
	Temp (°C)	Time (sec)	Degradation (%)	Temp (°C)	Time (sec)	Degradation (%)
AFB <sub>1</sub>	193	63.28	100	200	63.28	100
AFB <sub>2</sub>	203	63.28	100	202	63.28	100
AFG <sub>1</sub>	196	63.28	100	200	63.28	100
AFG <sub>2</sub>	205	63.28	100	206	63.28	100
AME	204	63.28	100	217	63.28	80
	-	-	-	230*	63.28*	100
FB <sub>1</sub>	206	20.10	100	209	59.78	100
FB <sub>2</sub>	208	48.50	100	181	58.94	100
FB <sub>3</sub>	178	63.28	100	207	24.43	100
OTA	217	63.28	72	207	63.28	100
	239*	63.28*	100	-	-	-
OTB	217	63.28	66	213	63.28	100
	239*	63.28*	100	-	-	-
STEG	206	51.14	100	197	63.28	100
T-2	195	63.28	100	207	63.28	100
ZEA	202	63.28	100	204	63.28	100
$\alpha$ -ZEL	200	63.28	100	203	63.28	100
$\beta$ -ZEL	199	63.28	100	203	63.28	100

**Key:** Temp: Temperature. \* Out-of-experimental range optimal conditions. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.



## CHAPTER FOUR<sup>#</sup>

### DEVELOPMENT, CHEMOMETRIC-ASSISTED OPTIMIZATION AND IN-HOUSE VALIDATION OF A MODIFIED PRESSURIZED HOT WATER EXTRACTION METHODOLOGY FOR MULTI-MYCOTOXINS IN MAIZE

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#### Abstract

Effective management of mycotoxins rely on stringent regulation and routine surveillance of food/feed commodities via efficient analysis, hence the continuous need for improved methods. The present study developed, optimized and validated a modified pressurized hot water extraction (PHWE) method for the simultaneous extraction of multi-mycotoxins from maize and subsequent quantification on ultra-high performance liquid chromatography and tandem mass spectrometry (UHPLC-MS/MS). The PHWE system was modified using ethanol (EtOH) as a cosolvent, while a numerical modelling approach, the central composite design (CCD), was adopted for the optimization of the extraction conditions. The computed global optimal solution for the objective function (*i.e.*, the most efficient combination of temperature and solvent composition for maximum recovery of target mycotoxins simultaneously) was 162 °C and 45% ethanol (EtOH) for temperature and solvent composition, respectively. Using the optimized conditions, it was possible to effectively extract and quantify 15 different mycotoxins, including aflatoxins (AFs), fumonisins (FBs), ochratoxins (OTs), zearalenone and its analogues (ZEAs), T2-toxin (T-2), alternariol monomethyl ether (AME) and sterigmatocystine (STEG), from maize in a single step with satisfactory recoveries (71 to 124%) except for ochratoxin A (OTA) and  $\alpha$ -zearalenol ( $\alpha$ -ZEL) which had recoveries of 58 and 14%, respectively. The modified PHWE method also demonstrated adequate linearities (0.986 to 0.999), intra-day precisions (RSD<sub>r</sub> ranged from 0 to 27%) and inter-day precisions (RSD<sub>R</sub> ranged from 3 to 34%). Further efficacious application of the method to real

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samples re-affirmed the prospects of PHWE as a suitable, cost-effective and greener alternative to traditional methods of mycotoxin extraction.

### Highlights

- A modified PHWE method for mycotoxin extraction was developed and applied for the first time.
- The method validation parameters were consistent with standard guideline requirements for analytical method performance.
- In comparison to conventional methods of mycotoxin extraction, the method performed very well, and in some cases favourably.
- PHWE is promising as an alternative to traditional methods for survey-type work and exposure studies for mycotoxins.

**Keywords:** Mycotoxins, pressurized hot water extraction, chemometric-assisted optimization, central composite design

### 4.1 Introduction

Mycotoxins are poisonous secondary metabolites produced by certain fungal species that contaminate various agricultural commodities. Exposure to mycotoxin-contaminated foods results in various health-related problems, depending on the type of mycotoxin and level of exposure. Relative to their prevalence and potency, they have been identified as the most significant nutritional hazard, superior to other natural inherent plant toxins, pesticide residues, food additives and other synthetic contaminants in foods (Kuiper-Goodman, 1998; Bennett and Klich, 2003). Besides the health-related problems, mycotoxins also exert significant socio-economic effects on societies globally, particularly in the developing nations (Gbashi *et al.*, 2017a; Makun *et al.*, 2012). Annual losses in agricultural commodities due to mycotoxin contamination have been estimated at one billion metric tons (Schmale and Munkvold, 2009; Wilson *et al.*, 2017). All these coupled with the globalization of the food supply chain, has led to more stringent regulatory limits and routine surveillance of the levels of these environmental pollutants in food and feed (Gbashi *et al.*, 2017a; Rahmani *et al.*, 2009). As such, analysis plays a critical tool in the control and management of mycotoxins (Gbashi *et al.*, 2017a).

Development of improved methods for mycotoxin analysis, particularly extraction methods, has been an active research field (Anfossi *et al.*, 2010; Arroyo-Manzanares *et al.*, 2014; Karsten *et al.*, 2008). Fundamental interests have been sensitivity, speed, ease, cost-effectiveness, and environmental friendliness. However, most of the conventional methods of mycotoxin extraction such as liquid-liquid solvent extraction, immuno-affinity column extraction, solid-phase extraction falls short of these qualities in one way or the other (Gbashi *et al.*, 2017a). Pressurized hot water extraction (PHWE) seems very promising in this regard, as it is more environmentally friendly, efficient, cheap, fast, and relatively easy (Teo *et al.*, 2010). Extraction with this method can be easily maneuvered to achieve extractability of a wide array of analytes with some degree of selectivity and efficiency by adjusting the extraction temperature and/or introduction of a co-solvent (Teo *et al.*, 2010; Plaza & Turner, 2015). Moreover, preliminary studies have yielded good results for PHWE of aflatoxin B<sub>1</sub> (AFB<sub>1</sub>) from maize (Gbashi *et al.*, 2017b).

Because the performance of PHWE is determined by a number of factors, in particular temperature and solvent composition, optimization is essential in order to achieve maximum efficiency. This is important when developing a method for the simultaneous extraction of multiple analytes with varying physicochemical properties such as mycotoxins. For this purpose, the utilization of chemometric tools, such as the response surface methodology (RSM) is suitable (Díez *et al.*, 2011; Gbashi *et al.*, 2016; Li *et al.*, 2017). Further driven by the need to save time, cost and physical efforts, the central composite design (CCD) (Bajer *et al.*, 2015) approach of RSM is an important mathematical tool for optimizing complex multivariate and multi-analyte problems (Asghar *et al.*, 2014), and has been widely used in the optimization of various extraction techniques for different analytes (Ali *et al.*, 2016; Gbashi *et al.*, 2016; Khazaeli *et al.*, 2016).

The CCD offers the advantage of a reduced number of experimental runs for response optimization, and is useful in simultaneously studying the effects of different control variables on an objective variable (Gbashi *et al.*, 2016; Zulkipli, 2012). Rakić *et al.* (2014) compared four different RSM models for the development of a chromatographic method for determining fluconazole and its impurities, and found CCD superior in terms of generation of better models and a reduced number of experimental runs (Rakić *et al.*, 2014). The present study describes the development and optimization of a PHWE method for multi-mycotoxin extraction from maize

using the CCD, and subsequent validation of the optimized method against standard analytical guidelines.

## 4.2 Materials and methods

### 4.2.1 Materials

Mycotoxin reference standards used in this study included aflatoxin B<sub>1</sub> (AFB<sub>1</sub>), aflatoxin B<sub>2</sub> (AFB<sub>2</sub>), aflatoxin G<sub>1</sub> (AFG<sub>1</sub>), aflatoxin G<sub>2</sub> (AFG<sub>2</sub>), fumonisin B<sub>1</sub> (FB<sub>1</sub>), fumonisin B<sub>2</sub> (FB<sub>2</sub>), fumonisin B<sub>3</sub> (FB<sub>3</sub>), ochratoxin A (OTA), ochratoxin B (OTB), T-2 toxin (T-2), zearalenone (ZEA),  $\alpha$ -zearalenol ( $\alpha$ -ZEL),  $\beta$ -zearalenol ( $\beta$ -ZEL), alternariol monomethyl ether (AME), and sterigmatocystin (STEG) were purchased from the National Metrological Institute of South Africa (NMISA). Mycotoxin standards used for the solvent extraction included all of the above listed mycotoxins purchased from Biopure (RomerLabs, Tulln, Austria), except for AME and FB<sub>3</sub> purchased from Sigma-Aldrich (Bornem, Belgium) and Promec unit (Tygerberg, South Africa), respectively. Deepoxy-deoxynivalenol (DOM) and zearalanone (ZAN) were used as internal standards and were purchased from Sigma-Aldrich (Bornem, Belgium) and Biopure (RomerLabs, Tulln, Austria), respectively.

Biotage® Isolute SAX cartridges were purchased from Anatech Instruments (Pty) Ltd (South Africa). C18-SPE cartridge and MultiSep®226 AflaZon+ multifunctional columns were purchased from Alltech (Lokeren, Belgium) and Romer Labs (Gernsheim, Germany), respectively. PVDF syringe filters (0.22  $\mu$ m, with Luer lock) and 10 mL NORM-JECT plastic syringe (with Luer lock) were purchased from Restek (Restek Corporation, Pennsylvania USA). Whatman® glass microfiber filters (47 mm diameter, grade GF/A) was purchased from VWR International (VWR International, Leuven, Belgium), while Ultrafree®-MC PVDF centrifugal filters (0.22  $\mu$ m) were purchased from Millipore (Bredford, MA, USA). Diatomaceous earth, potassium chloride, sodium sulphate, sodium bicarbonate, anhydrous sodium sulphate and dialysis tubing were purchased from Sigma (South Africa).

Solvents used for PHWE, extraction by Method 1 and extraction by Method 2 (as described in Section 4.2.4) included mass spectrometry (MS)-grade acetonitrile, MS-grade methanol and MS-grade formic acid, dichloromethane (DCM), ethanol (EtOH), iso-octane and sulphuric acid which

were also purchased from Sigma (South Africa). Ultrapure water was obtained from a Milli-Q Gradient A10 dispensing system (Millipore, Billerica, MA, USA). Solvents used for extraction by Method 3 (as described in Section 4.2.4) included HPLC grade acetonitrile (Biosolve BV, Valkenswaard, The Netherlands), LC-MS grade methanol, acetonitrile, glacial acetic acid all from (Biosolve BV, Valkenswaard, The Netherlands) and ammonium acetate from Merck (Merck KGaA, Darmstadt, Germany). N-hexane was purchased from BDH Hipersolv Chromanorm (VWR International, Leuven, Belgium) and nitrogen gas (Air Liquide, Aalter, Belgium). The water used for this method (i.e. Method 3) was obtained from a Milli-Q®SP Reagent water system (Millipore Corp., Brussels, Belgium). Maize flour was purchased from a local vendor in Johannesburg, South Africa. All other consumables were of analytical grade and purchased from accredited suppliers within South Africa.

## 4.2.2 Methods

### 4.2.2.1 Sampling

A total of 25 maize meal samples from different households in Ngwalemong village in Limpopo Province of South Africa destined for human consumption were collected. Incremental sampling was performed from different locations within the sampling lot to achieve a combined mass of 1 kg which was thoroughly mixed and placed in sterile, airtight ziplock plastic bags. The samples were kept chilled in a cooler box and transported to the Food, Environment and Health Research Group (FEHRG) Laboratory, University of Johannesburg, Doornfontein Campus where they were stored at  $-4^{\circ}$  until analysis.

### 4.2.2.2 Experimental design

Using Statistica (version 7, StatSoft, USA), a set of experiments were designed based on the CCD RSM in order to optimize two important PHWE parameters temperature ( $^{\circ}\text{C}$ ) and solvent composition (% EtOH) for maximum recovery of multi-mycotoxins. By adopting the CCD approach for two factors and 1 block, 10 experimental levels were obtained (Table 4.1): 2 levels of fractional factorial design for each of the factors, a replicated center point to improve the precision of the optimization model, and a set of axial points (*i.e.*,  $\alpha$  and  $-\alpha$ ) that allows for rotatability of the model and estimation of response curvature. Curvature estimation of the model is particularly important because one of the factors (temperature) exhibits a strong quadratic effect

on analyte recovery during PHWE (Gbashi *et al.*, 2016). Rotatability of the model is desirable because it allows for equal variance of prediction for all points equal-distance from the center point irrespective of the direction. The experimental domain was selected based on preliminary laboratory trials (Gbashi *et al.*, 2017b).

**Table 4.1:** Two-factor, 1 block standard order CCD experimental design for temperature and solvent composition optimization during PHWE of multi-mycotoxins.

S/No	Temperature (°C)	Solvent composition (% EtOH)	RSM Codes	Comment
1	50.00	0.000	-1, -1	Factorial level
2	50.00	40.00	-1, +1	Factorial level
3	150.0	0.000	+1, -1	Factorial level
4	150.0	40.00	+1, +1	Factorial level
5	29.29	20.00	- $\alpha$ , 0	Axial point
6	170.7	20.00	+ $\alpha$ , 0	Axial point
7	100.0	-8.280	0, - $\alpha$	Axial point
8	100.0	48.28	0, + $\alpha$	Axial point
9	100.0	20.00	+1, +1	Center point
10	100.0	20.00	+1, +1	Center point

Key: S/No.: serial number. EtOH: ethanol. RSM: response surface methodology.

After conducting experiments at the above stated experimental levels, a second-order optimization model represented in Equation 4.1 (Adebo *et al.*, 2018), was fitted to the experimental data using the method of least squares (MSL) which generates the lowest possible residuals (Bas & Boyaci, 2007). Adequacy of the model-fit was determined by evaluating various model-fit validation parameters described by Adebo *et al.* (2017). The parameters include coefficient of determination ( $R^2$ ), adjusted coefficient of determination ( $R^2$  adjusted), MS residual ( $MSR$ ), average absolute deviation ( $AAD$ ), bias factor ( $B_f$ ), accuracy factor ( $A_f$ ) and Pearson's correlation coefficient ( $r$ ). Model parameters and significance were determined at a probability level of 95% (*i.e.*,  $p < 0.05$ ).

$$z = \beta_0 + \sum_{i=1}^k \beta_i x_i + \sum_{i=1}^k \beta_{ii} x_i^2 + \sum_{i=1}^k \sum_{j=1}^k \beta_{ij} x_i x_j \quad \text{Equation 4.1}$$

Where  $z$  is the response variable *i.e.*, recovery (%),  $x_i$  and  $x_j$  are the factors *i.e.*, temperature (°C) and solvent composition (% EtOH) respectively,  $\beta_0$  is the model constant,  $\beta_i$ ,  $\beta_{ii}$  and  $\beta_{ij}$  are the coefficients for the linear, quadratic and interaction terms.

#### 4.2.2.3 Pressurized hot water extraction (PHWE)

Pressurized hot water extraction was performed using a make-shift laboratory setup described by Gbashi *et al.* (2016). The system consisted of an HPLC pump (Waters 6000 fluid controller, Waters Corporation, Manchester, UK), a stainless steel extraction cell (70 x 30 mm and approximately 20 mL), a refurbished GC 600 Vega Series 2 oven (Carlo Erba Instruments, Italy) with a digital temperature controllable unit ( $\pm 1$  °C), stainless tubing (1.58 mm in outer dimension (OD) and 0.18 mm inner dimension (ID)), a back-pressure valve (Swagelok, Johannesburg, South Africa), and a collection flask. For the extraction, 4 g of spiked maize flour was thoroughly mixed with 3 g of diatomaceous earth and placed inside the extraction cell. Extraction was performed at the different pre-designed experimental conditions of temperature (°C) and solvent composition (% EtOH) described previously in Table 4.1. The solvent was made to flow through the extraction cell at a steady flow rate of 5 mL/min with pressure maintained at  $1000 \pm 200$  psi using the back-pressure valve. The extract was collected into a 50 mL centrifugal tube up to the 50 mL mark. Each extraction experiment was performed in duplicate. The extracts were filtered using a 0.22  $\mu$ m nylon syringe filter into a 1.5 mL HPLC vial, and subsequently analyzed on the UHPLC-MS/MS.

#### 4.2.2.4 Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS)

Mycotoxins were quantified using a Shimadzu UHPLC-MS/MS 8030 equipment (Shimadzu Corporation, Tokyo, Japan), which consisted of an LC-30AD Nexera chromatograph connected to an autosampler (SIL-30 AC Nexera) and a column oven (CTO-20 AC Prominence) maintained at a constant temperature of 40 °C. Chromatographic separation of multi-mycotoxins was achieved on a Raptor<sup>TM</sup> ARC-18 column (2.7  $\mu$ m, 2.1 mm  $\times$  100 mm) (Restek Corporation, Pennsylvania USA). The sample injection volume was 2  $\mu$ L, and the mobile phases were composed of an aqueous phase *i.e.*, solvent A: 0.1% formic acid (FA) in deionized water, and an organic phase *i.e.*, solvent B: 0.1% FA in methanol/acetonitrile (50/50 v/v).

The gradient elution program began with 10% B for 0.1 min, ramped to 95% B in 8.4 min, maintained at this condition for 3 min, and the initial condition *i.e.*, 10% B re-established for 1 min, after which the column was allowed to re-equilibrate for 4.5 min for the next run. The mobile phase was delivered at a constant flow rate of 0.2 mL/min, and the total run time was 17 min. The LC was connected to a Shimadzu triple-quadrupole MS model 8030 (Shimadzu Corporation,



Kyoto, Japan) detector with an electron spray ionization source where mycotoxins were detected and quantified in positive ionization mode (ESI<sup>+</sup>). The MS method consisted of a multiple reaction monitoring (MRM) method operated at optimized MS conditions for the analytes (Table 4.2). The heat block temperature was 400 °C, desolvation line (DL) temperature was 250 °C, interface nebulizing gas flow rate was 3 L/min and drying gas flow rate was 15 L/min. The Shimadzu LabSolutions software was used for subsequent processing and visualization of the data.

**Table 4.2:** MRM transitions, optimized MS conditions and retention times of multi-mycotoxins

S/No	Mycotoxin	Ret. time (min)	Precursor	Products	Q1 Pre bias (V)	CE (eV)	Q3 Pre bias (V)
1.	AFB <sub>1</sub>	8.25	313.00	241.00*	-22.00	-41.00	-23.00
				285.10	-22.00	-24.00	-29.00
2.	AFB <sub>2</sub>	8.01	315.00	259.10*	-22.00	-31.00	-25.00
				287.00	-23.00	-26.00	-30.00
3.	AFG <sub>1</sub>	7.77	329.00	243.00*	-12.00	-28.00	-23.00
				311.10	-16.00	-24.00	-14.00
4.	AFG <sub>2</sub>	7.51	331.00	245.10*	-12.00	-32.00	-24.00
				313.00	-12.00	-24.00	-20.00
5.	AME	10.13	273.00	128.10*	-10.00	-49.00	-21.00
				115.10	-18.00	-54.00	-19.00
6.	FB <sub>1</sub>	7.97	722.20	352.20*	-34.00	-42.00	-11.00
				334.30	-20.00	-42.00	-11.00
7.	FB <sub>2</sub>	8.95	706.10	336.30*	-20.00	-38.00	-22.00
				318.30	-26.00	-41.00	-22.00
8.	FB <sub>3</sub>	8.75	706.30	336.30*	-40.00	-39.00	-11.00
				354.40	-20.00	-35.00	-24.00
9.	OTA	10.13	403.80	239.00*	-15.00	-27.00	-24.00
				221.00	-12.00	-38.00	-21.00
10.	OTB	9.33	370.10	205.00*	-13.00	-22.00	-21.00
				324.10	-13.00	-14.00	-22.00
11.	STEG	10.45	324.90	310.00*	-22.00	-24.00	-30.00
				281.10	-22.00	-40.00	-27.00
12.	T-2	9.67	467.20	245.10*	-13.00	-11.00	-16.00
				305.20	-22.00	-11.00	-20.00
13.	ZEA	10.06	319.10	185.00*	-12.00	-27.00	-30.00
				187.10	-15.00	-21.00	-19.00
14.	a-ZEA	9.42	323.10	277.20*	-17.00	-17.00	-18.00
				305.20	-24.00	-9.000	-20.00
15.	B-ZEA	8.95	323.10	277.20*	-16.00	-16.00	-18.00
				305.20	-16.00	-11.00	-20.00

Key: S/No.: serial number. Ret. Time: retention time. Q1 Pre bias: quadruple one pre-rod bias. Q3 Pre bias: quadruple three pre-rod bias. CE: collision energy. \* Quantitative product ion. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

### 4.2.3 Validation of the modified PHWE method for multi-mycotoxins extraction

Matrix effects (ME) for the different mycotoxins were determined using the signal enhancement or suppression approaches of Arroyo-Manzanares *et al.* (2018) and Sulyok *et al.* (2006). For this purpose, calibration curves were plotted for standards prepared in extracts obtained from blank samples, as well as, for standards prepared in neat solvents. Matrix effect was calculated using the difference in the slopes of the calibration curves as described in Equation 4.2. The linearity of the PHWE method was determined by evaluating the coefficient of determination ( $R^2$ ) between the instrumental responses and the analyte concentrations at 5 concentration levels within the range of 160 to 5,000  $\mu\text{g/mL}$ . The limits of detection (LOD) and limits of quantification (LOQ) (Equation 4.3) of the analytes were determined using the signal to noise ratio of the matrix-matched standards as described by Kim *et al.* (2017).

$$ME = \frac{Slope_m - Slope_n}{Slope_n} \times 100 \quad \text{Equation 4.2}$$

Where  $ME$  is the matrix effect,  $Slope_m$  is the slope of calibration curve of standards prepared in sample extracts and  $Slope_n$  is the slope of standards prepared in neat solvent.

$$Limit_{DQ} = F \times \left[ \frac{C}{\left(\frac{S}{N}\right)} \right] \quad \text{Equation 4.3}$$

Where  $Limit_{DQ}$  is the  $LOD$  or  $LOQ$  depending on the value of the multiplication factor  $F$ , which is 3.33 for  $LOD$  and 10 for  $LOQ$ .  $C$  is the concentration, while  $S$  is the signal at concentration  $C$ , and  $N$  is the noise level at similar concentration.

For accuracy (recovery) measurement, spiked maize samples (previously confirmed to be free of any of the analytes on UHPLC-MS/MS) were extracted using PHWE and the results presented as the percentage ratio of the recovered concentration to that of the originally spiked concentration (Equation 4.4) (Arroyo-Manzanares *et al.*, 2018). The spiking concentration was determined in accordance with the maximum theoretical extraction for the PHWE setup (described in Section 4.2.2.3) using a 20 mL extraction cell. Accordingly, sample spiking was achieved by adding 4 mL

of multi-mycotoxin mix standard solution (1 µg/mL) to 4 g of blank maize flour, mixing thoroughly and storing for 24 h in the dark at ambient conditions. Intra-day precision or repeatability (RSD<sub>r</sub>) of the method was determined by evaluating the coefficient of variation of recoveries of three PHWE procedures performed under the same working conditions within the period of 24 h at two different spiking levels, 250 and 1,000 µg/kg, levels 1 and levels 2, respectively. Inter-day precision or intermediate precision (RSD<sub>R</sub>), was determined in a similar manner to RSD<sub>r</sub>, however, 3 PHWE operations at the two spiking levels were performed over three consecutive days, and the coefficient of variation of the recoveries computed. Where  $E_r$  is the recovered concentration after spiking and  $E_i$  is the spiked concentration.

$$\text{Recovery (\%)} = \frac{E_r}{E_i} \times 100 \quad \text{Equation 4.4}$$

#### 4.2.4 Comparative assessment of the recovery of PHWE with other conventional methods of mycotoxin extraction

The extraction efficiency of the modified PHWE method was compared with those of some well-defined and validated methods for multi-mycotoxin extraction reported in literature. Method 1 is the method of Patterson and Roberts (1979) as described by Chilaka *et al.* (2012). Briefly, extraction was executed with acetonitrile/4% potassium chloride (KCl) (90/10, v/v), followed by defatting with iso-octane, phase separation by addition of DCM and saturated sodium bicarbonate. After separation, the aqueous phase was acidified with sulphuric acid (H<sub>2</sub>SO<sub>4</sub>), and further extracted with DCM. The organic phase was dialysed against 30% acetone overnight, and re-extracted into DCM. Both fractions were quantified for appropriate mycotoxins using the UHPLC-MS/MS. Extraction time was 48 h.

Method 2 is a solvent extraction method adapted from Sulyok *et al.* (2007). Extraction involved adding acetonitrile/water/acetic acid (79/20/1, v/v/v) to the sample in the ratio of 1/4. The samples were agitated for 90 min, centrifuged for 10 min at 4,000 g. To 350 µL of aliquot 350 µL of extraction solvent was added, filtered through a 0.22 µm PVDF syringe filter into a 1.5 mL HPLC vial without further sample clean-up, and injected into the UHPLC-MS/MS.

