

Deliverable 3.1

FOODSAFER

Review report on available models for fungal infection and mycotoxins in food commodities



Deliverable D3.1: Review report on available models for fungal infection and mycotoxins in food commodities



Work package number and title	WP3: Chemical Risks emergence
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Relevant Task	Task 3.1 Advancement of prediction
	tools for the emergence of mycotoxins
	and plant toxins using machine learning
	and
	big data
Participants	BAR, FFoQSI
Dissemination Level	Public
Due Date (month)	M12 – 30 September 2023

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This project has received funding from the European Union's Horizon Europe research and innovation programme under grant agreement No 101060698





Abstract

Food safety remains a concern worldwide, with annually millions of consumers vulnerable to food borne illnesses caused by various hazards. In this report we focus on mycotoxins, a group of chemical hazards with both chronic and acute health impacts. Mycotoxins are secondary fungal metabolites which are primarily produced by Fusarium spp., Aspergillus spp. and Penicillium spp. in various foods. The behavior of the fungi and the production of mycotoxins is dependent on environmental, agronomical, and geographical factors. These factors can be used to predict fungal growth and mycotoxin contamination in foods with modeling techniques and the relevant input data. This study aimed to identify the latest development in the field of predictive modeling of mycotoxins in feed and food crops at harvest, and input data used. A literature review was performed using the databases Scopus and Web of Science, with the aim to create an overview of existing mycotoxin prediction models. From the 190 hits, 26 records were used in the following step. This step is the data extraction and organization, where the records are read systematically, and 12 key characteristics are extracted. Most of the records focused on grains, with only three of the 26 looking at other foods, of which only one looked at tomatoes. Most of the predictive models are empirical and some of the most recent studies employed machine learning techniques as well. The top five most used input variables are temperature, relative humidity, preceding crop, rainfall and location. From the data extraction, four major themes emerged: data types and prediction, modeling and machine learning, model and data integration and fungal (Fusarium spp.) behavior. These themes collectively shape the overview of the current mycotoxin prediction models available. There is a strong emphasis on the need for integration of data and model types, climate change awareness and adaptation and the expansion of current research. The major advice is to conduct more research towards tomatoes, as well as to integrate modeling techniques and input variables.

Overview and objectives

This report is part of the Food SafeR, a Horizon Europe funded project.

The objective of the specific work package (WP3): "Chemical Risks Emergence" to extend the available tools and methods for combatting chemical hazards that can pose a human risk in Europe. Within WP3, several smaller goals are set which work in synchronicity. This includes studying secondary metabolites from plants and fungi via horizon scanning and mass spectrometric screening, advancing smartphone-based sensing and diagnostic tools for pyrrolizidine alkaloids, degradation of furans via innovative food processing techniques and big data machine learning prediction of mycotoxin and plant toxin occurrence. This report is part of the advancement of prediction tools for mycotoxin and plant toxin emergence (Task 3.1). The research objective of this report (deliverable 3.1) is creating an overview of the currently available prediction models for fungal infection and mycotoxin production in grains and tomatoes.



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Introduction

Food safety

Every year, millions of consumers are at risk of illnesses caused by food safety hazards (World Health Organization, 2015). These hazards can be biological, chemical and physical (World Health Organization & Nations, 2006). Chemical food safety hazards can cause serious food borne illnesses and bring the safety of food and trust in the food system in jeopardy. One of the main group of chemical hazards are mycotoxins and plant toxins, which are both natural toxins occurrent in arable crops.

Mycotoxin and fungal species

Mycotoxins are secondary fungal metabolites produced by filamentous fungi, which are harmful to humans and animals (Medina et al., 2017). The prominent fungi for mycotoxin production are *Fusarium* spp., *Aspergillus* spp. and *Penicillium* spp. species. These fungal species can infiltrate the food chain by contaminating plants or by developing on finished products. Here they can produce mycotoxins, the most common and commercially important being Aflatoxin (AF), ochratoxins (OTA), fumonisins, trichothecenes (TH), patulin (PAT), citrinin (CIT), and zearalenone (ZEA) (El-Sayed et al., 2022). Some of the fungal species can produce more than one type of mycotoxin (Wang, Liu, et al., 2022), and at the same time, some of these mycotoxins can be different fungal species Mycotoxins are the most toxic chemical agents found in food and feed, they can affect various organs and cause acute or chronic poisoning (Yin et al., 2018). Table 1 - adapted from El-Sayed et al., 2022 - present an overview of the mycotoxins, fungal species and major foods they can contaminate.

Mycotoxins	Genus/species	Major Foods
Aflatoxin	Aspergillus flavus	Cereals, oilseeds, coconut
	A. parasiticus	
	A. nomius	
Fumonisin	Fusarium verticillioides	Cereals, corn
	F. culmorum	
Ochratoxin	Aspergillus ochraceus	Cereals, herbs, oilseeds, figs,
	Penicillium nordicum	beef jerky, fruits, and wine
	P. verrucosum	
Patulin	Aspergillus terreus	Wheat, apples, grapes,
	A. clavatus	peaches, pears, apricots,
	Penicillium carneum	olives, cereals

Table 1. An overview of major mycotoxins, their corresponding generating fungal species and major food groups they are commonly found in. Table is adapted from El-Sayed et al., 2022.



	Penicillium clavigerum	
	P. griseofulvum	
Trichothecenes	Fusarium oxysporum	Cereals, legumes, fruits, and
	<i>Fusarium</i> spp.	
	Cephalosporium	
	Trichoderma	
Zearalenone	F. graminearum	Cereals, corn
	F. culmorum	
	Fusarium spp.	

Factors affecting