Method 3 is a multi-analyte solvent partitioning method comprising of an extraction phase, extensive sample clean-up steps using solid phase extraction (SPE) cartridges, and a thorough quality control procedure via addition of internal standards described by Majeed *et al.* (2018). To

5 g of spiked sample, 20 mL of extraction solvent acetonitrile/water/acetic acid (79/20/1, v/v/v) was added, vortexed for 5 min, agitated for 60 min using an end-over-end shaker (Exacta, Delhi, India), and centrifuged at 4,000 g for 15 min. The supernatant was filtered through a pre-conditioned C18-SPE cartridge under ambient pressure, and the extracts defatted with 20 mL of hexane. The defatted extract was divided into two portions. The first portion (10 mL) was made up to 30 mL using acetonitrile/acetic acid (99/1, v/v), and passed through a MultiSep®226 AflaZon<sup>+</sup> multifunctional column. The second portion (10 mL) was filtered using a glass microfilter (0.22 µm), and 2 mL of the filtrate added to the eluent of the first portion. The combined portions were evaporated to complete dryness over a stream of nitrogen gas at 40 °C, and reconstituted with 150 µL of mobile phase [5 mM ammonium acetate in water/methanol/acetic acid (94/5/1, v/v/v) and 5 mM ammonium acetate in acetonitrile/acetic acid (99/1, v/v), in the ratio of 3/2, v/v]. The reconstituted extract was subsequently thoroughly agitated for 4 min on a vortex machine (Labinco, Breda, The Netherlands), and filtered using a Ultrafree® PVDF centrifuge filter prior to injection on the LC-MS/MS.

## 4.3 Results and discussion

### 4.3.1 Method development and optimization

A modified PHWE method was developed for the simultaneous extraction of 15 different mycotoxins from maize. The mechanism and dynamics behind PHWE had been previously described in detail (Gbashi *et al.*, 2017a). Maize was selected based on the fact that it is a widely-consumed staple food also in South Africa and a favored substrate for fungal contamination and subsequent mycotoxin production (Chilaka *et al.*, 2012; Ranum *et al.*, 2014). Preliminary attempts at adopting a conventional PHWE system (which uses only hot water as the extraction solvent) for multi-mycotoxin extraction was unsuccessful due to low recoveries for many of the mycotoxins. As such, in order to improve the extractability multi-mycotoxin using PHWE, ethanol was incorporated as a co-solvent. Ethanol is an environmentally friendly, cheap and readily available solvent that has been proven to be effective in improving the efficiency of PHWE (Herrero *et al.*, 2011; Shang *et al.*, 2014; Shang *et al.*, 2017).

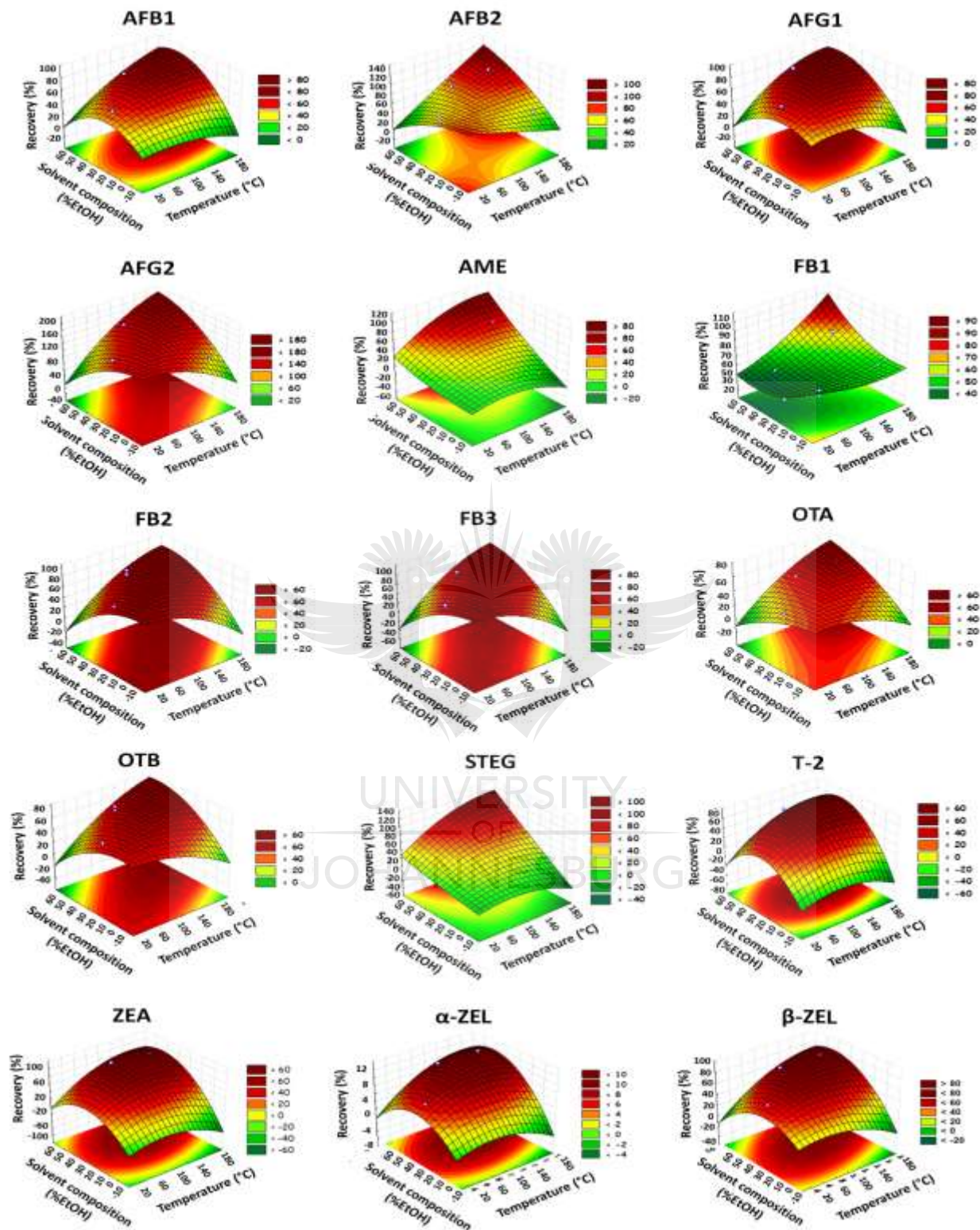
The extraction conditions of temperature and solvent composition were thus optimized using the CCD model in order to ensure an optimum performance of the modified PHWE method. In this

regard, experiments were conducted at a set of statistically pre-designed experimental conditions (Table 4.1) and a quadratic optimization function (Equation 4.1) fitted to the experimental data (Appendix 4.A). The resultant regression models [Appendix 4.B (columns 2-7)] were validated using standard model-fit validation parameters of  $R^2$ ,  $B_f$  and  $A_f$  [Appendix 4.B (columns 8-14)] as described by Adebo *et al.* (2018). The  $R^2$  values ranged from 0.56 to 0.97 indicating that the models were well-fit, whereas, the  $B_f$  and  $A_f$  values ranged from 0.98 to 1.22 and 1.10 to 1.59, respectively, indicating that the models presented a good estimation of the true relationship between the dependent variable (i.e. recovery) and the control variables (i.e. temperature and solvent composition). This functional relationship can be clearly visualized on the generated 3-D surface plots (Figure 4.1).

Following the model-fit, the multi-objective optimum solution for the dependent variables (i.e., the most efficient combination of temperature and solvent composition for the maximum recovery of all mycotoxins simultaneously) was computed using the global optimization function of the Minitab 17 statistical software (Minitab Inc., Pennsylvania, US) as described by Adebo *et al.* (2018). This optimum solution was 162 °C and 45% EtOH for temperature and solvent composition, respectively. Subsequent validation of this optimized conditions by laboratory experiments showed a clear enhancement in recovery of the analytes with recoveries ranging from 14 to 124%, with 13 out of 15 of the analytes having recoveries above 70% in one single extraction (Figure 4.2). Even T-2 which had a pre-optimization recovery of 0% using conventional PHWE, had a post-optimization recovery of over 82% using the optimized PHWE method. Alternariol monomethyl ether had the highest recovery rate (129%), followed in descending order by AFB<sub>1</sub> (127%), AFG<sub>1</sub> (125%), FB<sub>2</sub> (118%), ZEA (114%), AFB<sub>2</sub> (110%),  $\beta$ -ZEL (108%), OTB (98%), AFG<sub>2</sub> (94%), FB<sub>3</sub> (90%), T-2 (83%), STEG (73%), FB<sub>1</sub> (71%), OTA (58%) and  $\alpha$ -ZEL (14%).

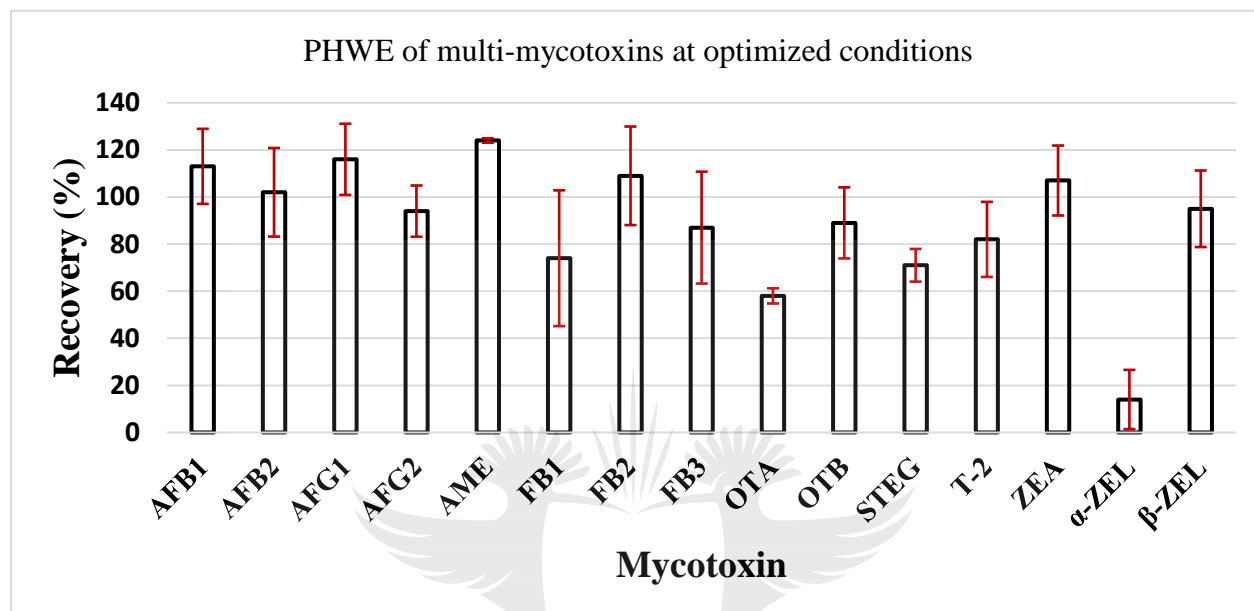
In addition to obtaining the optimal extraction condition, the model-fit also provided details on how the two extraction variables individually and interactively affected the recovery of each mycotoxin (Figure 4.3). These Pareto charts summarize the relative importance of the linear, quadratic and interaction effects of temperature and solvent composition on the recovery of individual mycotoxins. The effects are displayed on the y-axis and their corresponding magnitudes are plotted as horizontal bars on the x-axis. Bars that extended beyond the red line on the chart are significant at a 95% probability.





**Figure 4.1:** Response surface plots showing the relationship between mycotoxin recovery and extraction parameters (temperature and solvent composition). EtOH: ethanol. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>.

AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.



**Figure 4.2:** PHWE of multi-mycotoxins using CCD-optimized extraction conditions of 162 °C for temperature and 45% for solvent composition. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

Eight (8) out of 15 of the mycotoxins were most strongly influenced by the linear effect of solvent composition (S1L) indicating that an increase the solvent composition results in a corresponding increase in recoveries of these mycotoxins. This observed strong positive linear effect of solvent composition on the extractability of mycotoxins could be due to the polarity interactions, lower surface tension and higher diffusivity of the water-ethanol mixture as compared to water only. These features allow for greater permeability of the extraction solvent into matrix cellular structures, as well as, higher solubility of some of the analytes in the extraction solvent (Gbashi *et al.*, 2016; Teo *et al.*, 2010). Six (6) of the mycotoxins (i.e. OTs, FB<sub>2</sub>, FB<sub>3</sub>, AFB<sub>2</sub> and AFG<sub>2</sub>) were



most strongly influenced by the interaction effect of temperature and solvent composition (S1byT1) while only FB<sub>1</sub> was most strongly influenced by the linear effect of temperature (T1L).

### 4.3.3 Validation of the optimized PHWE method performance characteristics

Subsequent to optimization, the performance of the modified PHWE method was validated against benchmark standards of legislation and criteria. This was necessary for further authentication of the extraction process, and to compare the results obtained to established specifications of mycotoxin extraction and analysis.

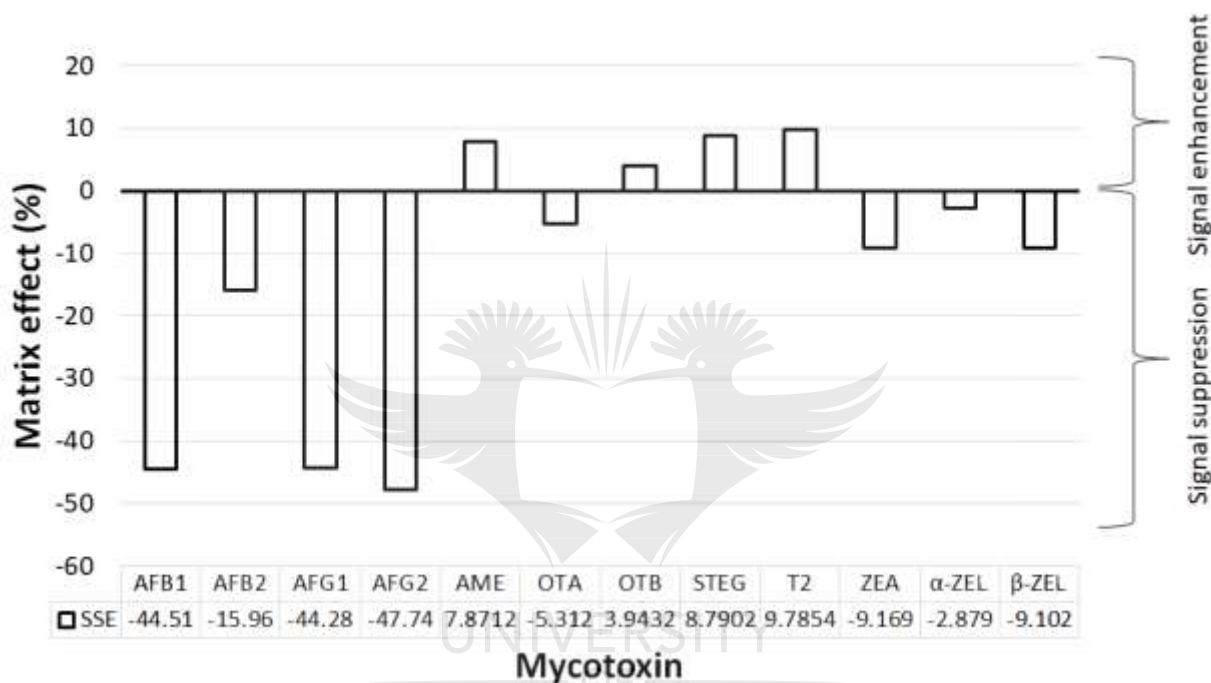
#### 4.3.3.1 Matrix effect (ME)

The possibility of co-extracted matrix components interfering with the signals of target analytes in the MS could not be ruled out, as such we investigated the ME of the modified PHWE method to determine whether a matrix-matched calibration was needed for quantitation of the analytes. Matrix effect can occur by way of signal suppression or amplification in the MS depending on the nature of the analyte and type of matrix (Kim *et al.*, 2017). From Figure 4.5, it can be seen that AFs, OTA, and ZEAs demonstrated matrix-induced signal suppression with AFG<sub>2</sub> having the highest suppression of 48%, followed in descending order by AFB<sub>1</sub> (45%), AFG<sub>1</sub> (44%), AFB<sub>2</sub> (15%), ZEA and  $\beta$ -ZEL (9%), OTA (5%) and  $\alpha$ -ZEL (3%). In contrast, OTB, T-2, AME and STEG demonstrated signal enhancement, with T-2 being the most enhanced at 10% (Figure 4.5). Apart from the AFs, all signal interferences were negligible ( $\leq 10\%$ ). The main components in maize which are likely to cause matrix effects during LC-MS/MS analysis are lysophospholipids (Xia & Jemal, 2009; Panuwet *et al.*, 2016). The mechanism behind this phenomenon is not yet well understood, however a commonly acknowledged explanation for ion suppression is that matrix components compete with analytes for available charges in the liquid phase hence limiting ionization (Cappiello *et al.*, 2010; Panuwet *et al.*, 2016). Also, at higher concentrations of co-eluting components, there may be an increase in surface tension and viscosity of the eluents in the ESI interface, leading to an inefficient transfer of the analyte to the gas phase (Panuwet *et al.*, 2016).



**Figure 4.3:** Pareto charts of standardized factor effects for pressurized hot water extraction (PHWE) of multi-mycotoxins. S1L: linear effect of solvent composition. S1Q: quadratic effect of

solvent composition. T1L: linear effect of temperature. T1Q: quadratic effect of temperature. S1byT1: interaction effect of solvent composition and temperature. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.



**Figure 4.4:** Matrix-induced signal suppression/enhancement for mycotoxins using pressurized hot water extraction (PHWE). AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

The AOAC recommends the use of matrix-matched external standard calibration to compensate for quantitation bias in the absence of isotopically-labeled standards (Lehotay, 2007; Liu *et al.*, 2015; Zrostlikova *et al.*, 2002). To this effect, quantitation of analytes was achieved using matrix-matched calibration curves, except for FBs, which for reasons unclear, did not yield linear calibration curves using matrix-matched solutions, as such, were quantified using calibration curves of standards prepared in neat solutions. Elsewhere, under different circumstances, a similar

phenomenon was observed for AFGs when using a solvent-based extraction method (Sameni *et al.*, 2014).

#### 4.3.3.2 Linearity, accuracy, LOD and LOQ

The UHPLC-MS/MS method demonstrated an adequate linearity with  $R^2$  values ranging from 0.986 to 0.999 (Table 4.3). The International Conference on Harmonization (ICH) recommends that coefficients of determination for biologics should be  $\geq 0.950$  (Shabir, 2005). In all cases, the y-intercept was zero which did not violate the maximum of 2% (of the target concentration response) recommended by the ICH (Shabir, 2005). Computed values for LOD and LOQ ranged from 0.06 to 40.85  $\mu\text{g}/\text{kg}$  and 0.18 to 122.60  $\mu\text{g}/\text{kg}$ , respectively (Table 4.3).

**Table 4.3:** Accuracy or recovery efficiency (%), linear calibration function, coefficient of linearity ( $R^2$ ), LOD and LOQ ( $\mu\text{g}/\text{kg}$ ).

Mycotoxin	Accuracy (%)	Equation	$R^2$	LOD ( $\mu\text{g}/\text{kg}$ )	LOQ ( $\mu\text{g}/\text{kg}$ )	Intra-day precision (RSD <sub>r</sub> )		Inter-day precision (RSD <sub>R</sub> )	
						Level 1	Level 2	Level 1	Level 2
AFB <sub>1</sub>	113	$y=963239.00x+0$	0.986	0.94	2.8	5	3	16	18
AFB <sub>2</sub>	102	$y=11376.000x+0$	0.997	0.08	0.3	10	21	19	23
AFG <sub>1</sub>	116	$y=1133280.0x+0$	0.996	0.43	1.3	20	11	15	16
AFG <sub>2</sub>	94	$y=603053.00x+0$	0.998	1.7	5.1	ND	ND	ND	ND
AME	124	$y=159974.00x+0$	0.996	2.4	7.2	ND	ND	ND	ND
FB <sub>1</sub>	74	$y=17830.000x+0$	0.998	2.3	6.8	10	10	29	20
FB <sub>2</sub>	109	$y=9478.7900x+0$	0.999	4.3	13	9	7	21	34
FB <sub>3</sub>	87	$y=28677.900x+0$	0.999	0.1	0.2	19	25	24	34
OTA	58	$y=2539650.0x+0$	0.998	0.4	1.3	22	20	3	30
OTB	89	$y=22408600x+0$	0.987	0.1	0.3	25	23	15	28
STEG	71	$y=2407810.0x+0$	0.998	0.5	1.5	5	19	7	20
T-2	82	$y=18644.300x+0$	0.999	16	47.3	27	23	16	31
ZEA	107	$y=370444.00x+0$	0.996	1.6	4.9	16	24	15	26
$\alpha$ -ZEL	14	$y=35358.600x+0$	0.999	41	123	0.00	6	13	30
$\beta$ -ZEL	95	$y=218599.00x+0$	0.999	12	36	23	17	16	30

**Key:** LOD: limit of detection. LOQ: limit of quantification. ND: not determined. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin

B<sub>3</sub>: OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

Results of accuracy of the method revealed that analytes were determined with reasonable accuracy ranging from 71 to 124%, with the exception of OTA and  $\alpha$ -ZEL which had recoveries of 58 and 14%, respectively (Table 4.3). The FDA recommends values between 80-110% for concentrations ranging from 1000 to 10,000  $\mu\text{g}/\text{kg}$  (FDA, 2015). The EC recommends recovery values between 60 and 130% (Commission Regulation, 2006a), the AOAC recommends 60 to 125% (AOAC, 2009) in foodstuffs contaminated with 10  $\mu\text{g}/\text{kg}$  of mycotoxins, whereas, the CODEX recommends 80 to 110% (CODEX, 2015) for accuracy in agricultural commodities contaminated with mycotoxins depending on the type of mycotoxins and level of contamination.

#### 4.3.3.3 Intra-day precision (RSD<sub>r</sub>) and inter-day precision (RSD<sub>R</sub>)

The results for the method precision i.e. RSD<sub>r</sub> and RSD<sub>R</sub> are presented in Table 4.3 (Columns 7-10). The method demonstrated good intra-day precision with all RSD<sub>r</sub> values  $\leq 27\%$ . These values did not vary wide from the requirements by the EC and AOAC. The AOAC recommends a repeatability variation coefficient of  $< 25\%$  for each mycotoxin (AOAC, 2009) and the EC recommends  $\leq 20\%$  for OTA,  $\leq 25$  for ZEA,  $\leq 20\%$  for FBs,  $\leq 30$  for T-2 (Commission Regulation, 2006a). The RSD<sub>R</sub> values for inter-day precision ranged from 3 to 34%. The AOAC recommends RSD<sub>R</sub> values less than 40% for each mycotoxin (AOAC, 2009) whereas the EC recommends RSD<sub>R</sub> values of  $\leq 30$  for OTA (at a concentration  $> 1 \mu\text{g}/\text{kg}$ ),  $\leq 30$  for FB<sub>1</sub> and FB<sub>3</sub> (at a concentration  $> 500 \mu\text{g}/\text{kg}$ ),  $\leq 40$  for ZEA (at a concentration  $> 50 \mu\text{g}/\text{kg}$ ), and  $\leq 40$  for T-2 (at a concentration  $> 250 \mu\text{g}/\text{kg}$ ) (Commission Regulation, 2014).

#### 4.3.4 Comparison with other conventional mycotoxin extraction methods

The recovery efficiency of our method for the extraction of multi-mycotoxins in maize was compared to those of other validated and widely-referenced methods reported in literature. The results showed significantly different ( $\alpha=0.05$ ) recovery patterns amongst the different extraction methods for some of the analytes. Relative to the performance of the conventional methods in terms of recovery, Method 1 (0 to 124%), Method 2 (0.80 to 184%), and Method 3 (99 to 100%), our method performed sufficiently (71 to 124%) with the exception of OTA (58%) and  $\alpha$ -ZEL (14%), and in some cases favorably (Table 4.4). Particularly, the recovery of FBs was poor using

the tested conventional methods with maximum recoveries <10%, whereas, the recovery of FBs with PHWE ranged from 74 to 109%. Chilaka *et al.* (2012) noted the difficulty of extracting FBs from maize using Method 1, and rather adopted a separate extraction procedure for this purpose using SAX SPE. Method 3 (Majeed *et al.*, 2018) involved the use of a strong organic eluent (acetonitrile/water) and 1% acetic acid for extraction, followed by defatting and an extensive clean-up using two different SPE clean-up. Further to this, two internal standards deepoxy-deoxynivalenol (DOM) and zearalanone (ZAN) were used for quality control to correct for unintended losses of analytes during the extraction and clean-up processes, as well as, during sample injection into the UHPLC-MS/MS as described in Section 4.2.4.

**Table 4.4:** Comparison of method performance (recovery) between PHWE and conventional extraction methods

Mycotoxin	Recovery (%)			
	PHWE	Method 1 (MME)	Method 2 (SOLV-DS)	Method 3 (SOLV-SPE)
AFB <sub>1</sub>	113 <sup>a</sup> ±16	118 <sup>a</sup> ±0.64	159 <sup>b</sup> ±3.4	100 <sup>a</sup> ±1.6
AFB <sub>2</sub>	102 <sup>a</sup> ±19	69 <sup>a</sup> ±2.2	98 <sup>a</sup> ±2.7	100 <sup>a</sup> ±0
AFG <sub>1</sub>	116 <sup>a</sup> ±15	124 <sup>a</sup> ±4.5	184 <sup>b</sup> ±1.7	100 <sup>a</sup> ±0.83
AFG <sub>2</sub>	94 <sup>b</sup> ±11	54 <sup>a</sup> ±1.3	73 <sup>ab</sup> ±2.3	100 <sup>b</sup> ±0.85
AME	124 <sup>d</sup> ±0.93	51 <sup>a</sup> ±1.2	77 <sup>b</sup> ±2.8	100 <sup>c</sup> ±3
FB <sub>1</sub>	74 <sup>b</sup> ±29	0.1 <sup>a</sup> ±0.1	3 <sup>a</sup> ±4.6	100 <sup>b</sup> ±2.7
FB <sub>2</sub>	109 <sup>b</sup> ±21	0 <sup>a</sup> ±0.	0.8 <sup>a</sup> ±0	100 <sup>b</sup> ±1.8
FB <sub>3</sub>	87 <sup>b</sup> ±24	0.3 <sup>a</sup> ±0.4	5 <sup>a</sup> ±0.45	100 <sup>b</sup> ±0.77
OTA	58 <sup>b</sup> ±3.2	41 <sup>a</sup> ±2.6	101 <sup>c</sup> ±0.79	100 <sup>c</sup> ±1.4
OTB	89 <sup>b</sup> ±15	51 <sup>a</sup> ±1.6	124 <sup>c</sup> ±9.6	NI
STEG	71 <sup>a</sup> ±6.9	108 <sup>b</sup> ±0.98	133 <sup>c</sup> ±0.62	100 <sup>b</sup> ±1.6
T-2	82 <sup>a</sup> ±16	78 <sup>ab</sup> ±0.13	112 <sup>b</sup> ±0.51	100 <sup>ab</sup> ±1.1
ZEA	107 <sup>a</sup> ±15	95 <sup>a</sup> ±4.9	115 <sup>a</sup> ±1.6	99 <sup>a</sup> ±4.6
α-ZEL	14 <sup>b</sup> ±13	17 <sup>a</sup> ±0.54	22 <sup>a</sup> ±0.57	NI
β-ZEL	95 <sup>a</sup> ±16	107 <sup>a</sup> ±1.2	105 <sup>a</sup> ±2.6	NI

Key: Values represent the mean recoveries of duplicate extractions ± standard deviations. Significant differences amongst the recovery values are indicated by superscripted alphabets on the means, and were compared using Tukey's pairwise multiple comparison test following a one-way ANOVA. Values in the same row followed by the same alphabet are not significantly different ( $p > 0.05$ ). MME: multi-mycotoxin extraction using a combination of solvents and organic salts (Chilaka *et al.*, 2012). SOLV-DS: solvent extraction followed by dilute and shoot injection (Sulyok *et al.*, 2007). SOLV-SPE: solvent extraction followed by clean-up using different SPE cartridges (Majeed *et al.*, 2018). NI: not investigated. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.

In terms of cost, effort and time, the PHWE method was more desirable. Despite foregoing clean-up, the observed recoveries were in the range of other single-laboratory validated methods widely reported in literature which required extensive clean-up procedures (Di Mavungu *et al.*, 2009; Monbaliu *et al.*, 2009, 2010; Bardsley & Oliver, 2015; Liu *et al.*, 2015; Solfrizzo *et al.*, 2018). For example, the recovery of the modified PHWE (which ranged from 58 to 124%, with the exception of  $\alpha$ -ZEL) is in line with those of Lattanzio *et al.* (2014) and Kim *et al.* (2017) who reported recoveries ranging from 63 to 93% and 74 to 133%, respectively, for multi-mycotoxin extraction in cereals (maize inclusive) followed by immuno-affinity column cleanup prior to LC-MS/MS analysis.

#### 4.3.6 Sample analysis

Sequel to adequate performance, the developed PHWE method was applied for the extraction of the understudied mycotoxins in 25 maize meal samples intended for human consumption obtained from rural households in Ngwalemong village in Limpopo Province (South Africa). The results revealed that all samples were free from AFBs, OTS and STEG. Ninety-six percent of the samples (n=25) were positive for FB<sub>1</sub>, 52% positive for FB<sub>3</sub>, and 48% positive for T-2 (Table 4.7). Fumonisin B<sub>1</sub> was the highest contaminant of the food products with a mean contamination levels of 119  $\mu\text{g}/\text{kg}$ , followed in descending order by  $\alpha$ -ZEL (24  $\mu\text{g}/\text{kg}$ ), and FB<sub>3</sub> (5.1  $\mu\text{g}/\text{kg}$ ). For all samples, the contamination levels for the tested mycotoxins were all below the maximum levels stipulated by the South African government, EC, CODEX, and other regulatory bodies (Arroyo-Manzanares *et al.*, 2018; CODEX, 1995; Commission Regulation, 2006b, 2013; FAO, 2004). It can thus be inferred that household maize meal in the aforementioned village in South Africa was safe for human consumption in terms of mycotoxins. Our observations further reiterate the adequacy of our developed PHWE method for the analysis of multi-mycotoxins in food using UHPLC-MS/MS.

**Table 4.5:** Mycotoxin contamination of maize meal from Ngwalemong village in Limpopo Province of South Africa.

Mycotoxin	Number of positive samples (n=25)	Mean* ( $\mu\text{g}/\text{kg}$ ) $\pm$ STD	Contamination range ( $\mu\text{g}/\text{kg}$ )
AFB <sub>1</sub>	<LOQ	<LOQ	NA
AFB <sub>2</sub>	<LOQ	<LOQ	NA



Mycotoxin	Number of positive samples (n=25)	Mean* ( $\mu\text{g/kg}$ ) $\pm$ STD	Contamination range ( $\mu\text{g/kg}$ )
AFG <sub>1</sub>	0	<LOQ	NA
AFG <sub>2</sub>	0	<LOQ	NA
AME	9	4.1 $\pm$ 7.2	<LOQ-32
FB <sub>1</sub>	24	119 $\pm$ 84	<LOQ-297
FB <sub>2</sub>	0	<LOQ	NA
FB <sub>3</sub>	13	5.1 $\pm$ 5.8	<LOQ-16
OTA	0	<LOQ	NA
OTB	0	<LOQ	NA
STEG	0	<LOQ	NA
T-2	12	4.3 $\pm$ 5.2	<LOQ-18
ZEA	3	0.99 $\pm$ 2.7	<LOQ-8.8
$\alpha$ -ZEL	6	24 $\pm$ 46	<LOQ-160
$\beta$ -ZEL	8	4.4 $\pm$ 6.9	<LOQ-18

Key: Mean\*: average contamination of the samples including positive (i.e. >LOD) and negative (i.e. <LOD) samples. STD: standard deviation. <LOD: below limit of detection. NA: not applicable. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

#### 4.4 Conclusion

The occurrence of mycotoxins in food and feed and their consequent severe effects in animals and humans have made it essential to routinely monitor the levels of these contaminants in various agricultural products. This has positioned analysis as a critical element in the management and control of mycotoxins. Extraction is an important step during mycotoxin analysis, hence improvement in extraction methods has been a recurrent interest in mycotoxicology. Shortcomings of other conventional methods have led to the development of new applications. Herein is reported for the first time the use of PHWE for the extraction of multi-mycotoxins and their subsequent quantitation on UHPLC-MS/MS. This method was developed as an efficient, safer, greener and faster alternative to other conventional methods for multi-mycotoxin extraction. All these were conveniently achieved in one single step extraction process with good values obtained for the accuracy and linearity and other associated validation parameters. The adoption of a chemometric approach for method optimization not only resulted in the optimal performance of the method, but also allows for the possibility of future optimizations geared towards analyte-specific applications. In any case, there is need to improve on some important aspects of the method, such as the working range of the method and the recovery values of OTA and  $\alpha$ -ZEL. Notwithstanding, the overall

performance of the method is highly promising for mycotoxin research and survey work. While the method is promising, further studies in the future can focus on the cost-benefit analysis of using PHWE for extraction, as compared to other conventional mycotoxin extraction techniques.

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## APPENDIX 4

**Appendix 4.A:** Pressurized hot water extraction (PHWE) of multi-mycotoxins at different levels of temperature and solvent composition based on the central composite design (CCD)

Mycotoxin	Recovery of mycotoxins (%) at different solvent composition and temperature conditions							
	50 °C/ 0% EtOH	50 °C/ 40% EtOH	150 °C/ 0% EtOH	150 °C/ 40% EtOH	29 °C/ 20% EtOH	170 °C/ 20% EtOH	100 °C/ 48.28% EtOH	100 °C/ 20% EtOH
AFB <sub>1</sub>	31±0.93	38±1.48	38±0.75	84±0.93	61±1.12	64±2.42	72±0.56	68±0.56
AFB <sub>2</sub>	66±2.05	38±10.05	51±8.19	89±15.07	74±3.54	72±15.26	76±2.42	70±3.54
AFG <sub>1</sub>	45±1.31	38±0.37	45±1.12	82±0.74	67±0.93	60±1.49	80±1.68	74±4.09
AFG <sub>2</sub>	128±0.93	76±0.37	98±1.68	159±3.16	136±0.56	123±1.67	147±0.37	145±0.74
AME	1±0.00	27±2.52	1±0.00	64±2.17	5±1.08	11±0.72	60±3.61	27±1.08
FB <sub>1</sub>	53±4.65	45±8.56	52±10.98	70±2.05	38±3.54	52±7.81	44±0.18	43±1.86
FB <sub>2</sub>	64±0.56	33±1.86	32±3.16	71±0.75	63±0.56	54±1.12	68±5.21	71±4.84
FB <sub>3</sub>	61±4.09	26±6.70	28±2.23	70±6.14	59±2.98	46±2.05	65±0.00	66±5.21
OTA	38±0.19	23±1.12	31±0.37	59±0.74	38±1.12	38±1.68	47±0.93	46±0.93
OTB	48±1.12	28±0.37	36±0.74	67±1.48	53±0.75	53±0.37	59±4.28	60±1.68
STEG	0±0.00	34±1.31	0±0.00	76±0.56	13±0.00	19±0.19	72±2.23	34±1.12
T-2	0±0.00	25±0.93	0±0.00	61±1.48	34±1.68	49±3.16	59±0.00	56±4.29
ZEA	0±0.00	35±0.56	1±0.00	79±2.42	39±0.18	39±1.12	69±1.87	61±0.37
α-ZEL	2±0.00	5±0.00	3±0.00	11±0.37	7±0.00	6±0.00	9±0.00	9±0.19
β-ZEL	35±0.19	38±0.93	35±0.74	83±1.48	61±0.93	55±0.93	70±1.12	71±1.12

**Key:** Sol. comp.: solvent composition. Temp.: Temperature. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.

## Appendix 4.B: Model-fit regression coefficients and validation parameters

Mycotoxin	$z(x,y) = C_{00} + C_{10}x + C_{20}x^2 + C_{01}y + C_{02}y^2 + C_{11}xy$						$R^2$	$R^2$ Adj	Residual	$\rho$	AAD	$B_f$	$A_f$
	$c_{00}$	$c_{10}$	$c_{20}$	$c_{01}$	$c_{02}$	$c_{11}$							
AFB <sub>1</sub>	27.40	0.310	0.000	1.070	-0.030	0.010	0.830	0.740	84.36	0.910	0.130	1.010	1.130
AFB <sub>2</sub>	83.02	-0.220	0.000	-0.880	-0.010	0.020	0.660	0.490	139.9	0.810	0.140	1.010	1.140
AFG <sub>1</sub>	37.08	0.480	0.000	0.360	-0.020	0.010	0.690	0.540	125.5	0.830	0.140	1.010	1.150
AFG <sub>2</sub>	129.56	0.400	0.000	-1.330	-0.030	0.030	0.760	0.640	253.0	0.870	0.090	1.010	1.100
AME	-19.11	0.630	0.000	-0.130	0.010	0.010	0.970	0.950	30.47	0.980	1.960	1.200	1.590
FB <sub>1</sub>	61.88	-0.250	0.000	-1.140	0.010	0.010	0.560	0.350	71.09	0.750	0.110	1.010	1.110
FB <sub>2</sub>	61.88	-0.250	0.000	-1.140	0.010	0.010	0.860	0.780	52.23	0.920	0.090	1.010	1.100
FB <sub>3</sub>	60.39	0.290	0.000	-0.980	-0.020	0.020	0.840	0.750	71.03	0.910	0.130	1.010	1.130
OTA	34.67	0.240	0.000	-0.550	-0.010	0.010	0.870	0.810	21.41	0.930	0.090	1.010	1.100
OTB	46.92	0.220	0.000	-0.320	-0.020	0.010	0.810	0.720	45.71	0.900	0.100	1.010	1.100
STEG	-18.18	0.620	0.000	0.190	0.000	0.010	0.970	0.960	31.09	0.990	2.270	0.980	1.140
T-2	-23.82	0.730	0.000	2.390	-0.050	0.010	0.940	0.900	56.69	0.970	0.120	1.000	1.120
ZEA	-23.29	0.840	0.000	2.260	-0.050	0.010	0.950	0.920	59.51	0.970	2.150	1.220	1.340
$\alpha$ -ZEL	-0.450	0.090	0.000	0.240	-0.010	0.000	0.870	0.810	1.780	0.930	0.220	1.020	1.230
$\beta$ -ZEL	25.32	0.490	0.000	0.930	-0.030	0.010	0.810	0.720	89.98	0.900	0.140	1.010	1.150

**Key:**  $c_{00}$  is a constant.  $c_{10}$  and  $c_{01}$  are the linear coefficients of  $x$  (temperature) and  $y$  (solvent composition), respectively.  $c_{20}$  and  $c_{02}$  are the quadratic coefficients of  $x$  and  $y$ , respectively.  $c_{11}$  is the interaction coefficient. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

## CHAPTER FIVE<sup>#</sup>

### COMPARISON OF PRESSURIZED HOT WATER EXTRACTION (PHWE) AND A SOLVENT-BASED EXTRACTION METHOD FOR THE ESTIMATION OF MULTI-MYCOTOXIN LEVELS IN CEREALS

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#### Abstract

Mycotoxin contamination of crops has contributed significantly to the elusive sustainable development in Africa. Routine analysis of food commodities is critical for control and management of these toxins in foods. In the present study, 15 different mycotoxins were estimated in three staple cereals from selected agro-ecological regions in Nigeria using a ‘novel’ green extraction method, pressurized hot water extraction (PHWE) in comparison to a conventional solvent extraction method. Tested mycotoxins included zearalenone and its analogues (ZEAs), ochratoxins (OTs), T-2 toxin (T-2), fumonisins (FBs), aflatoxins (AFs), alternariol monomethyl ether (AME) and sterigmatocystin (STEG). Further discrimination of the results of PHWE and solvent extraction using principal component analysis (PCA) and orthogonal projection to latent structures discriminate analysis (OPLS-DA) did not yield any differential clustering patterns, indicating the relative similarities of the results obtained from the two extraction methods. All the maize samples (n=16) and 32% (n=38) of sorghum and 35% (n=37) of millet samples were positive for at least one of the 15 tested mycotoxins. The FBs, in particular FB<sub>1</sub> had the highest prevalence in terms of rate of occurrence and levels of contamination in all three cereals. Maize samples generally had higher mycotoxin contamination levels for FB<sub>1</sub> (17 to 7,947 µg/kg), as compared to sorghum (188 to 248 µg/kg) and millet which was negative for the toxin. Contamination levels

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for the cereals were higher in the warm humid rain forest region and gradually decreased towards the hot and arid region in the north of the country. Co-occurrence of multiple mycotoxins was observed in many of the analyzed samples. A total of 14 different combinations were observed from the 5 major groups of regulated mycotoxins (*i.e.*, AFs, FBs, OTs, T-2 and ZEAs). The highest co-occurrence was AFs+FBs that occurred in 38% (n=16) of the maize samples, while AFs+OTs+ZEAs occurred in 3% (n=38) of the sorghum samples. These results indicate the relative risk of exposure of the Nigerian populace to mycotoxins, hence the need to prioritize food safety interventions, including establishing appropriate legislation to safeguard the public, particularly those from the southern part of the country where climatic conditions are warm and humid, and mycotoxins are prevalent. The results also demonstrate the applicability of PHWE as a possible alternative extraction method to conventional methods of extraction which are solvent based, hence promoting analytical techniques that are greener and more environmentally sustainable.

**Key words:** Mycotoxins, pressurized hot water extraction (PHWE), agroecological zones, co-occurrence, LC-MS/MS, green extraction, principal component analysis (PCA), orthogonal projection to latent structures discriminate analysis (OPLS-DA).

## 5.1 Introduction

Mycotoxins are well-known food and feed contaminants that are produced by ubiquitous toxigenic fungal species belonging mainly to the *Aspergillus*, *Penicillium*, *Fusarium*, *Claviceps* and *Alternaria* genera (Njobeh *et al.*, 2010a; Chilaka *et al.*, 2012; Atanda *et al.*, 2013). It has been estimated that approximately 4.5 billion people in the world, of which a majority from sub-Saharan Africa are chronically exposed to uncontrolled amounts of these toxins *via* exposure to contaminated foods (Turner *et al.*, 2007). Although about 300 to 400 different mycotoxins have been clearly identified in nature, only a few have received significant research attention due to their economic and health significance (Gbashi *et al.*, 2018), some of which include fumonisins (FBs), aflatoxins (AFs), zearalenone (ZEA) and its analogues, ochratoxins (OTs), T-2 toxin (T-2), and some emerging ones such as alternariol monomethyl ether (AME) and sterigmatocystin (STEG).

Relative to their incessant prevalence in the sub-Saharan African food supply chain, mycotoxins have been implicated in a number of adverse socio-economic effects, ranging from human and animal health, impact on food security, impact on livelihood, damage to the African agricultural export market brand, and impact on Africa's self-sustainability and increased dependence on foreign aid (Wagacha & Muthomi, 2008; Darwish *et al.*, 2014; Gbashi *et al.*, 2018). In the global food market, annual losses associated with mycotoxins have been estimated at approximately one billion metric tons of agricultural produce and food commodities (Schmale and Munkvold, 2009; Wilson *et al.*, 2017). Nigeria, a sub-Saharan African nation, and the most populous country on the continent, is one of the countries that have been severely plagued by the mycotoxin menace in Africa (Makun *et al.*, 2012; Atanda *et al.*, 2013; Ezekiel *et al.*, 2014).

Amidst several factors, favorable environmental conditions for colonization of crops by toxigenic fungi species, coupled with susceptibility of endemic staple crops such as maize, sorghum and millet to mycotoxin proliferation have been identified as a critical precursor to the pervasive impact of the toxins in Nigeria (Oyelami *et al.*, 1997; Atanda *et al.*, 2015; Apeh *et al.*, 2016; Chilaka *et al.*, 2016). Majority of the Nigerian populace (78 to >85%) rely on these cereal grains for dietary supply of energy, household incomes, as well as food and feed ingredients for their livestock (Awotide, 2012; Nicely *et al.*, 2012; Chilaka *et al.*, 2016). The farmers produce these crops under varying agronomic practices and different climatic conditions across the country. Nigeria has a humid tropical climate in its southern region which is close to the equator, and a hot arid climate gradually unfolds towards the northern part of the country, resulting in definable floral and agroecological patterns across the country.

Since these cereal crops are mostly produced by peasant farmers and marketed in local markets within the country and to other neighboring countries *via* unofficial sales channels (Bandyopadhyay *et al.*, 2007; Akhidenor & Nzeka, 2018), surveillance of mycotoxin contamination levels seldom occurs (Adetunji *et al.*, 2014). In this regard, despite the compelling evidence of risk exposure to mycotoxins on the Nigerian populace and their effects thereof (Liu & Wu, 2010; Atanda *et al.*, 2013), there is limited data on mycotoxins in Nigeria. It is thus imperative to routinely monitor the prevalence and levels of these toxins in food/feed in order to adopt appropriate control measures and policies. While it is important to adopt sensitive testing methods for mycotoxins, it is equally expedient to use methods that are fast, effective, more sustainable and



environmentally friendly. The present study describes the screening of samples of three staple cereals (maize, sorghum and millet) obtained from selected regions within Nigeria for possible contamination with mycotoxins using a novel green and effective method, pressurized hot water extraction (PHWE) in contrast to a conventional solvent-based extraction followed by UHPLC and tandem MS analysis.

## 5.2 Materials and methods

### 5.2.1 Materials

Mycotoxin reference standards used in this study included aflatoxin B<sub>1</sub> (AFB<sub>1</sub>), aflatoxin B<sub>2</sub> (AFB<sub>2</sub>), aflatoxin G<sub>1</sub> (AFG<sub>1</sub>), aflatoxin G<sub>2</sub> (AFG<sub>2</sub>), fumonisin B<sub>1</sub> (FB<sub>1</sub>), fumonisin B<sub>2</sub> (FB<sub>2</sub>), fumonisin B<sub>3</sub> (FB<sub>3</sub>), ochratoxin A (OTA), ochratoxin B (OTB), T-2 toxin (T-2), zearalenone (ZEA),  $\alpha$ -zearalenol ( $\alpha$ -ZEL),  $\beta$ -zearalenol ( $\beta$ -ZEL), alternariol monomethyl ether (AME), and sterigmatocystin (STEG) were purchased from the National Metrological Institute of South Africa (NMISA). Mycotoxin standards used for the solvent extraction included all of the above purchased from Biopure (RomerLabs, Tulln, Austria), except for AME and FB<sub>3</sub> purchased from Sigma-Aldrich (Bornem, Belgium) and Promec unit (Tygerberg, South Africa), respectively. Deepoxy-deoxynivalenol (DOM) and zearalanone (ZAN) were used as internal standards and were purchased from Sigma-Aldrich (Bornem, Belgium) and Biopure (RomerLabs, Tulln, Austria), respectively.

Biotage® Isolute SAX cartridges were purchased from Anatech Instruments (Pty) Ltd (South Africa). C18 solid phase extraction (SPE) columns and MultiSep®226 AflaZon+ multifunctional columns were purchased from Alltech (Lokeren, Belgium) and Romer Labs (Gernsheim, Germany), respectively. PVDF syringe filters (0.22  $\mu$ m, with Luer lock) and 10 mL NORM-JECT plastic syringe (with Luer lock) from Restek (Restek Corporation, Pennsylvania USA). Whatman® glass microfiber filters (47 mm diameter, grade GF/A) was purchased from VWR International (VWR International, Leuven, Belgium), while Ultrafree®-MC PVDF centrifugal filters (0.22  $\mu$ m) were purchased from Millipore (Bredford, MA, USA). Diatomaceous earth, potassium chloride, sodium sulphate, sodium bicarbonate, anhydrous sodium sulphate and dialysis tubing were purchased from Sigma (South Africa).

Solvents used for PHWE included MS-grade acetonitrile, MS-grade methanol and MS-grade formic acid, dichloromethane (DCM), ethanol (EtOH), iso-octane and sulphuric acid which were also purchased from Sigma (South Africa). Ultrapure water was obtained from a Milli-Q Gradient A10 dispensing system (Millipore, Billerica, MA, USA). Solvents used for the solvent extraction method included HPLC grade acetonitrile (Biosolve BV, Valkenswaard, The Netherlands), LC-MS grade methanol, acetonitrile, glacial acetic acid all from (Biosolve BV, Valkenswaard, The Netherlands) and ammonium acetate from Merck (Merck KGaA, Darmstadt, Germany). N-hexane was purchased from BDH Hipersolv Chromanorm (VWR International, Leuven, Belgium) and nitrogen gas (Air Liquide, Aalter, Belgium). The water used for this method (i.e. solvent extraction) was obtained from a Milli-Q®SP Reagent water system (Millipore Corp., Brussels, Belgium).

## 5.2.2 Methods

### 5.2.2.1 Sampling and sampling preparations

#### *Sampling*

Sampling was done as described by Atehnkeng *et al.* (2008). Sixteen maize (*Zea mays*) samples, 38 sorghum (*Sorghum bicolor*) samples and 37 millet (*Pennisetum glaucum*) samples were obtained from farmers/traders from five different agroecological zones in Nigeria (Adetuniji *et al.*, 2014; Ezekiel *et al.*, 2014) as described in Table 5.1. Choice of grains was based on consumption patterns of the West African diet, which is characterized by increased consumption of the selected cereals.

The Humid Rain Forest zone (HRF) falls within latitudes 6°4' & 7°5' N and longitudes 3°5' & 8°8' E, with maximum temperatures ranging from 26 to 28 °C, and average rainfall between 1,300 and 2,000 mm from two raining seasons in a year. Lying between latitudes 6°8' & 9°30' N and longitudes 2°40' & 12°15' E is the Derived Savannah zone (DRS), with maximum temperatures in a year averaging 25 to 35 °C and a bimodal rainfall averaging between 1,300 mm and 1,500 mm annually. The Southern Guinea Savannah (SGS) is characterized by a mean bimodal rainfall distribution between 1000 mm to 1300 mm per annum, maximum temperatures averaging 26 to 38 °C, and lies within latitudes 8°4' & 11°3' N and longitudes 2°41' & 13° 33' E, while the Northern

Guinea Savannah (NGS) is characterized by a single raining season per annum averaging between 900 mm to 1000 mm, and maximum temperatures ranging between 28 and 40 °C, and lies within latitudes 9°10' & 11°59' N and longitudes 3°19' & 13°37' E. The Sahel Savannah (SHS) lies within latitudes 12°2' & 13°8' N and longitudes 3°9' & 13°9' E, and is characterized by a Saharan climate, with maximum temperatures averaging between 30 to 40 °C and a single raining season per annum with rainfall distribution averaging between 650 and 1,000 mm (Atehnkeng *et al.*, 2008; Adetuniji *et al.*, 2014).

**Table 5.1:** Selected sampling locations for maize, sorghum and millet in Nigeria

Crop	Number of samples	Agroecological zone	Sub regions	Cultural/Geopolitical jurisdiction
Maize	16	Humid Rain Forest and Derived Savannah (HRF/DRS)	Lagos, Ondo, Ogun, Osun and Ekiti	Southern Nigeria
Sorghum	12	Humid Rain Forest and Derived Savannah (HRF/DRS)	Ondo, Ogun, Osun and Ekiti	Southern Nigeria
	26	Sahel Savannah (SHS)	Sokoto, Katsina, Kebbi, Jigawa and Kano	Northern Nigeria
Millet	20	Humid Rain Forest and Derived Savannah (HRF/DRS)	Ondo, Ogun, Osun and Ekiti	Southern Nigeria
	9	Northern and Southern Guinea Savannah (NGS/SGS)	Niger, Bauchi, Plateau, Kogi, Benue and Kwara,	North-Central Nigeria
	8	Sahel Savannah	Kebbi and Sokoto	Northern Nigeria

### ***Pressurized hot water extraction (PHWE)***

The cereal samples (maize, sorghum and millet) were milled to sieve size of < 0.6 to 1 mm using a mechanical blender. Extraction was performed using a laboratory-scale PHWE equipment (Addendum A) (Gbashi *et al.*, 2017) operated at previously optimized extraction conditions of 45% EtOH solvent composition and 162 °C temperature (Gbashi *et al.*, 2019a). For the extraction, 4 g of grounded cereal sample was thoroughly mixed with 3 g of diatomaceous earth and transferred into the extraction cell (70 x 30 mm and approximately 20 mL) which was contained in a GC oven (Carlo Erba Instruments, Italy) maintained at a temperature of 162 °C using a digital

temperature controllable unit ( $\pm 1$  °C). The extraction solvent (45% EtOH) was pumped at a constant flow rate of 5 mL/min through the extraction cell *via* a stainless-steel tubing (1.58 mm in outer dimension and 0.18 mm inner dimension), and the pressure maintained at  $1000 \pm 200$  psi by means of a back-pressure valve (Swagelok, Johannesburg, South Africa). The extract was made to pass through a cooling coil and collected into a 50 mL centrifuge tube up to the 50 mL mark. Two (2) mL of the extracts were filtered through a 0.22  $\mu$ m PVDF syringe filter into a 2 mL HPLC vial for subsequent analysis on UHPLC-MS/MS.

### ***Solvent extraction***

Solvent extraction was performed using the method of Majeed *et al.* (2018). Briefly, five (5) grams of samples were spiked with internal standards, DOM (1  $\mu$ g/kg) and ZAN (1  $\mu$ g/kg), prior to extraction. For the extraction, 20 mL of extraction solvent, acetonitrile/water/acetic acid (79/20/1, v/v/v), was added to the spiked samples, agitated for 1 h on an overhead shaker (AG 6A, Exacta, Mery sour Oise, France) and centrifuged for 15 min at 3,300 g using an IEC Central (type MP4) centrifuge (VWR International, Leuven Belgium). The supernatant was passed through a pre-conditioned (10 mL of the extraction solvent) octadecyl (C18) solid phase extraction (SPE) column (Grace octadecyl C18, Lokeren, Belgium) under gravity. A second extraction was performed on the samples by adding 5 mL of extraction solvent, agitating, centrifuging and passing through the SPE column as described above. The total volume of the eluate was adjusted to 25 mL and defatted with 10 mL n-hexane. The defatted extract was split into two equal parts for further clean-up using different approaches. The first portion (10 mL defatted extract) was diluted with 20 mL acetonitrile/acetic acid (99/1, v/v) and was subjected to clean-up by a Multisep226, Afla-ZON+ multifunctional column, under gravity, followed by further column washing using 5 mL of acetonitrile/acetic acid (99/1, v/v). The second portion (10 mL defatted extract) was filtered using a Whatman glass microfilter (VWR International, Zaventem, Belgium). The first extract was combined with 2 mL of the second extract, evaporated to dryness under a stream of nitrogen gas at 40 °C. The residue was reconstituted in 150  $\mu$ L of mobile phase, methanol/water/acetic acid (57.20/41.80/1, v/v/v) and 5 mM ammonium acetate, and filtered through a 0.22  $\mu$ m Ultrafree®-MC centrifugal filter (Bedford, MA, USA) at 14,000 g for 5 min.

### 5.2.2.2 Liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS)

#### *Chromatographic separation and UHPLC-MS/MS for PHWE*

Chromatographic separation, detection and quantitation of mycotoxin levels was achieved using Shimadzu UHPLC-MS/MS 8030 equipment (Shimadzu Corporation, Tokyo, Japan). The system consisted of a chromatograph (LC-30AD Nexera) linked to an autosampler (SIL-30 AC Nexera). Two (2) microlitres of sample were injected and pumped through a Raptor™ ARC-18 column (2.7 µm, 2.1 mm × 100 mm) (Restek Corporation, Pennsylvania USA) maintained at 40 °C in a column oven (CTO-20 AC Prominence). A binary pump (LC-20AD) connected to the system was used to pump the mobile phases A (aqueous phase) and B (organic phase) through the column at a constant flow rate of 0.2 mL/min. Mobile phase A consisted of 0.1% formic acid (FA) in deionized water, and mobile phase B consisted of 0.1% FA in methanol/acetonitrile (50/50 v/v). The elution gradient program started with pumping 10% B for 0.1 min, which was steadily increased to 95% B within 8.4 min, held constant at 95% B for 3 min, initial gradient condition of 10% B re-established within 1 min, and then the column was allowed to re-equilibrate at this condition for 4.5 min prior to the next injection, making a total run time of 17 min.

Separated analytes were delivered to a Shimadzu triple-quadrupole MS model 8030 (Shimadzu Corporation, Kyoto, Japan) detector equipped with an electron spray ionization operated in positive mode (ESI<sup>+</sup>). A time-scheduled ultrafast multiple reaction monitoring (MRM) MS method was used for the quantification and identification of the analytes of interest. To improve specificity and confidence in analytical detection, two MRM-transitions were monitored per analyte. The desolvation line (DL) temperature was 250 °C, heat block temperature was 400 °C, drying gas flow rate was 15 L/min, and interface nebulizing gas flow rate was 3 L/min. The Shimadzu LabSolutions software was used for subsequent data visualization and analysis. The optimized chromatographic and MS method parameters of the 15 mycotoxins under investigation are presented in Table 5.2.

**Table 5.2:** MRM transitions, optimized MS conditions and retention times of mycotoxins.

S/No	Mycotoxin	Ret. time (min)	Precursor (mz)	Products (mz)	Q1 Pre bias (V)	CE (eV)	Q3 Pre bias (V)
1.	AFB <sub>1</sub>	8.25	313.00	241.00*	-22.00	-41.00	-23.00
				285.10	-22.00	-24.00	-29.00
2.	AFB <sub>2</sub>	8.01	315.00	259.10*	-22.00	-31.00	-25.00

S/No	Mycotoxin	Ret. time (min)	Precursor (mz)	Products (mz)	Q1 Pre bias (V)	CE (eV)	Q3 Pre bias (V)
				287.00	-23.00	-26.00	-30.00
3.	AFG <sub>1</sub>	7.77	329.00	243.00*	-12.00	-28.00	-23.00
				311.10	-16.00	-24.00	-14.00
4.	AFG <sub>2</sub>	7.17	331.00	245.10*	-12.00	-32.00	-24.00
				313.00	-12.00	-24.00	-20.00
5.	AME	10.13	273.00	128.10*	-10.00	-49.00	-21.00
				115.05	-18.00	-54.00	-19.00
6.	FB <sub>1</sub>	7.97	722.20	352.20*	-34.00	-42.00	-11.00
				334.30	-20.00	-42.00	-11.00
7.	FB <sub>2</sub>	8.95	706.10	336.30*	-20.00	-38.00	-22.00
				318.30	-26.00	-41.00	-22.00
8.	FB <sub>3</sub>	8.75	706.30	336.30*	-40.00	-39.00	-11.00
				354.40	-20.00	-35.00	-24.00
9.	OTA	10.13	403.80	239.00*	-15.00	-27.00	-24.00
				221.00	-12.00	-38.00	-21.00
10.	OTB	9.33	370.10	205.00*	-13.00	-22.00	-21.00
				324.10	-13.00	-14.00	-22.00
11.	STEG	10.45	324.90	310.00*	-22.00	-24.00	-30.00
				281.10	-22.00	-40.00	-27.00
12.	T-2	9.67	467.20	245.10*	-13.00	-11.00	-16.00
				305.20	-22.00	-11.00	-20.00
13.	ZEA	10.06	319.10	185.00*	-12.00	-27.00	-30.00
				187.10	-15.00	-21.00	-19.00
14.	$\alpha$ -ZEL	9.42	323.10	277.20*	-17.00	-17.00	-18.00
				305.20	-24.00	-9.000	-20.00
15.	$\beta$ -ZEL	8.95	323.10	277.20*	-16.00	-16.00	-18.00
				305.20	-16.00	-11.00	-20.00

Key: S/No: serial number. Ret. Time: retention time. Q1 Pre bias: quadruple one pre-rod bias. Q3 Pre bias: quadruple three pre-rod bias. CE: collision energy. \* Quantitative product ion. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>, AFB<sub>2</sub>: aflatoxin B<sub>2</sub>, AFG<sub>1</sub>: aflatoxin G<sub>1</sub>, AFG<sub>2</sub>: aflatoxin G<sub>2</sub>, AME: alternariol monomethyl ether, FB<sub>1</sub>: fumonisin B<sub>1</sub>, FB<sub>2</sub>: fumonisin B<sub>2</sub>, FB<sub>3</sub>: fumonisin B<sub>3</sub>, OTA: ochratoxin A, OTB: ochratoxin B, STEG: sterigmatocystin, T-2: T-2 toxin, ZEA: zearalenone.  $\alpha$ -ZEL:  $\alpha$ -zearalenol.  $\beta$ -ZEL:  $\beta$ -zearalenol.

### ***Chromatographic separation and LC-MS/MS for solvent extraction***

A Waters Acquity UPLC system (Waters, Milford, MA, USA) linked to a Waters Micromass Quattro Micro triple-quadrupole mass spectrometer (Waters, Milford, MA, USA), was used for chromatographic separation, detection and quantification of the extracts obtained from the solvent extraction. The above described LC-MS/MS system was equipped with a Waters Symmetry C18 analytical column (5  $\mu$ m, 2.1  $\times$  150 mm) and a Waters Sentry guard column (3.5  $\mu$ m 2.1  $\times$  10 mm)

purchased from the same vendor. The column oven was kept at room temperature (25 °C), and 20 µL of sample was injected into the column. The aqueous part of the mobile phase (*i.e.*, mobile phase A) consisted of water/methanol/acetic acid (94/5/1, v/v/v) and 5 mM ammonium acetate, and the organic part of the mobile phase (*i.e.*, mobile phase B) consisted of methanol/water/acetic acid (97/2/1, v/v/v) and 5 mM, ammonium acetate. The gradient elution program and MS parameters are as described by Monbaliu *et al.* (2009).

### 5.2.2.3 Validation of the modified PHWE method for multi-mycotoxin extraction

The effects of the cereal-matrix components on the analytical signals of the different mycotoxins in the MS were determined using the signal suppression/enhancement method described by Arroyo-Manzanares *et al.* (2018) and Sulyok *et al.* (2006). Calibration curves were plotted for standards prepared in analyte-free sample extracts, as well as for standards prepared in neat organic solvents (100% methanol). Matrix-effect (ME) was determined as the percentage ratio of the difference between the slope of matrix-matched calibration curve and neat standards calibration curve divided by the slope of neat standards calibration curve (Equation 5.1).

$$ME = \frac{Slope_m - Slope_n}{Slope_n} \times 100 \quad \text{Equation 5.1}$$

Where *ME* is the matrix effect, *Slope<sub>m</sub>* is the slope of calibration curve of standards prepared in sample extracts and *Slope<sub>n</sub>* is the slope of standards prepared in neat solvent.

The limits of detection (LOD) and limits of quantification (LOQ) (Equation 5.2) of the mycotoxins were determined using the signal-to-noise ratio of the matrix-matched standards as described by Kim *et al.* (2017). Linearity was determined by least-square regression of a 6-point matrix-matched calibration curve within the ranges of 9 to 5,000 µg/kg depending on the mycotoxin. Recovery efficiency of the method was determined by spiking analyte-free samples with known concentrations of mycotoxins, extracting the analytes the same day using PHWE as described above. The percentage ratio of post-extraction concentration (recovered concentration) to that of pre-extraction concentration (initial concentration) was taken as the recovery value (Equation 5.3) (Arroyo-Manzanares *et al.*, 2018).

$$Limit_{DQ} = F \times \left[ \frac{C}{\left(\frac{S}{N}\right)} \right] \quad \text{Equation 5.2}$$



$$\text{Recovery (\%)} = \frac{E_r}{E_i} \times 100 \quad \text{Equation 5.3}$$

Where  $Limit_{DQ}$  is the  $LOD$  or  $LOQ$  depending on the value of the multiplication factor  $F$ , which is 3.33 for  $LOD$  and 10 for  $LOQ$ .  $C$  is the concentration, while  $S$  is the signal at concentration  $C$ , and  $N$  is the noise level at similar concentration.  $E_r$  is the recovered concentration after spiking, and  $E_i$  is the spiked concentration.

#### 5.2.2.4 Multivariate discriminant analysis

The pre-processed data set was subjected to multivariate discriminant analysis in order to scrutinize for discriminatory patterns between the two extraction methods. Using the SIMCA-P<sup>+</sup> 14.0 chemometrics software (Umetrics, MKS Instruments Inc., Sweden), the data was mean-centered, Pareto-scaled (Aliferis *et al.*, 2010) and subjected to PCA and OPLSD-DA analysis in order to extract maximum information from the data set. The adopted models, PCA and OPLS-DA, are advanced dimensionality reduction tools which highlights contrasts or similarities between data groups *via* construction of few interpretable linearly uncorrelated variables called latent variable or principal components from the dataset (Worley & Powers, 2013). PCA does not supervise the construction of latent variables from the dataset while the OPLS-DA supervises the construction of latent variables from the dataset (Aliferis *et al.*, 2010; Worley & Powers, 2013).

For the OPLS-DA model, the data variables were classified into two major groups depending on the adopted method of analysis, either PHWE or solvent extraction. This was critical because, OPLS-DA is a supervised model, as such, information regarding variable class member is a prerequisite for location of the principal components. Usually, OPLS-DA is best applicable when there are only two classification groups in the data set, such as a control group and a dependent group. As such, classification of the data set into two groups permitted the extraction of a between-class variation referred to as the Y-predictive block, and a within-class variation referred to as the Y-orthogonal block or uncorrelated variation (Song *et al.*, 2013). By doing so, OPLS-DA maximizes the discrimination of the two groups of variables and provides an improved model interpretability without modifying its predictive power (Trygg & Wold, 2002).

For the evaluation of model performances, the quantitative *goodness-of-fit* parameters *i.e.*,  $R2X(\text{cum})$  and  $Q2X(\text{cum})$  values, and the *goodness-of-prediction* parameters *i.e.*, the  $Q2(\text{cum})$

values, were calculated. The  $R^2X(\text{cum})$  and  $Q^2X(\text{cum})$  values for the PCA model were used to measure the degree to which the latent structures (*i.e.*, principal components) describe the variations and patterns in the data set (Worley & Powers, 2013). Whereas for the OPLS-DA model, the  $R^2X(\text{cum})$  was used to estimate the cumulative fraction of the variation of the  $X$  variables explained by the model,  $R^2Y(\text{cum})$  was used to measure the cumulative ratio of the variation of the  $Y$  variables explained by the model, and the  $Q^2(\text{cum})$  estimated the cumulative predictive capacity of the full model (Aliferis *et al.*, 2010; Matthews *et al.*, 2012). For internal validation of the OPLS-DA models to assess the statistical significance of the model, the goodness-of-fit and goodness-of-prediction of the OPLS-DA model was compared with those of 100 random  $Y$ -permuted models, which generates a distribution of  $Q^2$  values that are suitable for testing the null hypothesis for a model's  $Q^2$  (Worley & Powers, 2013; Zhang *et al.*, 2015b).

### 5.3 Results and discussion

Pressurized hot water extraction, a 'novel' green extraction technique was adopted for the analysis of multi-mycotoxin in 91 samples of maize, sorghum and millet intended for human consumption obtained from different agroecological zones in Nigeria as described in Section 5.2.2.1. In order to authenticate the PHWE method, a method validation was performed, as well as, a comparison with a solvent-based extraction method.

#### 5.3.1 Method validation and comparative evaluation of PHWE and solvent extraction

The results of PHWE method validation in comparison with solvent extraction is presented in Appendix 5.A and Table 5.3. In order to compensate for matrix effects, matrix-matched calibrations were adopted for quantification of the mycotoxin concentrations in the samples for the two methods.

##### 5.3.1.1 Validation of PHWE and solvent extraction

The performances of both methods showed good consistency with EC, AOAC, and ICH guidelines (EC, 2002; Shabir, 2005; Commission Regulation, 2006a; AOAC, 2009; Arroyo-Manzanares *et al.*, 2018). The linearity correlation ( $R^2$ ) of PHWE ranged from 0.98 to 1.00 for the 15 mycotoxins in all 3 sample matrices within the linear ranges of 60 to 2,000  $\mu\text{g}/\text{kg}$  for  $\text{FB}_1$ , 16 to 500  $\mu\text{g}/\text{kg}$  for  $\text{FB}_2$ , 10 to 300  $\mu\text{g}/\text{kg}$  for  $\text{AFB}_1$  and 30 to 1,000  $\mu\text{g}/\text{kg}$  for the other analytes (Appendix 5.A). The

benchmark for the acceptance of linearity of  $R^2$  equal or higher than 0.95 by the International Conference on Harmonization (ICH) was fulfilled for all understudied analytes (Shabir, 2005), though there existed a significant difference ( $p \leq 0.05$ ) in the linearities of the two methods. The sensitivity of the methods was determined by assessing the LOD's and LOQ's of the method for each of the mycotoxins. For PHWE, the LOD's and LOQ's ranged respectively from 0.06 to 41  $\mu\text{g}/\text{kg}$  and 0.32 to 123  $\mu\text{g}/\text{kg}$  for maize, 0.07 to 98  $\mu\text{g}/\text{kg}$  and 0.21 to 295  $\mu\text{g}/\text{kg}$  for sorghum, and 0 to 26  $\mu\text{g}/\text{kg}$  and 0.01 to 79  $\mu\text{g}/\text{kg}$  for millet (Table 5.3). These values were sufficiently low for detection and quantitation of small amounts of the analytes under investigation in cereal grains (Chilaka *et al.*, 2016; Kim *et al.*, 2017), as such, trace amounts of the analytes in the sample extracts can be quantitatively reported with a high degree of confidence. There was no statistically significant difference ( $p \leq 0.05$ ) between the LOD's and LOQ's of PHWE and the solvent extraction method.

The recovery rates of the 15 mycotoxins varied from 74 to 126% in maize, 73 to 115% in sorghum and 67 to 133% in millet for PHWE, which is not far from the AOAC recommendations of between 60% to 125% for foodstuff contaminated with 10  $\mu\text{g}/\text{kg}$  of mycotoxins, and the EC recommendations of 60 and 130% (Commission Regulation, 2006a; Arroyo-Manzanares *et al.*, 2018). The recovery rates for the solvent extraction method varied from 99 to 100% for maize, 100 to 101% in sorghum, and 100 to 102% for millet. Though the recoveries of the solvent extraction method were more consistent and closer to 100%, when compared to those of PHWE using the Independent Sample's T-test at a 95% probability, there existed no statistically significant differences in the mean recoveries of the two methods. The RSDr values for all the analytes in maize, sorghum and millet matrices ranged from 2 to 19% for PHWE and satisfied the guideline criterion of  $<25\%$  by CODEX and the EC (Commission Regulation, 2006a; AOAC, 2009; Arroyo-Manzanares *et al.*, 2018). In comparison with the RSD values for the solvent extraction, those of maize ranged from 0 to 5% and 5 to 20% for sorghum. These values were significantly different ( $p \leq 0.05$ ) from the corresponding RSD values for PHWE while those of millet (3 to 15%) were not significantly different ( $p > 0.05$ ).

**Table 5.3:** Method validation parameters for PHWE and solvent extraction<sup>#</sup> of multi-mycotoxin in maize, sorghum and millet matrices.

Mycotoxin	Maize				Sorghum				Millet			
	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)
AFB <sub>1</sub>	0.94	2.8	108	3.1	0.37	1.1	104	1.7	2.2	6.6	97	10
	0.28 <sup>#</sup>	0.9 <sup>#</sup>	100 <sup>#</sup>	1.6 <sup>#</sup>	0.89 <sup>#</sup>	2.7 <sup>#</sup>	101 <sup>#</sup>	6.4 <sup>#</sup>	2.0 <sup>#</sup>	6.0 <sup>#</sup>	101 <sup>#</sup>	5.3 <sup>#</sup>
AFB <sub>2</sub>	0.08	0.25	98	12	0.07	0.20	108	3.2	1.0	3.1	72	9.0
	0.04 <sup>#</sup>	0.13 <sup>#</sup>	100 <sup>#</sup>	0 <sup>#</sup>	0.76 <sup>#</sup>	2.3 <sup>#</sup>	101 <sup>#</sup>	11 <sup>#</sup>	3.4 <sup>#</sup>	10 <sup>#</sup>	101 <sup>#</sup>	8.0 <sup>#</sup>
AFG <sub>1</sub>	0.43	1.3	126	13	1.2	3.7	125	4.3	2.7	8.2	96	8.3
	0.13 <sup>#</sup>	0.38 <sup>#</sup>	100 <sup>#</sup>	0.83 <sup>#</sup>	0.27 <sup>#</sup>	0.80 <sup>#</sup>	101 <sup>#</sup>	9.6 <sup>#</sup>	1.0 <sup>#</sup>	2.9 <sup>#</sup>	100 <sup>#</sup>	4.1 <sup>#</sup>
AFG <sub>2</sub>	1.2	3.6	107	8.2	1.2	3.7	115	2.6	2.7	8.1	85	6.5
	4.2 <sup>#</sup>	13 <sup>#</sup>	100 <sup>#</sup>	0.85 <sup>#</sup>	1.7 <sup>#</sup>	4.9 <sup>#</sup>	102 <sup>#</sup>	11 <sup>#</sup>	7.3 <sup>#</sup>	22 <sup>#</sup>	100 <sup>#</sup>	6.4 <sup>#</sup>
AME	2.4	7.2	77	11	5.7	17	79	11	26	78	72	14
	0.86 <sup>#</sup>	2.6 <sup>#</sup>	100 <sup>#</sup>	2.9 <sup>#</sup>	3.9 <sup>#</sup>	12 <sup>#</sup>	101 <sup>#</sup>	5.3 <sup>#</sup>	6.8 <sup>#</sup>	21 <sup>#</sup>	101 <sup>#</sup>	7.8 <sup>#</sup>
FB <sub>1</sub>	2.3	6.8	111	9.6	1.1	3.2	81	2.9	2.2	6.5	133	6.8
	1.3 <sup>#</sup>	3.8 <sup>#</sup>	100 <sup>#</sup>	2.7 <sup>#</sup>	1.3 <sup>#</sup>	3.9 <sup>#</sup>	101 <sup>#</sup>	8.6 <sup>#</sup>	5.1 <sup>#</sup>	15 <sup>#</sup>	102 <sup>#</sup>	9.4 <sup>#</sup>
FB <sub>2</sub>	4.3	13	89	1.7	7.3	22	78	5.2	0	0.01	119	11
	3.3 <sup>#</sup>	9.8 <sup>#</sup>	100 <sup>#</sup>	1.8 <sup>#</sup>	4.7 <sup>#</sup>	14 <sup>#</sup>	101 <sup>#</sup>	7.0 <sup>#</sup>	5.6 <sup>#</sup>	17 <sup>#</sup>	102 <sup>#</sup>	11 <sup>#</sup>
FB <sub>3</sub>	0.06	0.18	95	5.5	0.07	0.20	84	6.3	0.0	0.01	72	8.3
	2.7 <sup>#</sup>	8.2 <sup>#</sup>	100 <sup>#</sup>	0.77 <sup>#</sup>	0.63 <sup>#</sup>	1.9 <sup>#</sup>	101 <sup>#</sup>	8.0 <sup>#</sup>	1.3 <sup>#</sup>	4.0 <sup>#</sup>	102 <sup>#</sup>	14 <sup>#</sup>
OTA	0.44	1.3	75	8.8	0.17	0.50	72	8.9	0.40	1.2	67	12
	0.32 <sup>#</sup>	0.95 <sup>#</sup>	100 <sup>#</sup>	1.4 <sup>#</sup>	1.1 <sup>#</sup>	3.3 <sup>#</sup>	101 <sup>#</sup>	7.8 <sup>#</sup>	0.54 <sup>#</sup>	1.6 <sup>#</sup>	100 <sup>#</sup>	8.3 <sup>#</sup>
OTB	0.11	0.32	77	6.3	0.07	0.21	79	4.9	0.18	0.55	72	7.9
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
STEG	0.50	1.5	95	8.7	0.33	0.99	90	3.2	1.6	4.7	92	13
	0.07 <sup>#</sup>	0.21 <sup>#</sup>	100 <sup>#</sup>	1.6 <sup>#</sup>	0.68 <sup>#</sup>	2.1 <sup>#</sup>	101 <sup>#</sup>	5.4 <sup>#</sup>	1.4 <sup>#</sup>	4.3 <sup>#</sup>	100 <sup>#</sup>	3.1 <sup>#</sup>
T-2	0.04	0.13	87	16	0.07	0.20	84	6.2	1.1	3.4	69	12

Mycotoxin	Maize				Sorghum				Millet			
	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)	LOD (µg/kg)	LOQ (µg/kg)	Recovery (%)	RSDr (%)
	0.86 <sup>#</sup>	2.6 <sup>#</sup>	100 <sup>#</sup>	1.1 <sup>#</sup>	2.5 <sup>#</sup>	7.4 <sup>#</sup>	101 <sup>#</sup>	6.6 <sup>#</sup>	2.6 <sup>#</sup>	7.7 <sup>#</sup>	100 <sup>#</sup>	5.8 <sup>#</sup>
ZEA	1.6	4.9	80	9.8	0.88	2.6	93	3.4	20	59	83	9.5
	4.2 <sup>#</sup>	13 <sup>#</sup>	99 <sup>#</sup>	4.7 <sup>#</sup>	15 <sup>#</sup>	44 <sup>#</sup>	102 <sup>#</sup>	20 <sup>#</sup>	16 <sup>#</sup>	47 <sup>#</sup>	102 <sup>#</sup>	15 <sup>#</sup>
α-ZEL	41	123	84	19	60	180	73	5.3	26	79	100	13
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
β-ZEL	12	36	74	7.4	17	50	83	4.1	14	42	73	12
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
Mean	1.2	3.6	96	8.9	1.5	4.6	93	4.9	5.0	15	88	10
	1.5 <sup>#</sup>	4.6 <sup>#</sup>	100 <sup>#</sup>	1.7 <sup>#</sup>	2.7 <sup>#</sup>	8.2 <sup>#</sup>	101 <sup>#</sup>	8.8 <sup>#</sup>	4.4 <sup>#</sup>	13 <sup>#</sup>	101 <sup>#</sup>	8.1 <sup>#</sup>
Sig. (2-tailed)	0.59	0.58	0.34	0	0.38	0.38	0.12	0.01	0.83	0.83	0.06	0.15

Key: <sup>#</sup> Parameter values for solvent extraction. ND: not determined. Recovery values are presented mean of duplicate determinations ± standard deviation of mean. LOD: Limit of detection; LOQ: Limit of quantification. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.

In general, there was less variability in the validation parameters (*i.e.*, recovery, linearity and RSD) of the solvent extraction method as compared to those of PHWE. This could be due to the fact that the solvent extraction method involved multiple clean-up steps (defatting and two SPE purification procedures using different SPE cartridges). This was in addition to the use of two internal standards to correct for loss of analytes during the sample preparation or injection steps in the analytical process. On the other hand, PHWE was designed with the aim of reduction of cost and the amount of harmful organic solvents used during extraction and increased speed of the analytical process. Forfeiture of a clean-up step facilitated the achievement of these objectives. This however contributed to the higher variations observed in the PHWE analytical results, which was not unexpected. Such variations are negligible provided they were within the acceptable limits stipulated by regulatory bodies (Anklam *et al.*, 2002; Commission Regulation, 2006a; AOAC, 2009; CODEX, 2015; FDA, 2015; Arroyo-Manzanares *et al.*, 2018). As would be discussed in the succeeding sections of this chapter, the overall variations between the two analytical procedures have been shown to be statistically insignificant.

### **5.3.1.2 Comparative evaluation of PHWE and solvent extraction**

Principal component analysis (PCA) and orthogonal projection to latent structures discriminant analysis (OPLS-DA) approaches were adopted to scrutinize the entire data set (*i.e.*, combined data from method validation and samples analysis) for inherent global discriminatory patterns such as multiple pairwise correlations and/or co-variances between the data obtained by the two extraction methods, which may not be readily observed by using conventional statistical analysis.

#### **5.3.1.2.1 Discriminatory analysis of PHWE and solvent extraction methods using PCA and OPLS-DA**

The results of the PCA and OPLS-DA analysis of the data and their corresponding model-fit quality parameters are shown in Table 5.4 and Figure 5.1. PCA was used for an initial screening of the overall structure of the data set for discriminatory patterns and detection of outliers. The results revealed a single latent variable, which indicated there were no differential patterns between the variables pertaining to PHWE and corresponding variables pertaining to the solvent extraction. Notwithstanding, the PCA model accounted for 97% of the variations in the data set [*i.e.*,

$R^2X(\text{cum})=0.97$ ], with a predictive ability of 77% [*i.e.*,  $Q^2X(\text{cum})=0.77$ ]. This observation was in agreement with the results of the Independent Samples T-test performed on each of the variables from the two extraction methods (Tables 5.3 & 5.5, and Appendix 5.A), where it was observed that the majority of the variables were not significantly different ( $p>0.05$ ).

**Table 5.4:** Summary of PCA-X model and OPLS-DA models with the corresponding model validation parameters

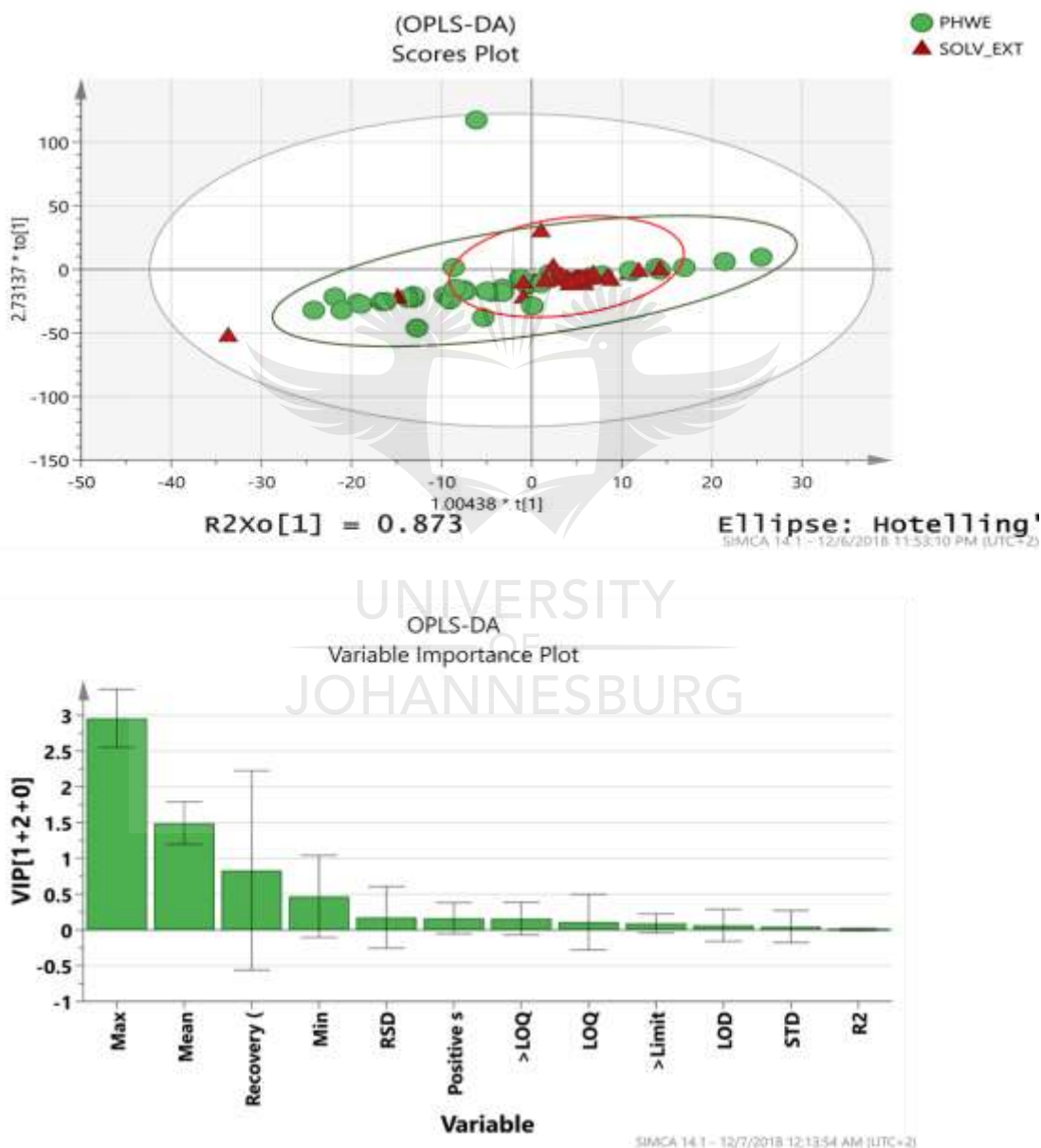
Model	Data classification	Number of observations	Number of components	$R^2X(\text{cum})$	$R^2Y(\text{cum})$	$Q^2(\text{cum})$
PCA	None	84 (X=14, Y=2)	1	0.97	-	0.77
OPLS-DA	PHWE & SOLV-EXT	84 (X=14, Y=2)	1 predictive and 2 orthogonal	0.99	-0.11	0.05

**Key:** PCA-principal component analysis. OPLS-DA-orthogonal projection to latent structures discriminate analysis. PHWE-pressurized hot water extraction. SOLV-EXT-solvent extraction

Since PCA does not take into account the classification label associated with the data set, discrimination of the data groups is not maximized. This problem is solved by the OPLS-DA model which supervises the construction of the latent variables, hence, yielding a more class-specific discrimination of the data. Results of the OPLS-DA analysis showed the construction of 2 explanatory and 1 predictive principal component with a 99% total explained variation in X [*i.e.*,  $R^2X(\text{cum})=0.99$ ]. However, the model could not account for the cumulative variations in Y [ $R^2Y(\text{cum})=-0.11$ ], and the total amount of predicted variability in the full model was low [*i.e.*,  $Q^2(\text{cum})=0.05$ ]. As such, despite the OPLS-DA models making reference to the pre-defined sample class membership in order to maximize separation of the data, there was no clear separation of the data groups. A pattern which can be more clearly visualized on the OPLS-DA scores plot (Figure 5.1). On this score plot, the green circular dots represent variables of the PHWE class, while the red triangular dots represent variables of the solvent extraction (*i.e.*, SOLV-EXT) class. Variables from the two data groups can be seen clustered together towards the middle of the plot and while some arbitrarily distributed across the graph. This is an indication of intrinsic similarities and randomness in the patterns within and between the groups.



This observation is in strong agreement to the results of PCA analysis as well as the Independent Sample's T-test. Overall, PHWE compared well with the solvent-based extraction method, and other validated methods for multi-mycotoxin extraction reported in literature (Sulyok *et al.*, 2006; Lattanzio *et al.*, 2014; Kim *et al.*, 2017; Arroyo-Manzanares *et al.*, 2018). Hence, considering its good validation performance, it was deemed adequate for investigating the natural occurrence of mycotoxins in food commodities.



**Figure 5.1:** OPLS-DA scores plot and variable importance plot (VIP) plot for discriminate analysis of PHWE and solvent extraction.

### 5.3.2 Mycotoxin contamination of staple cereals

The above validated PHWE method together with the solvent extraction method was used for the screening of 15 different mycotoxin in samples of maize (n=16), sorghum (n=38) and millet (n=37) obtained from six agroecological zones from Nigeria (Table 5.5). Only samples contaminated with mycotoxins at levels above the respective LODs were considered positive. The minor differences between the results from the two extraction methods, are possibly due to the differences in the LOD's and LOQ's, as well as the recovery rates of the two methods. For the sake of discussing the results, in the remaining sections of this paper, reference is made only to the results of the PHWE.

#### 5.3.2.1 Mycotoxin levels and incidence rate in maize, sorghum and millet from Nigeria

The incidence rates and levels of mycotoxin contamination in maize, sorghum and millet samples are presented in Table 5.5. All of the maize samples (n=16), 32% (n=38) of sorghum and 35% (n=37) of millet samples were non-complaint, *i.e.*, were positive for at least one of the 15 tested mycotoxins. Fumonisin, in particular FB<sub>1</sub> had the highest prevalence in terms of rate of occurrence and levels of contamination in all three cereals. All the maize samples (n=16) were positive for FBs with contamination levels ranging from 17 to 7,947 µg/kg for FB<sub>1</sub> and 30 to 14,603 µg/kg for ΣFB<sub>1</sub>&FB<sub>2</sub>. Out of the 16 analyzed maize samples, 7 samples (*i.e.*, 44%) contained ΣFB<sub>1</sub>&FB<sub>2</sub> at levels above the maximum levels of 4,000 µg/kg in unprocessed maize stipulated by the European Commission (EC) and CODEX (EC, 2007; WHO, 2017; Arroyo-Manzanares *et al.*, 2018). Previous studies have equally reported high incidence rates and levels of FBs contamination in maize from Nigeria (Afolabi *et al.*, 2006; Adetunji *et al.*, 2014). Bankole and Mabekoje (2004) found that FB<sub>1</sub> was the predominant mycotoxin, occurring in 79% of samples of maize obtained from a similar region from Nigeria as we sampled (Southern Nigeria).

Such high incidence rates and even higher levels of FBs contamination have likewise been reported in other West African countries. Ngoko *et al.* (2001) found FB<sub>1</sub> in 16 out of 18 maize samples from Cameroon at levels within the range 300 to 26,000 µg/kg. Fumonisin occurred in sorghum samples at relatively lower levels, with a mean value of 17 µg/kg and maximum value of 248 µg/kg for ΣFB<sub>1</sub>&FB<sub>2</sub>, while, no FBs contamination was recorded in millet samples. Chilaka *et al.* (2016) reported a mean value of 83 µg/kg and a maximum value of 180 µg/kg for ΣFB<sub>1</sub>&FB<sub>2</sub> in

sorghum. The International Agency for Research on Cancer (IARC) has classified FB<sub>1</sub> as a group 2B carcinogen (possibly carcinogenic to humans) (IARC, 2002). Consumption of foods contaminated with FBs have been directly linked with upper gastro-intestinal tract cancer (Soriano and Dragacci, 2004). Moreover, FBs are also nephrotoxic, hepatotoxic, immunosuppressive, atherogenic and embryotoxic in experimental animal systems (Nair, 1998).

AFs contamination was also relatively high in the cereal samples. In maize, levels for AFB<sub>1</sub> ranged from 6.5 to 315 µg/kg, with a mean of 54 µg/kg, while ΣAFs ranged from 16 to 323 µg/kg. Sixty-nine percent (n=16) of the maize samples were contaminated above the maximum level of 2 and 4 µg/kg for AFB<sub>1</sub> and ΣAFs, respectively, stipulated by the European Commission (EC) (Commission Regulation, 2006b; Arroyo-Manzanares *et al.*, 2018). These levels are similar to those reported by Bandyopadhyay *et al.* (2007), who reported ΣAFs contamination ranging from 1.1 to 480 µg/kg and a mean of 36 µg/kg in freshly harvested maize in Nigeria. In sorghum, 8% of samples were above the EC limits for AFB<sub>1</sub> (2 µg/kg) and ΣAFs (4 µg/kg), respectively, whereas, 5% of millet samples exceeded similar limits for AFB<sub>1</sub> and ΣAFs. Aflatoxin B<sub>2</sub>, AFG<sub>1</sub> and AFG<sub>2</sub> were not detected in any of the millet samples, however, the observed levels for AFB<sub>1</sub> (5.5 to 50 µg/kg) were in agreement to those reported by Apeh *et al.* (2016) (1.1 to 15 µg/kg) in millet grain from Nigeria. Observed levels for ΣAFs in sorghum (15 to 116 µg/kg) were less than those reported by Makun *et al.* (2009) (<LOQ to 1,164 µg/kg) in stored sorghum samples. This could be due to variations in fungi colonization of crops over different years which could be stimulated by annual variations in temperature and rainfall, in addition to other climatic conditions (Streit *et al.*, 2013; Guerre, 2016). Generally, AFs were more prevalent in maize, followed by sorghum and then millet. A similar trend was observed by Bandyopadhyay *et al.* (2007), in their study on the relative severity of AFs contamination of cereal crops in West Africa. In fact, they observed that Nigerians consume 138 kg cereals annually, and if the main cereal is sorghum instead of maize, associated AF problems will be diminished 4-fold, whereas, if it is millet, then the AF-related risks will be reduced at least 8-fold (Bandyopadhyay *et al.*, 2007). Diversification of diets, instead of diets that are heavily dependent on maize could greatly reduce exposure to AFs and their consequent health-related problems. Aflatoxins are highly carcinogenic and are equally recognized as being immunosuppressive. Among the AFs group, AFB<sub>1</sub> is considered the most toxic, and has been identified as the most potent naturally occurring carcinogen known to man (IARC, 2002; D'Mello, 2003).

**Table 5.5:** Mycotoxin contamination of maize, sorghum and millet from Nigeria using PHWE and solvent extraction<sup>#</sup>.

Mycotoxin	Maize (n=16)					Sorghum (n=38)					Millet (n=37)				
	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)
*AFB <sub>1</sub>	69	54	6.5-315	69	69	8	3.6	7.3-116	8	8	5	2.4	38-50	5	5
	44 <sup>#</sup>	18 <sup>#</sup>	15-74 <sup>#</sup>	44 <sup>#</sup>	44 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	3 <sup>#</sup>	0.33 <sup>#</sup>	<LOQ-9.4 <sup>#</sup>	3 <sup>#</sup>	3 <sup>#</sup>
AFB <sub>2</sub>	69	1.3	0.31-7.8	63	0	0	0 <sup>#</sup>	<LOQ	0	0	0	0	<LOQ	0	0
	44 <sup>#</sup>	7.0 <sup>#</sup>	3.3-13 <sup>#</sup>	44 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
AFG <sub>1</sub>	0	0	<LOQ	0	0	3	0.19	<LOQ-7.3	3	0	0	0	<LOQ	0	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
AFG <sub>2</sub>	0	0	<LOQ	0	0	0	0	<LOQ	0	0	0	0	<LOQ	0	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
*ΣAFs	69	56	16-323	50	69	8	3.8	15-116	8	8	5	2.4	38-50	5	5
	44 <sup>#</sup>	21 <sup>#</sup>	18-83 <sup>#</sup>	44 <sup>#</sup>	44 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	3 <sup>#</sup>	0.67 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	3 <sup>#</sup>
AME	0	0	<LOQ	0	0	3	0.99	<LOQ-38	3	0	8	21	128-343	8	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	3 <sup>#</sup>	0.89 <sup>#</sup>	<LOQ-34 <sup>#</sup>	3 <sup>#</sup>	0 <sup>#</sup>	16 <sup>#</sup>	8.5 <sup>#</sup>	24-117 <sup>#</sup>	16 <sup>#</sup>	0 <sup>#</sup>
*FB <sub>1</sub>	100	2,033	17-7,947	100	0	8	17	188-248	8	0	0	0	<LOQ	0	0
	94 <sup>#</sup>	1,644 <sup>#</sup>	68-7,105 <sup>#</sup>	94 <sup>#</sup>	0 <sup>#</sup>	5 <sup>#</sup>	6.8 <sup>#</sup>	97-159 <sup>#</sup>	5 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
FB <sub>2</sub>	100	1,525	37-5,961	94	6	0	0	<LOQ	0	0	0	0	<LOQ	0	0
	88 <sup>#</sup>	527 <sup>#</sup>	57-2,074 <sup>#</sup>	88 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
FB <sub>3</sub>	94	292	7.5-767	94	0	3	0.41	<LOQ -16	3	0	0	0	<LOQ	0	0
	81 <sup>#</sup>	186 <sup>#</sup>	33-689 <sup>#</sup>	81 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
*ΣFB <sub>1</sub> &B <sub>2</sub>	100	3,851	30-1,460	100	44	8	17	188-248	8	0	0	0	<LOQ	0	0
	94 <sup>#</sup>	2,171 <sup>#</sup>	68-9,179 <sup>#</sup>	94 <sup>#</sup>	19 <sup>#</sup>	5 <sup>#</sup>	6.8 <sup>#</sup>	97-159 <sup>#</sup>	5 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
*OTA	31	8.3	6.5-54	31	31	5	0.59	7.5-15	5	5	5	0.73	6.9-20	5	5
	13 <sup>#</sup>	4.0 <sup>#</sup>	4.7-54 <sup>#</sup>	13 <sup>#</sup>	6 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
OTB	13	1.5	7.8-17	13	0	3	0.20	<LOQ -7.5	3	0	5	0.37	6.8-6.9	5	0
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
ΣOTs	31	9.8	6.5-58	31	0	5	0.79	7.5-23	5	0	5	1.1	14-27	5	0
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>

Mycotoxin	Maize (n=16)					Sorghum (n=38)					Millet (n=37)				
	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)	Positive samples (%)	Mean* (µg/kg)	Range (µg/kg)	Samples >LOQ (%)	Samples >Limit (%)
STEG	13	0.86	6.5-7.3	13	0	13	15	1.9-330	13	0	24	7.4	5.0-208	14	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	13 <sup>#</sup>	18 <sup>#</sup>	9.9-272 <sup>#</sup>	13 <sup>#</sup>	0 <sup>#</sup>	5 <sup>#</sup>	6.9 <sup>#</sup>	5.0-188 <sup>#</sup>	5 <sup>#</sup>	0 <sup>#</sup>
*T-2	0	0	<LOQ	0	0	3	0.20	<LOQ -7.5	3	0	3	0.65	<LOQ-23	3	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
*ZEA	19	3.5	7.4-33	19	0	11	1.1	4.8-22	11	0	14	12	80-94	8	0
	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>	5 <sup>#</sup>	1.5 <sup>#</sup>	<LOQ <sup>#</sup>	0 <sup>#</sup>	0 <sup>#</sup>
α-ZEL	31	31	<LOQ-140	6	0	5	6.5	<LOQ	0	0	0	0	<LOQ	0	0
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
β-ZEL	19	4.7	<LOQ	0	0	8	2.9	<LOQ-63	3	0	0	0	<LOQ	0	0
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>
ΣZEAs	44	39	72-155	31	0	11	10	<LOQ	0	0	14	12	80-94	8	0
	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>	ND <sup>#</sup>

Key: <sup>#</sup> Parameter values for solvent extraction. % + ve Samples: percentage of positive samples (*i.e.* samples >LOD). Mean\*: average contamination of the samples including positive (*i.e.* >LOD) and negative (*i.e.* <LOD) samples. Samples >Limit: number of samples with contamination levels above the maximum limit set by the EC. N.D.: not detected. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol. ΣZEAs: sum of ZEAs. ΣOTs: sum of OTs. ΣFB<sub>1</sub>&FB<sub>2</sub>: sum of FB<sub>1</sub> and FB<sub>2</sub>. ΣAFs: sum of AFs. \*Indicate the mycotoxins that are regulated by the EC (Arroyo-Manzanares *et al.*, 2018. Commission Recommendation, 2013, 2006b), with their respective regulatory limits as follows: AFB<sub>1</sub> in all cereals and their derived products 2 µg/kg and 4 µg/kg for ΣAFs (Commission Regulation, 2006b), ΣFB<sub>1</sub>&FB<sub>2</sub> in unprocessed maize and maize flour/meal – 4,000 µg/kg (Arroyo-Manzanares *et al.*, 2018. EC, 2007. WHO, 2017), OTA in unprocessed cereals – 5 µg/kg (Commission Regulation, 2006b), Sum of T-2 and HT-2 in unprocessed cereals – 100 µg/kg (Commission Recommendation, 2013), ZEA in unprocessed cereals other than maize – 100 µg/kg (EC, 2007) and ZEA in unprocessed maize – 350 µg/kg (EC, 2007).

Ochratoxin A was present in 31% (n=16) of the maize samples at levels ranging from 6.5 to 54 µg/kg. All positive maize samples for OTA were above the maximum level of 5 µg/kg in unprocessed cereals stipulated by the EC (Commission Regulation, 2006b). In sorghum, the levels of OTs varied from 7.5 to 15 µg/kg, while those for millet ranged from 0.75 to 20 µg/kg. Sangare-Tigori *et al.* (2006) reported higher OTA levels (17 to 204 µg/kg) in millet from the West African country of Côte d'Ivoire sampled between 1998 to 2002, which may be due to yearly variations in mycotoxin contamination patterns across the continent (Streit *et al.*, 2013; Guerre, 2016; Van der Fels-Klerx *et al.*, 2016). Exposure to OTA has been linked with nephropathy (Maaroufi *et al.*, 1995), urinary tract tumors (Gazinska *et al.*, 2012) and oxidative DNA damage leading to mutagenesis and eventually cancer (Zepnik *et al.*, 2001). Based on its carcinogenicity in animal studies, OTA has also been classified as a group 2B possible human carcinogen by the International Agency for Research on Cancer (IARC) (IARC, 1993).

The incidence rate and contamination range of ZEA in maize and sorghum and millet was 19% (7.4 to 33 µg/kg) and 11% (4.8 to 22 µg/kg), respectively. These levels are negligible when compared with the EC maximum limit of 350 µg/kg for unprocessed maize and 100 µg/kg for unprocessed cereals other than maize, respectively (EC, 2007). On the other hand, 5 out of 37 millet samples were positive for ZEA within the range 80 to 94 µg/kg, none of which exceeded the EC limits of 100 µg/kg in unprocessed cereals other than maize (EC, 2007). The ZEA analogues,  $\alpha$ -ZEL and  $\beta$ -ZEL, were also detected in at least one of maize and sorghum samples each, while none of the analogues was detected in millet samples. Chilaka *et al.* (2016) and Adetunji *et al.* (2014) reported maize and millet contamination with  $\alpha$ -ZEL and  $\beta$ -ZEL (Adetunji *et al.*, 2014; Chilaka *et al.*, 2016).

Cereal contamination by ZEAs could be a major health concern as this toxin is known to be chemically stable both during various food processing operations such as cooking, heating, fermentation, milling etc., and has been quantified in a number of processed cereal-based products from Africa (Abia *et al.*, 2013; Hueza *et al.*, 2014; Adekoya *et al.*, 2017). Zearalenone has been implicated in the manifestations of gynecomastia with testicular atrophy in rural males in Southern Africa (Shephard, 2008b). Among human populations, children are the most vulnerable to ZEA exposure and the toxin has been implicated in several incidents of precocious pubertal changes

(Zain, 2011) and other fertility problems (Sherif *et al.*, 2009). The potency of ZEA's estrogenic activity is reportedly greater than that of many naturally occurring non-steroidal estrogens (Bennett and Klich, 2003). Exposure to high concentrations of ZEA in cattle feed has been linked with enlargement of the mammary gland, infertility, reduced milk production, vaginal secretions and vaginitis particularly in young dairy heifers (Zinedine *et al.*, 2007). Whereas in swine, effects of ZEA include enlargement of the uterus, vaginal prolapse, swelling of the vulva, infertility, reduced litter size and embryonic death (Agag, 2004).

The Alternaria toxin, AME, and the trichothecene toxin, T-2, were not detected in any of the maize samples. Bankole *et al.* (2010) also reported the absence of T-2 contamination in maize from Nigeria. In sorghum (n=38) and millet (n=37) samples, T-2 occurred in 3% each, whereas, the average AME contamination was 0.99 and 21 µg/kg for sorghum and millet, respectively. Sterigmatocystin occurred in 13% of both maize (n=16) and sorghum (n=38) samples within the ranges of 6.5 to 7.3 µg/kg and 1.9 to 330 µg/kg, respectively, whereas 9 out of 37 millet samples were positive for STEG at concentrations ranging from 5 to 208 µg/kg. Elsewhere, STEG was reported as a contaminant of Nigerian maize (Adetunji *et al.*, 2014). While the toxicity of T-2 has been established in literature (Li *et al.*, 2011; Adhikari *et al.*, 2017), the toxic effects of STEG and AME to humans have remained largely limited. Nonetheless, it is known that STEG is a precursor for the biosynthesis of AFB<sub>1</sub> and both have similar structural configurations, as such, STEG is considered as a potent mutagen, carcinogen, and teratogen (Davis, 1981; Chu, 2003). The IARC classifies STEG as a group 2B carcinogen (IARC, 1976; Chu, 2003).

A number of studies have demonstrated the stability of AME during extreme food processing conditions such as during wet baking of bread (Siegel *et al.*, 2010; Abia *et al.*, 2013), as such, there is a risk of secondary exposure to AME through processed cereal-based foods. Adekoya *et al.* (2017) reported AME contamination of gruels derived directly from maize and sorghum in Nigeria. Some studies have demonstrated the possible carcinogenicity and mutagenicity of AME (Liu *et al.*, 1992; Brugger *et al.*, 2006; Ostry, 2008). For example, NIH/3T3 cells mutated by AME caused subcutaneous tumors in mice (Liu *et al.*, 1991). It has also been shown to induce DNA strand breaks in cell cultures (Podlech & Marko, 2009). In general, mycotoxin contamination was higher in maize, followed by sorghum and then millet (Table 5.5). A similar trend was observed by Makun *et al.* (2013) and Gwary *et al.* (2012). It has been shown that tannin-rich varieties of



sorghum and millet are less susceptible to fungal colonization (Apeh *et al.*, 2016; Dykes & Rooney, 2006), indicating that phytochemicals present in these cereals could exert antimycological properties as such resulting in less mycotoxin contamination.

### **5.3.2.2 Mycotoxin distribution patterns in maize, sorghum and millet from different agroecological zones of Nigeria**

Geoclimatic conditions under which crops are cultivated are critical for fungi proliferation and attendant mycotoxin production (Leema *et al.*, 2011; Medina *et al.*, 2014; Apeh *et al.*, 2016). Table 5.6 presents the distribution patterns of mycotoxins in maize, sorghum and millet across 5 agroecological zones in Nigeria. Maize samples generally had higher incidence rate and mycotoxin contamination levels. This could be because all the maize samples were obtained from the HRF/DRS agroecological zones. Also, as stated earlier in Section 5.3.2.1, maize is generally more susceptible to contamination by mycotoxigenic fungal species and consequent mycotoxin production as compared to sorghum and millet (Chilaka *et al.*, 2016; Sirma *et al.*, 2016). Likewise, in millet samples contamination levels increased from Southern to Northern Nigeria, with samples from Northern having the lowest levels of contamination and incidence rates. A similar trend was observed by Chilaka *et al.* (2016), who reported contamination/incidence rate of multi-mycotoxin contamination in DRS>NGS>SHS.

The observed high incidence rate and contamination levels of mycotoxins in maize, sorghum and millet samples from the HRF/DRS agroecological zones could be partly due to the climatic conditions in these regions that favor the proliferation of mycotoxigenic fungi species and subsequent mycotoxin production (Atehnkeng *et al.*, 2008). As already described in Section 5.2.2.1, the HRS is characterized by abundant rainfall (1,500 to 2,000 mm/yr), high humidity (78 to 100%) and average temperatures between 25 to 28 °C (Afolabi *et al.*, 2013; Amajama *et al.*, 2016), while the DRS vegetation represents a transition between the humid rainforest and guinea savannah zones. Annual rainfall in this zone ranges from 1,200 mm to 1,700 mm, while average humidity and temperature are 66 to 78% and 26 to 27 °C, respectively (Adejumo & Adejoro, 2014). Adejumo and Adejoro (2014), noted that the important agroecological zones in terms of mycotoxin research in Nigeria are the HRF, DRS and SGS/NGS zones.

**Table 5.6:** Distribution of mycotoxins in maize, sorghum and millet across different agroecological zones in Nigeria as analyzed using PHWE followed by UHPLC-MS/MS.

Mycotoxin	Maize		Sorghum				Millet					
	HRF/DRS (n=16)		HRF/DRS (n=12)		SHS (n=26)		HRF/DRS (n=20)		NGS/SGS (n=9)		SHS (n=8)	
	Mean* (µg/kg)	Range (µg/kg)	Mean* (µg/kg)	Range (µg/kg)	Mean* (µg/kg)	Range (µg/kg)	Mean* (µg/kg)	Range (µg/kg)	Mean* (µg/kg)	Range (µg/kg)	Mean* (µg/kg)	Range (µg/kg)
AFB <sub>1</sub>	54.41	6.50-315.00	10.92	15.00-116.00	0.28	<LOQ-7.25	2.55	<LOQ-49.50	4.17	<LOQ-37.50	0.00	<LOQ
AFB <sub>2</sub>	1.30	0.31-7.80	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
AFG <sub>1</sub>	0.00	<LOQ	0.00	<LOQ	0.28	<LOQ-7.25	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
AFG <sub>2</sub>	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
ΣAFs	55.71	15.60-322.80	10.92	15.00-116.00	0.56	<LOQ-14.50	2.55	<LOQ-49.50	4.17	<LOQ-37.50	0.00	<LOQ
AME	0.00	<LOQ	0.00	<LOQ	1.44	<LOQ-37.50	24.30	127.50-343.00	30.50	<LOQ-274.50	0.00	<LOQ
FB <sub>1</sub>	2,033.00	16.92-7,947.00	0.00	<LOQ	24.25	187.50-248.00	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
FB <sub>2</sub>	1,525.00	36.56-5,961.00	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
FB <sub>3</sub>	292.10	7.50-767.30	0.00	<LOQ	0.60	15.50-15.50	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
ΣFB <sub>1</sub> &FB <sub>2</sub>	3,851.00	29.60-14,603.00	0.00	<LOQ	24.25	187.50-248.00	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
OTA	8.28	6.50-54.25	1.88	7.50-15.00	0.00	<LOQ	1.36	6.88-20.25	0.00	<LOQ	0.00	<LOQ
OTB	1.52	7.75-16.50	0.63	<LOQ-7.50	0.00	<LOQ	0.68	6.75-6.88	0.00	<LOQ	0.00	<LOQ
ΣOTs	9.80	6.50-57.75	2.50	7.50-22.50	0.00	<LOQ	2.04	13.75-27.00	0.00	<LOQ	0.00	<LOQ
STEG	0.86	6.50-7.25	27.81	3.75-330.00	9.64	1.94-204.80	12.81	11.00-207.70	1.74	<LOQ-5.00	0.00	<LOQ
T-2	0.00	<LOQ	0.00	<LOQ	0.29	<LOQ-7.50	0.04	<LOQ	2.58	<LOQ-23.25	0.00	<LOQ
ZEA	3.49	7.38-33.00	3.06	7.50-21.75	0.18	4.75-4.75	9.99	90.00-90.00	26.94	80.00-93.50	0.94	<LOQ
α-ZEL	30.53	139.50-139.50	0.00	<LOQ	9.19	<LOQ	0.00	<LOQ	0.00	<LOQ	0.00	<LOQ
β-ZEL	4.66	<LOQ	5.25	63.00-63.00	1.80	<LOQ	0.00	<LOQ	0.89	<LOQ	0.00	<LOQ
ΣZEAs	38.68	71.50-155.00	8.31	<LOQ	11.18	<LOQ	9.99	<LOQ-90.00	27.83	80.00-93.50	0.94	<LOQ

Key: HRF: Humid rain forest. DRS: Derived savannah. NGS: Northern guinea savannah. SGS: Southern guinea savannah. SHS: Sahel savannah. Mean\*: average contamination of the samples including positive (i.e. >LOD) and negative (i.e. <LOD) samples. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol. ΣZEAs: sum of ZEAs. ΣOTs: sum of OTs. ΣFB<sub>1</sub>&FB<sub>2</sub>: sum of FB<sub>1</sub> and FB<sub>2</sub>. ΣAFs: sum of AFs.

Interestingly, this HRF zone spans across many of the West African countries, as such, similar patterns of mycotoxin contamination have been recorded in some of these countries (Hell *et al.*, 2000; Ngoko *et al.*, 2001). Hell *et al.* (2000), Udoh *et al.* (2000) and Gong *et al.* (2003) observed significant AFs contamination of maize in lowland areas in Cameroon, Nigeria, Benin and Togo, respectively. A similar trend was reported for FBs (10 to 16,040  $\mu\text{g}/\text{kg}$ ) in maize from Burkina Faso (Nikiema *et al.*, 2004) and FB<sub>1</sub> (300 to 26,000  $\mu\text{g}/\text{kg}$ ) in maize from Cameroon (Ngoko *et al.*, 2001). On the other hand, the lower levels of mycotoxin contamination and incidence rates observed in the Middle-Belt and Northern parts of Nigeria *i.e.*, the SGS/NGS and SHS, respectively, could be due to dryer and more arid climatic conditions in these regions. Particularly the SHS has a much lower annual rain fall and humidity as compared to DRS and HRF. Temperatures can reach as high as 40 °C (Atehnkeng *et al.*, 2008; Benson *et al.*, 2017). Such conditions may not favor the proliferation of mycotoxigenic fungi species.

### 5.3.2.3 Simultaneous occurrence of multiple mycotoxins in maize, sorghum and millet from Nigeria as analyzed using PHWE followed by UHPLC-MS/MS

Based on the results of this study, exposure of humans and animals to multiple mycotoxins is highly likely in the selected regions in Nigeria, as we observed co-occurrence of different groups of mycotoxins in many of the analyzed samples. This observation is in line with previous literature reports (Chilaka *et al.*, 2016; Somorin *et al.*, 2016; Adekoya *et al.*, 2018). Mycotoxin co-contamination of crops is a complex phenomenon, and a number of interrelating factors, such as fungi specie, crop genotype, and climatic conditions may be responsible for the co-occurrence of mycotoxins in foods. It is known that a single fungal specie may be able to produce more than one mycotoxin (Bayman & Baker, 2006; McCormick *et al.*, 2011), while one mycotoxin can be produced by different fungi species (Alasiri *et al.*, 2013; Ismaiel & Papenbrock, 2015).

**Table 5.7:** Co-occurrence of different groups of regulated mycotoxins in maize, sorghum and millet samples from Nigeria.

Co-contaminants	Number of co-occurrences		
	Maize (n=16)	Sorghum (n=38)	Millet (n=37)
AFs+FBs	6	0	0
AFs+FBs+OTs	3	0	0

Co-contaminants	Number of co-occurrences		
	Maize (n=16)	Sorghum (n=38)	Millet (n=37)
AFs+FBs+OTs+ZEAs	1	0	0
AFs+FBs+ZEAs	1	0	0
AFs+OTs+ZEAs	0	1	0
AFs+ZEAs	0	1	0
FBs+OTs+ZEAs	1	0	0
FBs+T-2	0	1	0
OTs+ZEAs	0	0	1

**Key:** AFs: aflatoxins. FBs: fumonisins. OTs: ochratoxins. T-2: T-2 toxin. ZEAs: zearalenone and its analogues  $\alpha$ - and  $\beta$ -zearalenol

Table 5.7 and Appendix 5.B describe all the possible co-occurrence patterns of the five groups of regulated mycotoxins detected in the samples, which are AFs, FBs, OTs, T-2 and ZEAs. This was achieved using the Venn diagram web application (Bioinformatics and Evolutionary Genomics, Ghent University, Belgium) (BEG Group, 2018). The 5 groups of mycotoxins subjected to this analysis yielded 9 different unique intersections as summarized in Table 5.7. The highest co-occurrence of mycotoxins that appeared in the maize samples was the co-contamination of AFs and FBs (*i.e.* AFs+FBs) which occurred in 6 (n=16) of the maize samples, while 3 of the samples simultaneously contained AFs, FBs and OTs. A similar pattern was observed in 5,000 samples submitted to the GEMS/Food contaminants database between 2011 and 2016, where reiterations of FBs+AFs combinations occurred in approximately 6% of the maize samples, 1% of sorghum (JECFA, 2016). A combination of AFs+FBs+OTs+ZEAs also occurred in one (n=16) of the maize samples, whereas, a combination of AFs+OTs+ZEAs occurred in one (n=38) of the sorghum samples. The co-occurrence of OTs+ZEAs was observed in a single millet sample.

Such co-contamination patterns have previously been reported in cereals from Nigeria (Bankole & Mabekoje, 2004; Makun *et al.*, 2011; Adetunji *et al.*, 2014; Chilaka *et al.*, 2016). Bankole and Mabekoje (2004) reported that 15 samples (n=103) of pre-harvest maize from Southern Nigeria were contaminated with both FBs and AFs simultaneously. A prevalence rate of 10% and mean contamination level of 111  $\mu\text{g}/\text{kg}$  have been reported for OTA, concurrently with OTB 7% (7.5  $\mu\text{g}/\text{kg}$ ), STEG 37% (3  $\mu\text{g}/\text{kg}$ ), ZEA 17% (174  $\mu\text{g}/\text{kg}$ ),  $\alpha$ -ZEL 1% (17  $\mu\text{g}/\text{kg}$ ), and  $\beta$ -ZEL 1% (13  $\mu\text{g}/\text{kg}$ ) in stored maize from five different agroecological zones in Nigeria (Adetunji *et al.*, 2014). A review of over a hundred papers between 1987 to 2016, revealed 127 mycotoxin combinations, of which AFs+FBs, AFs+OTA, DON+ZEA, and FBs+ZEA were amongst the most frequently co-

occurring combinations in cereal crops (Smith *et al.*, 2016). In Tanzania, co-exposure to FBs+AFs has been confirmed by means of plasma or urinary biomarkers of AF<sub>1</sub> and FB<sub>1</sub> (JECFA, 2016). Co-occurrence can be caused by substrate colonization with a single fungus that produces more than one mycotoxin, or due to colonization by different fungi species that produce different mycotoxins. It has been reported that ZEA usually co-occurs with one or more of the THs, because of the ability of its producing fungi to synthesize more than one mycotoxin (Grenier & Oswald, 2011).

Since the individual toxins that make these combinations are all amongst the most potent mycotoxins, their co-existence must not be neglected (Smith *et al.*, 2016). The combined effects of different mycotoxins have been extensively reviewed in literature (De Ruyck *et al.*, 2015; JECFA, 2016; Smith *et al.*, 2016), and could manifest as additive, synergistic or antagonistic (JECFA, 2016). For example, exposure of F344 rats to FB<sub>1</sub>+AFB<sub>1</sub> combinations increased liver preneoplastic changes suggestive of a synergistic interaction (Qian *et al.*, 2016), whereas, health concerns in humans include possible childhood stunting (Chen *et al.*, 2018). All cytotoxic effects of the binary combinations of OTA, FB<sub>1</sub> and AFB<sub>1</sub> in low concentrations at their EU regulatory limits to MDBK cell lines were additive, and in the order OTA+FB<sub>1</sub> > AFB<sub>1</sub>+FB<sub>1</sub> > AFB<sub>1</sub>+OTA (Clarke *et al.*, 2014), while FB<sub>1</sub>+ $\alpha$ -ZEL combination significantly diminished interferon  $\gamma$  mRNA expression as compared to  $\alpha$ -ZEL alone (Luongo *et al.*, 2006).

### 5.3.3 Significance of mycotoxin contamination of Nigerian staple cereals

We reiterate that mycotoxin contamination of maize, sorghum and millet crops in Nigeria represents a major food safety concern because these crops are staples. Atanda *et al.* (2015) asserted that AF contamination in maize and peanuts in Nigeria contributed to at least 7,761 cases of liver cancer, resulting in a total burden of 100,965 Disability-Adjusted Life Years (DALYs) (Atanda *et al.*, 2015). Derived food products from these cereals such as *masa*, *tuwo*, *ogi*, *ogi-baba*, *kunu*, *burukutu* and others are also at risk of mycotoxin contamination (Kpodo *et al.*, 1996; Adejumo & Adejoro, 2014; Ezekiel *et al.*, 2015; Chilaka *et al.*, 2016, 2018; Adekoya *et al.*, 2017; Njobeh & Olotu, 2017). Some of these processed food products (e.g. *ogi* and *ogi-baba*) are used as weaning foods for children. Sadly, a number of studies have reported mycotoxin contamination in these weaning foods (Oluwafemi & Ibeh, 2011; Adekoya *et al.*, 2017; Adetunji *et al.*, 2017). In

fact, a study (Oluwafemi & Ibeh, 2011), reported AFB<sub>1</sub> contamination levels up to 4,806 µg/kg in home-made weaning food made from maize and soybeans (Oluwafemi & Ibeh, 2011). Moreover, a posthumous autopsy of infants who suffered from kwashiorkor showed a significant level of AFs in their brains, because of consumption of contaminated maize-derived gruels (Oyelami *et al.*, 1997).

Aside the health effects on humans and animals, mycotoxin prevalence in Nigeria and Africa as a whole has other significant socio-economic impacts, ranging from food security, decreased market value of crops, regulatory rejections of goods mainly at ports of exit, damage to the African agricultural export brand amongst others (Gbashi *et al.*, 2018). For example, in 2010, the monetized burden of AFs contamination in Nigeria was estimated to be between 112 million USD and 942 million USD, which accounts for roughly 0.5% of the nation's GDP (Atanda *et al.*, 2015). These enormous impacts of mycotoxin could significantly jeopardize prospects of attaining the UN's sustainable development goal number 2, of achieving food security, improved nutrition, and a healthy agro-economic growth by 2030 (Gbashi *et al.*, 2018).

#### 5.4 Conclusion

Mycotoxin contamination of food and feed continues to remain a major challenge to public health in Nigeria. In this study, an environmentally friendly extraction method (PHWE), coupled with UHPLC-MS/MS analysis in comparison to a solvent-based method of extraction was used to determine the natural occurrence of multi-mycotoxins in maize, sorghum and millet, collected from different agroecological regions in Nigeria. Aside the adequacy of the method validation parameters, both univariate and multivariate (PCA and OPLS-DA) statistical models indicated the relative similarities of the results obtained from the two methods, which further authenticated the applicability of PHWE as an effective method for a research-related survey of multi-mycotoxin screening in cereals.

The survey results revealed the presence of all fifteen analyzed mycotoxins, including FBs, AFs, OTs, ZEAs, T-2, AME and STEG, in at least one sample of each cereal. Fumonisin, AFs and ZEAs were the predominant contaminants of the cereals, and maize was the most susceptible substrate, followed by sorghum and millet. Some of the samples were contaminated with mycotoxins at levels significantly higher than the maximum limit by the EC and CODEX. Also,

elaborate combinations of the different groups of regulated mycotoxins were observed. This stimulates curiosity about the possibility of their synergistic effects on the local populace that consume these crops. We also observed some fairly discrete mycotoxin contamination patterns across the different agroecological zones in the country depending on the substrate.

Considering the economic importance of these cereals in Nigeria, it is thus imperative to prioritize the adoption of functional mitigation strategies that are both cost-effective, crop-specific and locally adapted to the climatic conditions and agronomic practices of the region, in order to adequately combat the prevalence of these toxins in Nigeria. Further to this, more research should be done to determine the toxicological effects of different mycotoxin combinations in order to better understand their associated public health risks. If this is done, then future establishment of regulatory limits or as the case may be, reassessment of already existing limits could take into account the effects of co-existing mycotoxins. The successful adoption of PHWE in this study further represents a step closer to sustainability in green-solvent extraction in the field of mycotoxicology.

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## APPENDIX 5

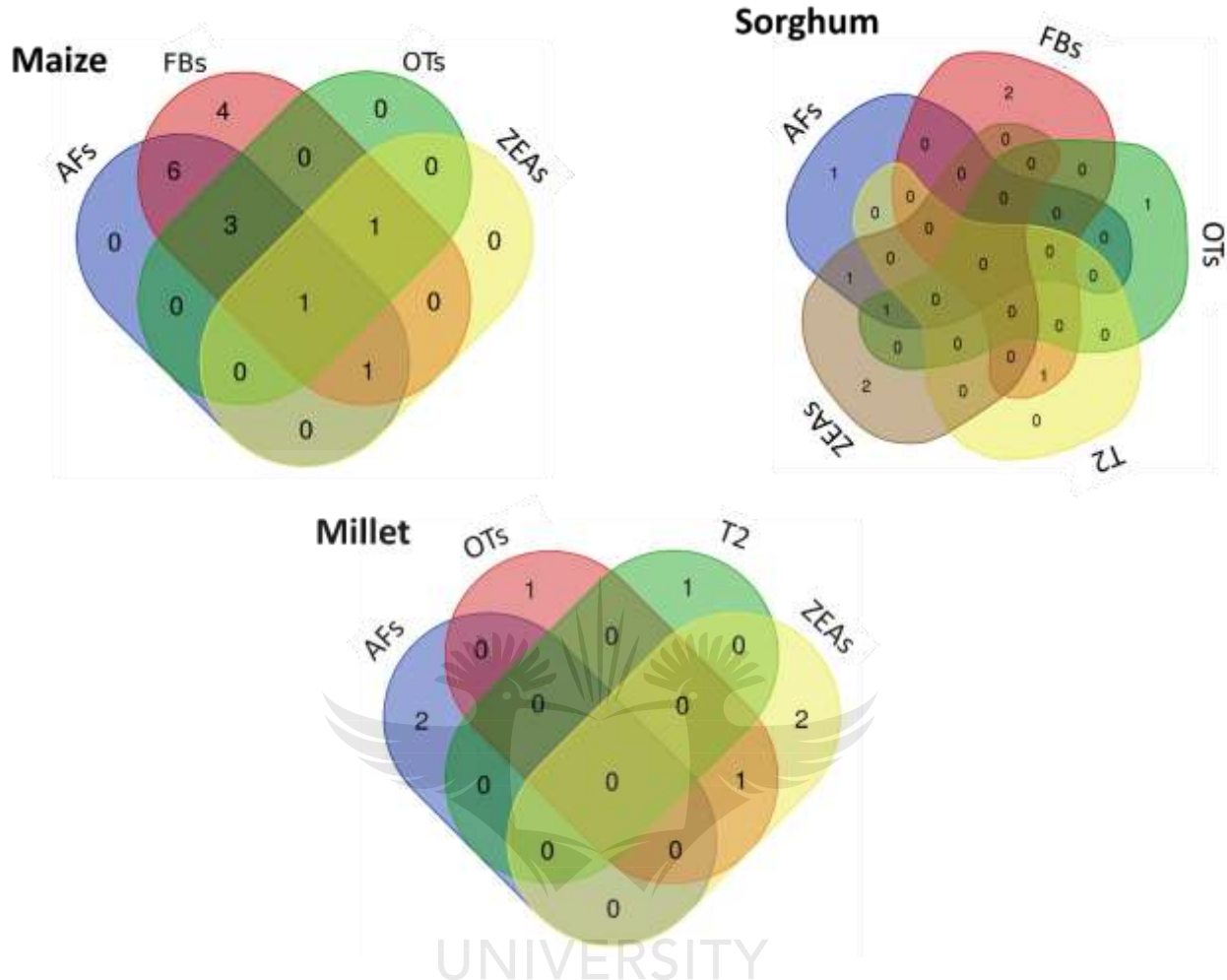
Appendix 5.A: Linearity parameters and matrix effect of PHWE of multi-mycotoxins in maize, sorghum and millet.

Myco	Linear Range (µg/kg)	Maize			Sorghum			Millet		
		Equation	R <sup>2</sup>	ME (%)	Equation	R <sup>2</sup>	ME (%)	Equation	R <sup>2</sup>	ME (%)
AFB <sub>1</sub>	30-1,000	y=726418.00x+0.0000000	0.998	43	y=758813.00x+0.0000000	0.998	45	y=394509.00x+0.0000000	0.998	-5
	10-40 <sup>#</sup>	y=0.0388236x-0.0297569 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.02246.00x-0.0551951 <sup>#</sup>	0.992 <sup>#</sup>	ND <sup>#</sup>	y= 0.0205976x-0.0481812 <sup>#</sup>	0.994 <sup>#</sup>	ND <sup>#</sup>
AFB <sub>2</sub>	10-300	y=29922.300x+0.0000000	0.990	ND	y=30003.100x+0.0000000	0.996	ND	y=1017810.0x+0.0000000	0.999	-14
	10-40 <sup>#</sup>	y= 0.0389391x-0.0724287 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.0217079x-0.0288360 <sup>#</sup>	0.972 <sup>#</sup>	ND <sup>#</sup>	y= 0.0182912x-0.0454976 <sup>#</sup>	0.988 <sup>#</sup>	ND <sup>#</sup>
AFG <sub>1</sub>	30-1,000	y=733883.00x+0.0000000	0.997	49	y=656177.00x+0.0000000	0.984	43	y=364241.00x+0.0000000	0.991	-3
	10-40 <sup>#</sup>	y= 0.0282378x-0.0290143 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y= 0.0190237x-0.0468256 <sup>#</sup>	0.988 <sup>#</sup>	ND <sup>#</sup>	y= 0.0155844x-0.0182782 <sup>#</sup>	0.993 <sup>#</sup>	ND <sup>#</sup>
AFG <sub>2</sub>	30-1,000	y=602178.00x+0.0000000	0.999	44	y=596522.00x+0.0000000	0.995	44	y=358975.00x+0.0000000	0.998	6
	10-40 <sup>#</sup>	y=0.0137443x -0.0346290 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y= 0.0197771x-0.0440019 <sup>#</sup>	0.984 <sup>#</sup>	ND <sup>#</sup>	y= 0.0117548x-0.0147432 <sup>#</sup>	0.982 <sup>#</sup>	ND <sup>#</sup>
AME	30-1,000	y=282992.00x+0.0000000	0.998	57	y=269502.00x+0.0000000	0.994	55	y=134284.00x+0.0000000	1.000	9
	10-40 <sup>#</sup>	y=0.0012392x-0.0053106 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.0006475x-0.0170763 <sup>#</sup>	0.996 <sup>#</sup>	ND <sup>#</sup>	y=0.0005798x-0.0085391 <sup>#</sup>	0.989 <sup>#</sup>	ND <sup>#</sup>
FB <sub>1</sub>	60-2,000	y=108498.00x+0.0000000	0.992	63	y=109.64500x+0.0000000	0.998	64	y=56694.100x+0.0000000	0.998	30
	20-80 <sup>#</sup>	y=0.0031071x-0.0163114 <sup>#</sup>	0.998 <sup>#</sup>	ND <sup>#</sup>	y=0.0021193x-0.0772540 <sup>#</sup>	0.989 <sup>#</sup>	ND <sup>#</sup>	y= 0.0014962x-0.0995423 <sup>#</sup>	0.984 <sup>#</sup>	ND <sup>#</sup>
FB <sub>2</sub>	16-500	y=15175200x+0.0000000	0.997	57	y=16315600x+0.0000000	0.996	60	y=9292170.0x+0.0000000	0.995	30
	20-80 <sup>#</sup>	y=0.0036764x+0.0021624 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.00188148x-0.0115376 <sup>#</sup>	0.989 <sup>#</sup>	ND <sup>#</sup>	y=0.0015081x-0.1082910 <sup>#</sup>	0.977 <sup>#</sup>	ND <sup>#</sup>
FB <sub>3</sub>	30-1,000	y=467233.00x+0.0000000	0.997	61	y=494279.00x+0.0000000	0.999	63	y=242114.00x+0.0000000	0.998	24
	20-80 <sup>#</sup>	y= 0.0051078x-0.0189341 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y= 0.0036043x-0.0766144 <sup>#</sup>	0.987 <sup>#</sup>	ND <sup>#</sup>	y=0.0023971x-0.1025880 <sup>#</sup>	0.974 <sup>#</sup>	ND <sup>#</sup>
OTA	30-1,000	y=2569440.0x+0.0000000	0.999	60	y=2462030.0x+0.0000000	0.998	59	y=1242000.0x+0.0000000	0.999	18
	25-100 <sup>#</sup>	y= 0.0059043x-0.0187238 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.0028299x-0.0278753 <sup>#</sup>	0.991 <sup>#</sup>	ND <sup>#</sup>	y= 0.0042255x-0.0060401 <sup>#</sup>	0.968 <sup>#</sup>	ND <sup>#</sup>
OTB	30-1,000	y=25504200x+0.0000000	0.996	62	y=21534600x+0.0000000	0.997	55	y=1165260.0x+0.0000000	1.000	18
	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>
STEG	30-1,000	y=1697490.0x+0.0000000	0.995	60	y=1766930.0x+0.0000000	0.997	61	y=794631.00x+0.0000000	0.999	14
	25-100 <sup>#</sup>	y=0.0189498x-0.0007388 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y= 0.0087249x-0.0812727 <sup>#</sup>	0.988 <sup>#</sup>	ND <sup>#</sup>	y=0.0097481x-0.0207013 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>
T-2	30-1,000	y=15881.200x+0.0000000	0.996	61	y=62117.600x+0.0000000	0.998	90	y=33360.200x+0.0000000	0.999	82



Myco	Linear Range (µg/kg)	Maize			Sorghum			Millet		
		Equation	R <sup>2</sup>	ME (%)	Equation	R <sup>2</sup>	ME (%)	Equation	R <sup>2</sup>	ME (%)
ZEA	50-200 <sup>#</sup>	y=0.00739964x-0.0429551 <sup>#</sup>	0.999 <sup>#</sup>	ND <sup>#</sup>	y=0.0033890x-0.0488755 <sup>#</sup>	0.993 <sup>#</sup>	ND <sup>#</sup>	y= 0.0038011x+0.0089581 <sup>#</sup>	0.987 <sup>#</sup>	ND <sup>#</sup>
	30-1,000	y=571027.00x+0.0000000	0.997	60	y=494014.00x+0.0000000	0.997	54	y=240378.00x+0.0000000	0.993	6
α-ZEL	50-200 <sup>#</sup>	y=0.0010048x-0.0007694 <sup>#</sup>	0.996 <sup>#</sup>	ND <sup>#</sup>	y=0.0002811x-0.0015622 <sup>#</sup>	0.917 <sup>#</sup>	ND <sup>#</sup>	y=0.0002970x-0.0043136 <sup>#</sup>	0.969 <sup>#</sup>	ND <sup>#</sup>
	30-1,000	y=48991.100x+0.0000000	0.999	61	y=45737.600x+0.0000000	0.999	58	y=20146.000x+0.0000000	0.998	5
β-ZEL	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>	N.D. <sup>#</sup>
	30-1,000	y=128721.00x+0.0000000	0.999	60	y=257624.00x+0.0000000	0.997	56	y=128721.00x+0.0000000	0.999	13
Mean <sup>#</sup>			0.996±0.00			0.996±0.00			0.996±0.00	
			0.999±0.00 <sup>#</sup>			0.982±0.01 <sup>#</sup>			0.999±0.00 <sup>#</sup>	
Sign (2-tailed)			0.01			0.04			0.01	

Key: <sup>#</sup>Parameter values for solvent extraction. Myco: mycotoxin. ME: Matrix effect. N.D.: not detected. R<sup>2</sup>: coefficient of determination. AFB<sub>1</sub>: aflatoxin B<sub>1</sub>. AFB<sub>2</sub>: aflatoxin B<sub>2</sub>. AFG<sub>1</sub>: aflatoxin G<sub>1</sub>. AFG<sub>2</sub>: aflatoxin G<sub>2</sub>. AME: alternariol monomethyl ether. FB<sub>1</sub>: fumonisin B<sub>1</sub>. FB<sub>2</sub>: fumonisin B<sub>2</sub>. FB<sub>3</sub>: fumonisin B<sub>3</sub>. OTA: ochratoxin A. OTB: ochratoxin B. STEG: sterigmatocystin. T-2: T-2 toxin. ZEA: zearalenone. α-ZEL: α-zearalenol. β-ZEL: β-zearalenol.



**Appendix 5.B:** Incidences of co-contamination of different classes of regulated mycotoxins in maize, sorghum and millet from Nigeria as analyzed using PHWE followed by UHPLC-MS/MS. Afs: aflatoxins. FBs: fumonisins. OTs: ochratoxins. T-2: T-2 toxin. ZEAs: zearalenone and its analogues  $\alpha$ - and  $\beta$ -zearalenol.

## CHAPTER SIX

### 6.0 GENERAL DISCUSSION AND CONCLUSION

#### 6.1 GENERAL DISCUSSION

Mycotoxins are one of the most notorious food contaminants due to their severe toxicity and perpetual proliferation in various agricultural commodities globally (Njobeh *et al.*, 2010a; Reddy *et al.*, 2010). Despite much efforts to control mycotoxin contamination, these contaminants remain incessantly prevalent in food and feed, to the detriment of consumers of such products (Aldred *et al.*, 2004; Zinedine *et al.*, 2007; Njobeh *et al.*, 2010a). Their presence in food/feed is highly unwanted and results in huge economic losses to the agricultural industry and international trade due to stringent trade policies to ensure public health and safety (Kimanya *et al.*, 2012; Mitchell *et al.*, 2016; Gbashi *et al.*, 2018). Reliable analytical data is critical for adequate risk assessment, legislative actions and provides a strong scientific basis for adoption of relevant mitigation strategies along the supply chain (Anklam *et al.*, 2002; Aldred *et al.*, 2004). Such data is based on efficient and validated methods of analysis (Gbashi *et al.*, 2018). It is therefore obligatory that such methods conform to certain performance criteria with respect to reliability, accuracy and sensitivity (Gilbert & Anklam, 2002; Commission Regulation, 2006a; Arroyo-Manzanares *et al.*, 2018). Due to the urgency to meet up with ever increasing demand for more healthy and safe foods, it is expedient that methods employed for quality control and surveillance are equally fast in addition to safety and cost-effectiveness, an aspect which many of the conventional methods of mycotoxin analysis are grossly lacking (Schenck & Hobbs, 2004; Karsten *et al.*, 2008; Frenich *et al.*, 2009; Arroyo-manzanares *et al.*, 2014).

In this research work, a fast, efficient and environmentally-friendly method called pressurized hot water extraction (PHWE), was developed, validated and applied for the extraction of multiple mycotoxins in a single step. This method depends on the heat- and pressure-induced dissolution, partitioning and solvation characteristics of water, which makes it act in a manner similar to organic solvents in terms of extractability (Teo *et al.*, 2010; Gbashi *et al.*, 2017c). Since PHWE is heat-dependent, there are concerns, which have been shown to be genuine (Khoza *et al.*, 2014, 2015; Sani *et al.*, 2014), that some analytes might experience thermal degradation resulting in lower recoveries during PHWE. It was thus imperative to first investigate the thermal degradation

patterns of the mycotoxins, in order to ascertain the feasibility of this extraction approach. This constituted the first objective of this research work which was successfully achieved (Gbashi *et al.*, 2019b) as described in Chapter Three of this thesis.

In this experiment, the thermal stability of 15 different mycotoxins was determined as a function of temperature and time for pure standards and maize matrix spiked with mycotoxins. Maize was chosen as the reference matrix because it is a widely-consumed staple food around the world and a favored substrate for fungal contamination and subsequent mycotoxin production. In order to optimize the degradation of the multi-mycotoxins, a set of experiments were statistically designed based on the response surface methodology (RSM). By adopting the central composite design (CCD) approach of the RSM, 10 experimental levels were obtained, with temperature values ranging from 50 to 150 °C and time values ranging from 10 to 50 min. After heat treatment, the residues were then quantified on an UHPLC-MS/MS. Inference from the obtained results indicated that depending on the type of mycotoxins and conditions of exposure, the test mycotoxins were stable during thermal treatment. This observation is in line with previously published reports on the thermal stability of mycotoxins (Castelo *et al.*, 1998; Raters & Matissek, 2008; Karlovsky *et al.*, 2016; Kim *et al.*, 2017). This implies that with a carefully optimized combination of temperature and time, the challenge of thermal degradation of mycotoxins may easily be overcome during PHWE.

After confirming the stability of the mycotoxins, the design, optimization and validation of the PHWE method was performed in fulfillment of Objective 2 of this research as described in Chapter Four of this thesis. For the method development and optimization, a similar chemometric approach to that of the previously performed experiment, *i.e.*, the CCD, was adopted. Two extraction parameters (temperature and solvent composition) were optimized to determine the best conditions for the simultaneous extraction of the 15 different mycotoxins spiked into maize. The computed results yielded a condition of 162 °C and 45% ethanol (EtOH) for temperature and solvent composition, respectively. Using this optimized condition, with the exception of OTA and  $\alpha$ -ZEL which had a recoveries of 58 and 14%, respectively, it was possible to achieve satisfactory recoveries (71 to 124%) for all analytes, which were consistent with regulatory requirements of

the EC, AOAC, CODEX, FDA and ICH (Shabir, 2005; Commission Regulation, 2006a; AOAC, 2009; CODEX, 2015; FDA, 2015).

Other method validation parameters such as linearity [0.986 to 0.999 (Addendums B-E)], limit of detection (LOD) (range: 0.06 to 41  $\mu\text{g}/\text{kg}$ ) and limit of quantification (LOQ) (range: 0.18 to 123  $\mu\text{g}/\text{kg}$ ), intra-day precision or repeatability (0 to 27%) and inter-day precision or reproducibility (3 to 34%) were also in line with analytical method performance criteria by same regulatory bodies (Shabir, 2005; Commission Regulation, 2006a; AOAC, 2009; CODEX, 2015; FDA, 2015). When compared with other conventional mycotoxin extraction methods, the extraction efficiency of the modified PHWE method was akin, and in some cases better. A small-scale pilot study was subsequently performed to test the applicability of the PHWE method for the analysis of mycotoxins in real samples. Twenty-five maize meal samples intended for human consumption obtained from rural households in Ngwalemong village in Limpopo Province (South Africa) were subjected to PHWE followed by UHPLC-MS/MS analysis to determine the levels of 15 different naturally occurring mycotoxins in the samples. The results revealed that though many of the samples were positive for the tested mycotoxins, none of the detected levels exceeded the regulatory limits set by the EC.

The pilot study was thus followed by a much larger scale study, to estimate multi-mycotoxin contamination levels in 91 samples of staple cereals, maize, sorghum and millet, collected from 5 different agroecological zones in Nigeria. This was in achieving Objective 3 of this research work as described in Chapter Five of this thesis. During this experiment for a larger scale application of the PHWE method, the 91 samples that were extracted using the modified PHWE method were also analyzed using a solvent extraction method which served as a control for cross-validation and authentication of the validity of the PHWE method. Discrimination of the results obtained by the two methods using the PCA and OPLS-DA multivariate discriminatory approach indicated that the variations in the results were not significantly different ( $p > 0.05$ ). The results of the PHWE analysis revealed that all the 15-tested mycotoxins were detected in at least one of the samples, some being contaminated with mycotoxins at levels significantly higher than the corresponding EC maximum levels in the food commodities. For example, 100% of the maize samples were positive for  $\text{FB}_1$  and  $\Sigma\text{FB}_1\&\text{FB}_2$  at levels ranging from 17 to 7,950  $\mu\text{g}/\text{kg}$  and 30 to 14,600  $\mu\text{g}/\text{kg}$ , respectively, with 44% of the samples exceeding the maximum levels of 4,000  $\mu\text{g}/\text{kg}$  in

unprocessed maize as stipulated by EC and CODEX (EC, 2007; WHO, 2017; Arroyo-Manzanares *et al.*, 2018).

Selected single ion chromatograms (SIM) showing the peaks of the different mycotoxins for the mycotoxin standards and contaminated maize, sorghum and millet samples are shown in Addendums F-G. Much lower levels of FBs were however, observed in sorghum samples (mean value of 17  $\mu\text{g}/\text{kg}$  and maximum value of 248  $\mu\text{g}/\text{kg}$  for  $\Sigma\text{FB}_1\&\text{FB}_2$ ) while none of the millet samples were contaminated with FBs. A similar trend was observed for AFs contamination in the cereals, with maize registering the highest prevalence, 54  $\mu\text{g}/\text{kg}$  for  $\text{AFB}_1$  and 56  $\mu\text{g}/\text{kg}$  for  $\Sigma\text{AFs}$ , while sorghum and millet had lower levels of  $\text{AFB}_1$  (3.6 and 2.4  $\mu\text{g}/\text{kg}$ , respectively) and  $\Sigma\text{AFs}$  (3.8 and 2.4  $\mu\text{g}/\text{kg}$ , respectively). This trend and the contamination levels thereof are in agreement with a number of previously published literature on mycotoxin contamination of maize, sorghum and millet in Nigeria (Bankole & Mabekoje, 2004; Afolabi *et al.*, 2006; Adetunji *et al.*, 2014; Chilaka *et al.*, 2016). It is evident from these results that mycotoxins, particularly AFs and FBs, still constitute a significant concern to food safety in Nigeria, and perhaps other West African countries.

## 6.2 CONCLUSION

In this research work, it was noted that risks of mycotoxins present in agricultural commodities are assessed by adequate analytical procedures. At present, mycotoxins are extracted using solvent-based extraction methods involving multiple steps, which are expensive, labor-intensive and time-consuming. We developed, validated and used a fast, low-cost and environmentally friendly extraction method, PHWE, for the extraction of multi-mycotoxins in food samples in comparison to the conventional methods routinely used. To the best of our knowledge, this constitutes the first report on the application of this method for the extraction mycotoxins in food. In the experiments that preceded the actual method development, the thermal degradation patterns of some of the understudied mycotoxins (*i.e.*, STEG and AME) were also reported for the first time. The use of multivariate chemometric models was fundamental in the overall experimental design, data analysis and interpretations of the results.

The efficacious application of the validated method to real samples and the results thereof not only re-affirm the adequacy of the modified PHWE method, but also offer insights on the risk of

exposure of the populace, as well as, contribute to existing knowledge on the prevalence of mycotoxins in commercially available cereals (maize, maize meal, sorghum and millet) in Nigeria and South Africa, where applicable. This further draws attention to the mycotoxin issue in Africa, and the need for more proactive approaches in tackling this problem such as routine surveillance of these toxins in the food and feed supply chain using efficient, fast and cheap analytical approaches. This is not undermining the need for preventive and other mitigation approaches. Furthermore, inference from the data obtained are expected to stimulate policy makers and stakeholders along the food supply chain to identify critical areas of collaboration and strengthen alliances in order to ameliorate the effects of these toxicants on the continent of Africa, and the world at large. In this regard, research objectives should be prioritized to ensure a positive impact for public health, food safety and security and economic development. Critical areas to concentrate efforts include development of efficient and cost-effective analytical and intervention strategies, public awareness, strengthening research and human capacity development as well as harmonizing and enforcing regulations.

In light of the focus of this thesis, possible future works include improvements in some aspects of the PHWE method, such as the recovery of OTA and  $\alpha$ -ZEL, as well as, the linear range of the method. In future developments, a sample concentration could improve the performance of the method. A collaborative inter-laboratory study to assess the performance characteristics of the PHWE could be organized between the Mycotoxin Laboratory, University of Johannesburg, Doornfontein Campus, South Africa and the Molecular Sciences Institute, School of Chemistry, University of Witwatersrand, South Africa, as both laboratories have a similar PHWE set up. Another future work includes extending the applicability of the PHWE method for the extraction of a wider range of other fungal metabolites and environmental pollutants that contaminate different food and feed substrates. Also, imminent developments could enable complete elimination of organic solvents from the PHWE method, as well as, the possibility to combine the method with other advanced chromatographic and mass spectrometric instruments such as the Pegasus GC-HRTOF-MS for the analysis of mycotoxins and other fungal metabolites where applicable. The choice of the Pegasus GC-HRTOF-MS can be explained in terms of its rich analytical capabilities (ultra-high mass resolution, accuracy and sensitivity) as well as its availability in our department. A further goal will be an accredited method for routine analysis for



the implementation of regulatory limits and trade specifications, as well as, obtaining a patent for the PHWE method by the end of 2020.

In general, based on the results of this study, the adoption of PHWE in combination with UHPLC and tandem MS techniques is very promising as an alternative to conventional methods for survey-type work and exposure studies for multi-mycotoxin levels in food products. Though several other benefits can be derived from reduced chemical usage, this study emphasizes the significance of greener methods of analysis in the field of mycotoxicology and bioanalysis, hence stimulating interest and contributing to green chemistry, environmental sustainability and public health in many ways.

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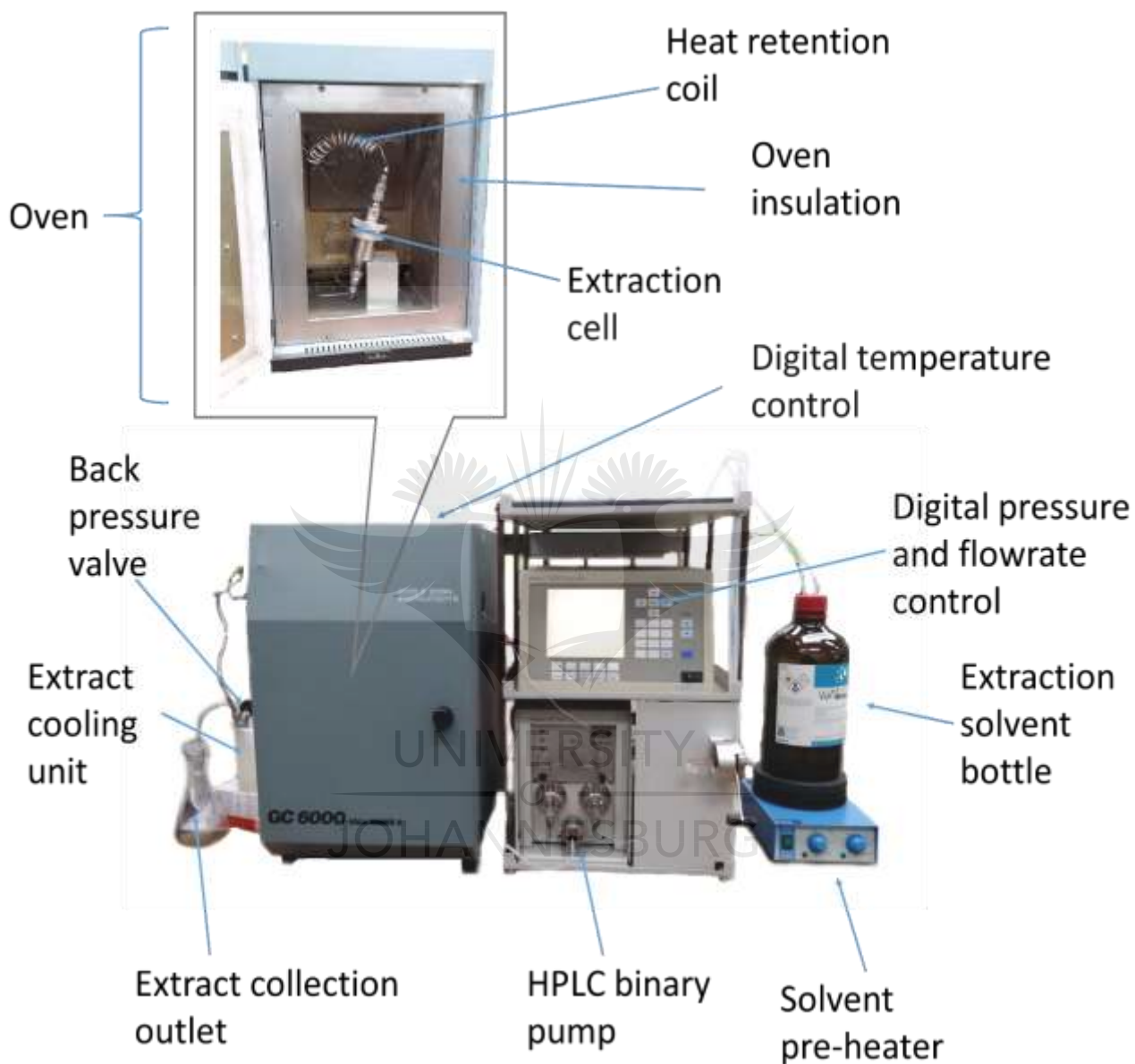
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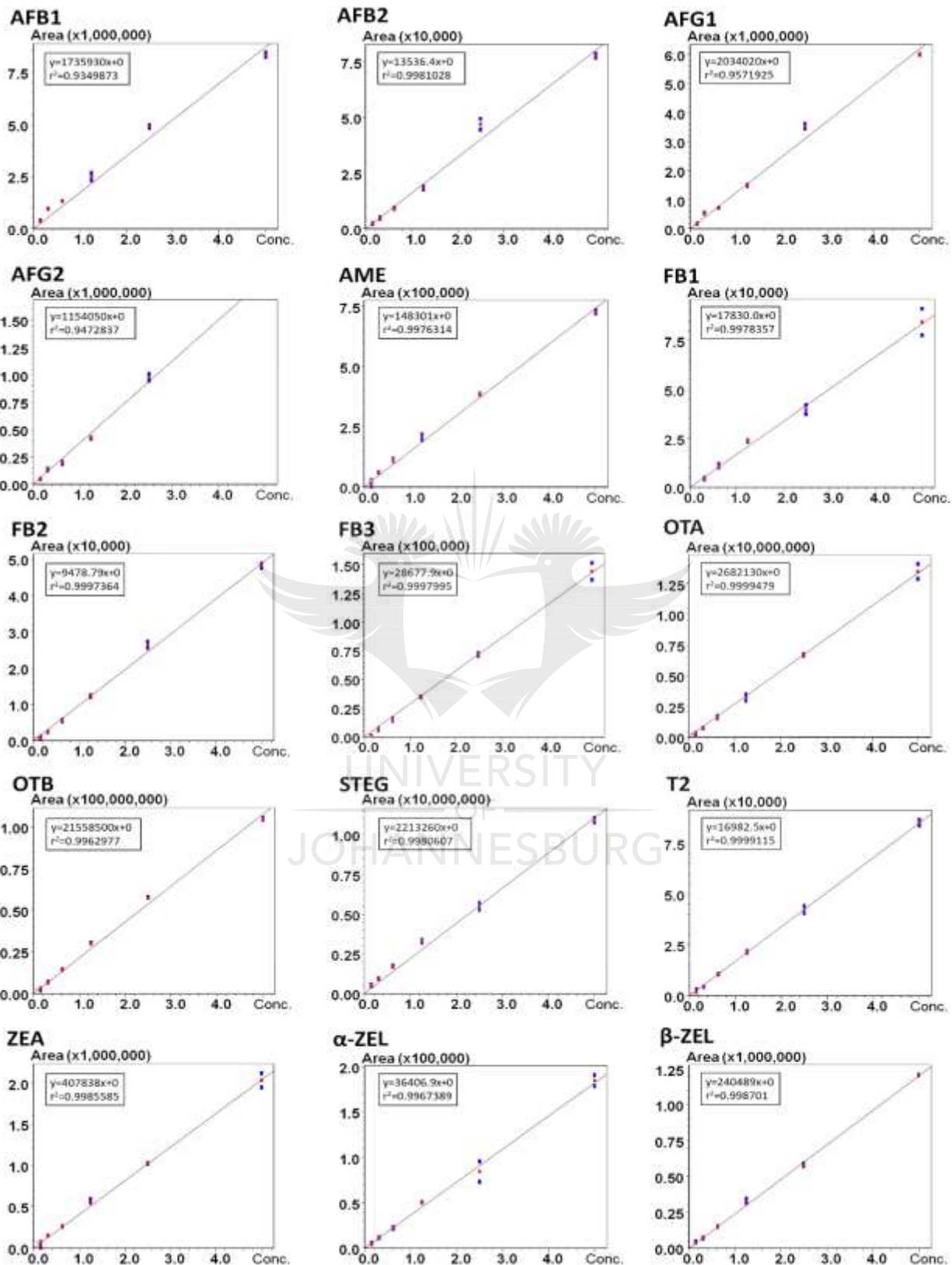


## ADDENDUM



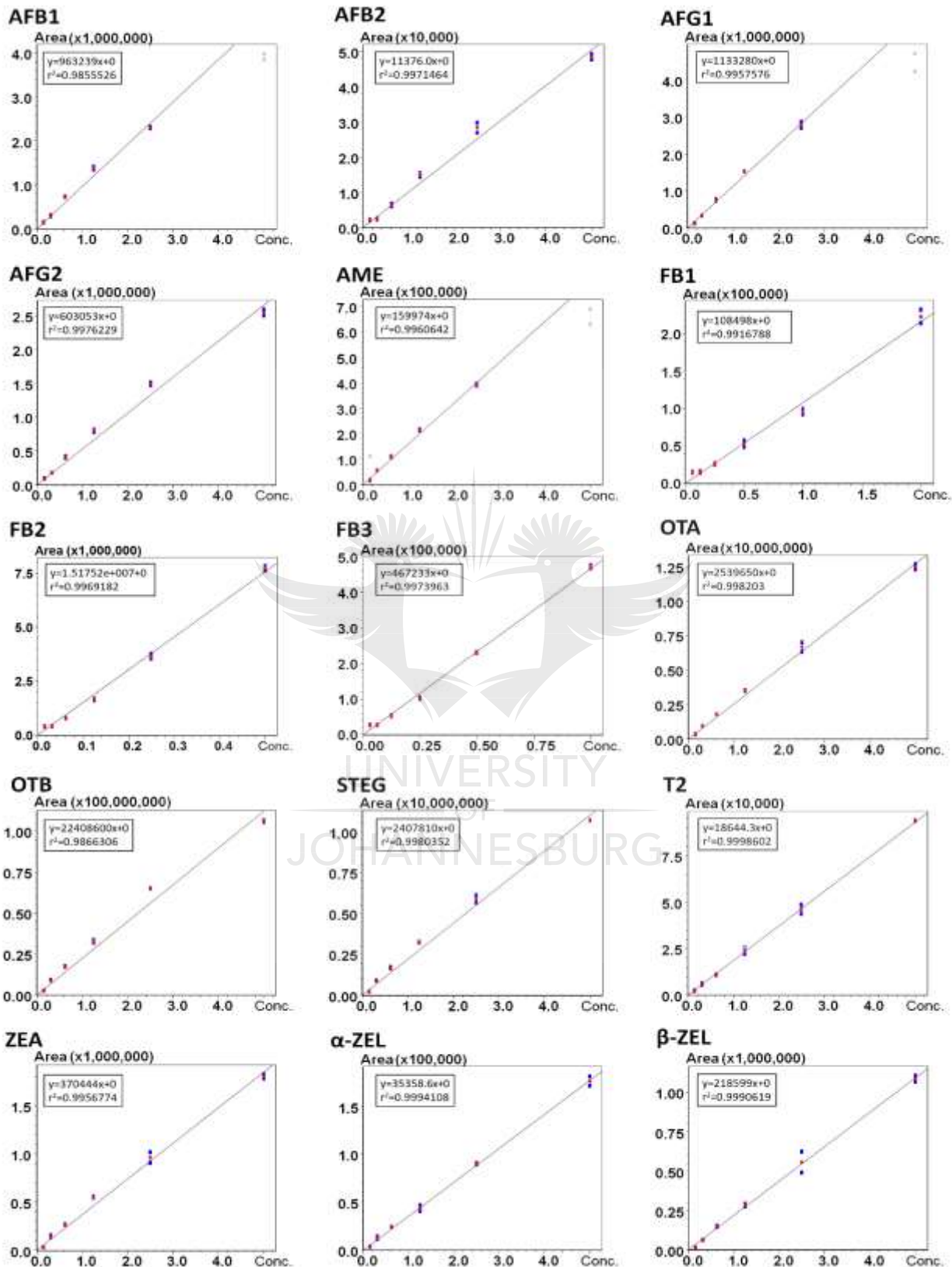
**Addendum A:** Picture of the homemade laboratory scale PHWE unit.



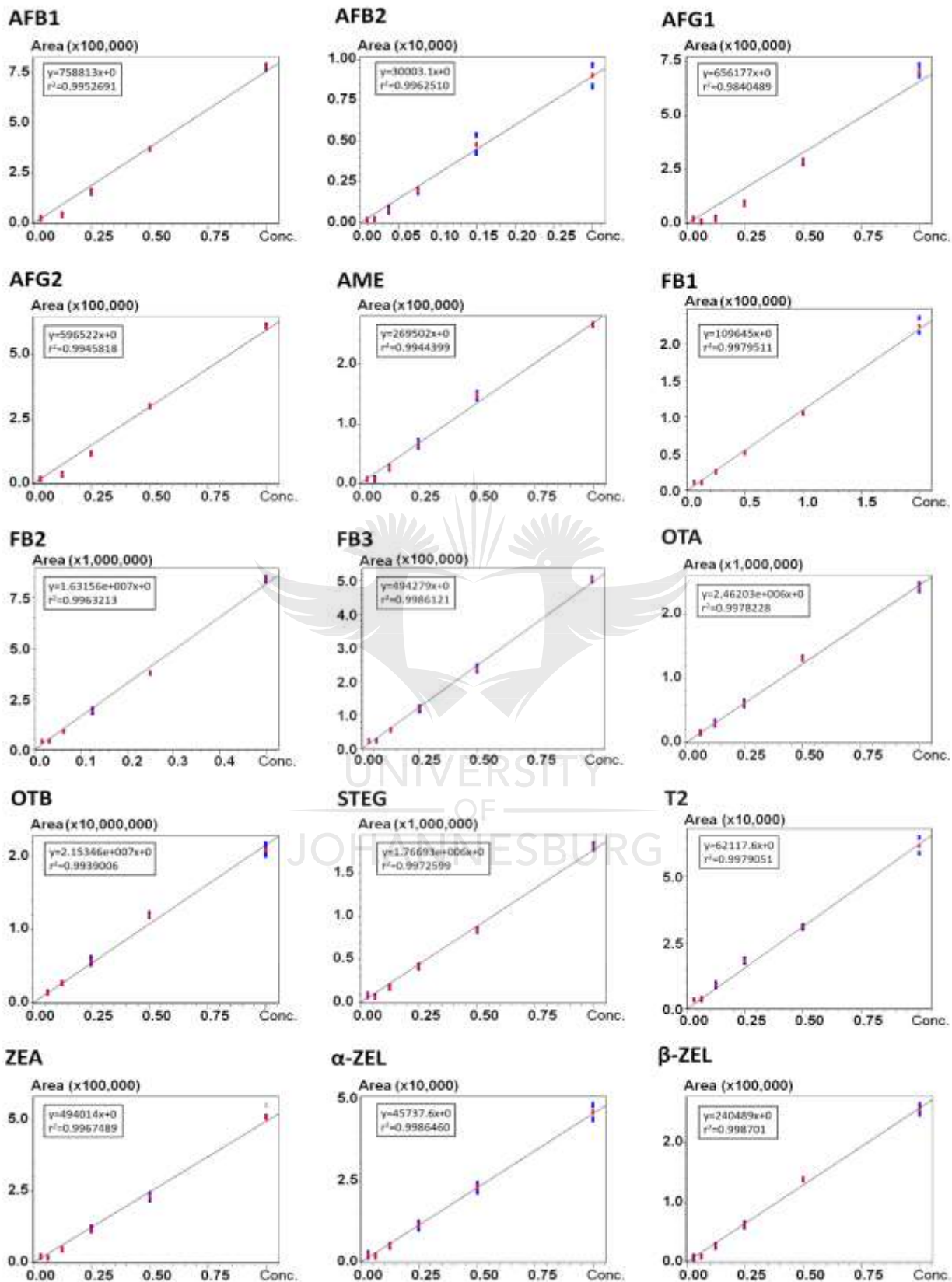


Addendum B: Calibration curves for mycotoxins prepared in neat solvent.

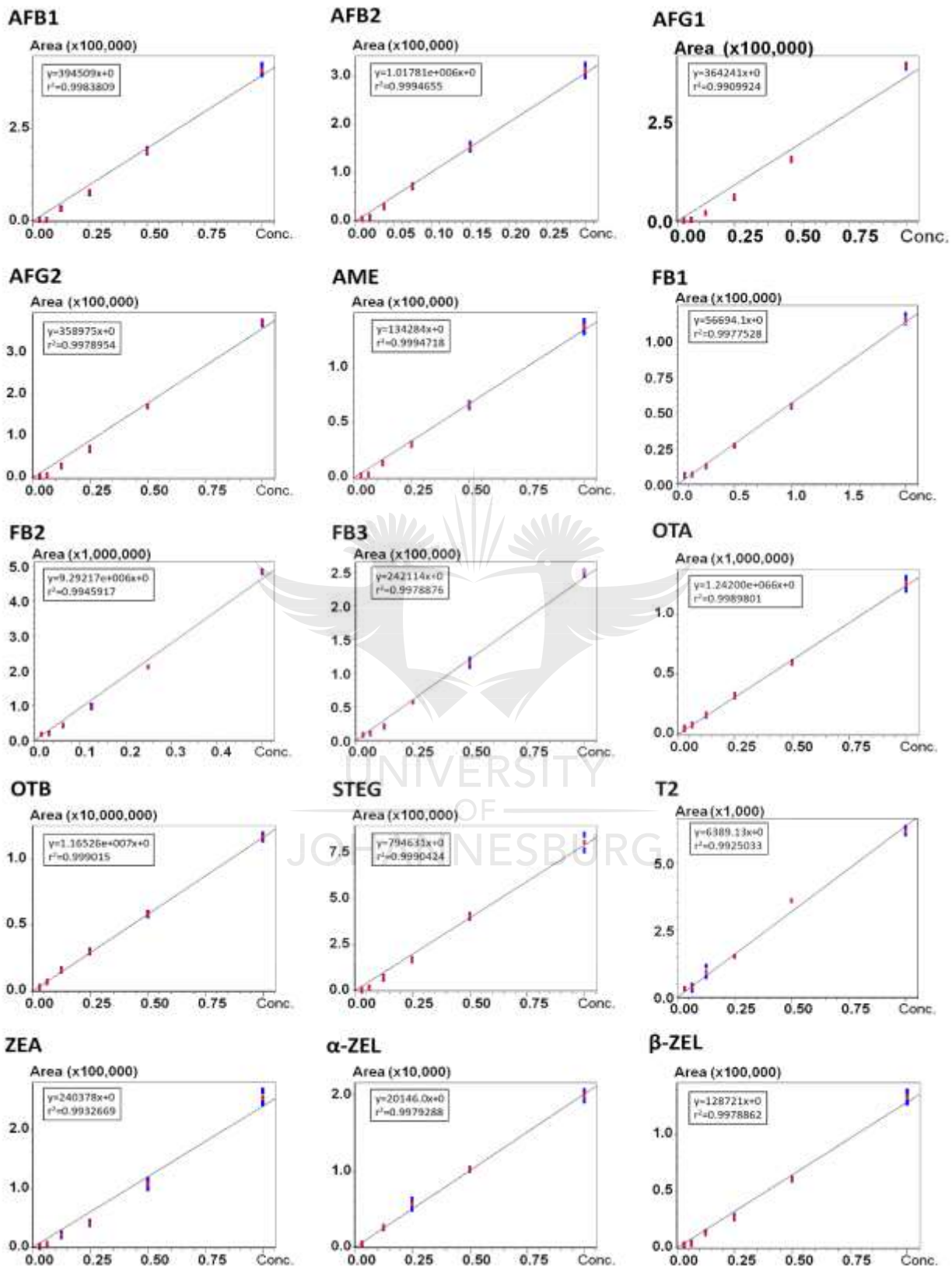




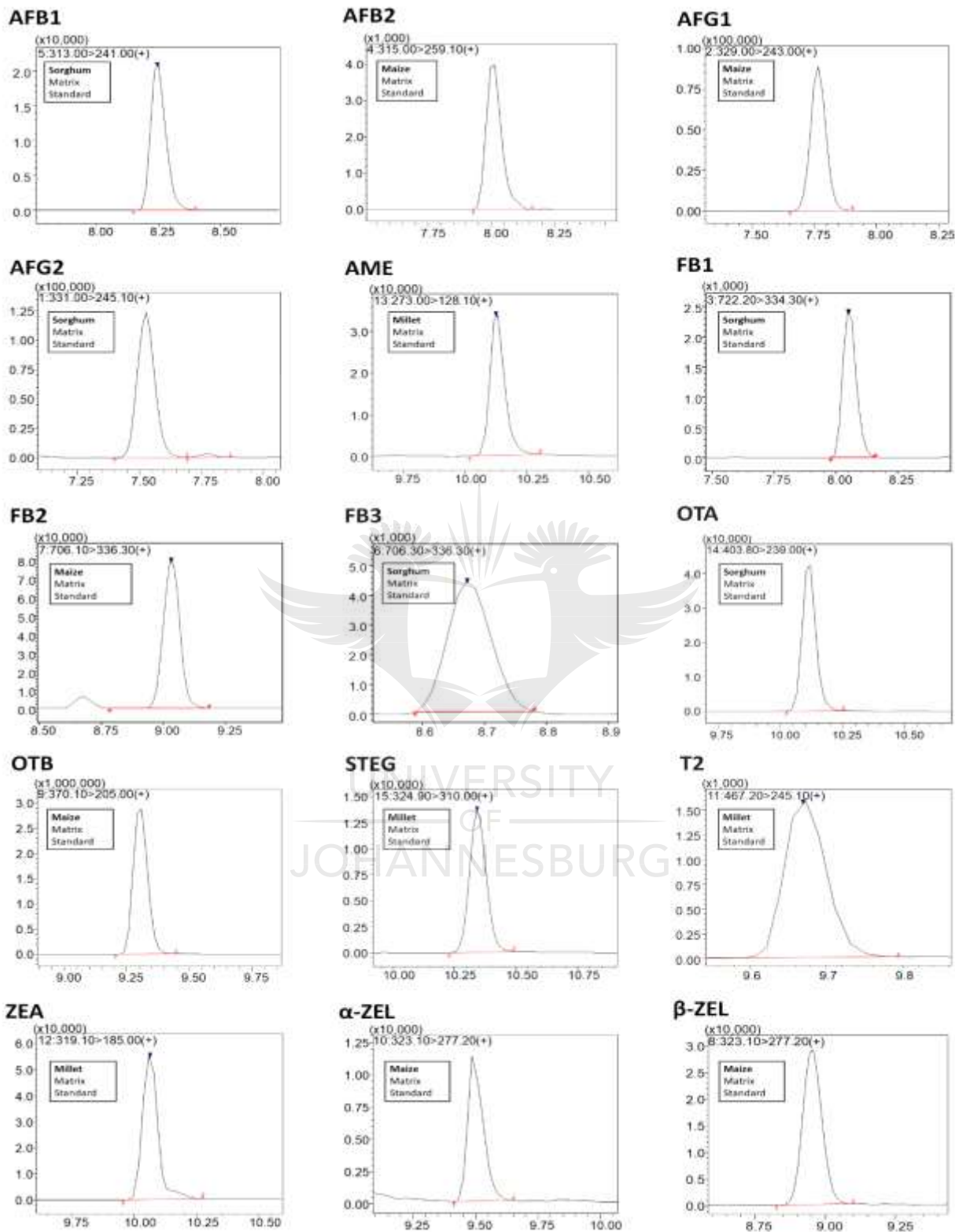
Addendum C: Maize matrix-matched calibration curves.



Addendum D: Sorghum matrix-matched calibration curves.

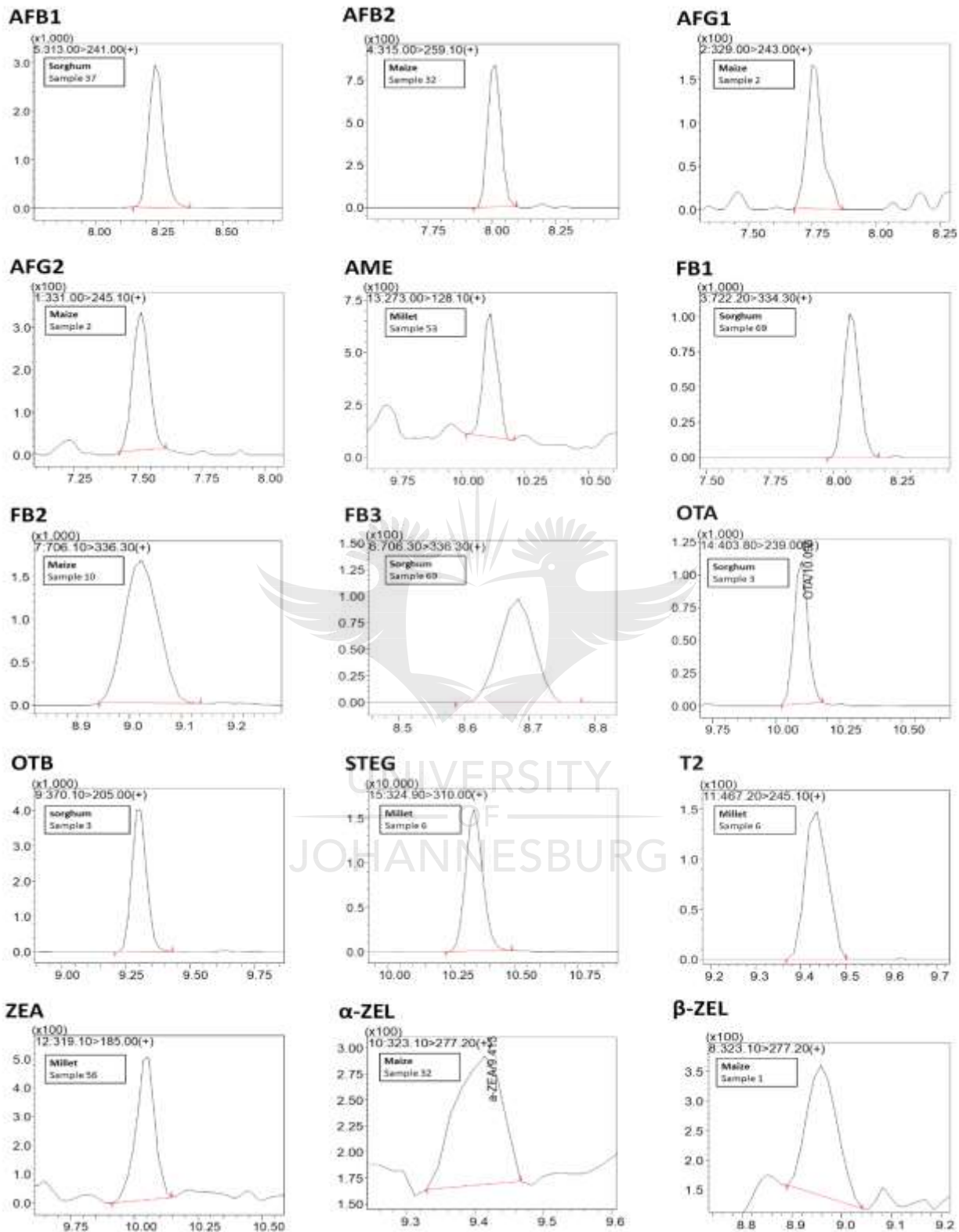


Addendum E: Millet matrix-matched calibration curves.



**Addendum F:** Selected single ion chromatograms (SIM) showing the peaks of the different mycotoxins prepared in neat solvent, maize-matrix, sorghum-matrix and millet-matrix.





**Addendum G:** Selected single ion chromatograms (SIM) showing the peaks of the different mycotoxins for contaminated maize, sorghum and millet samples.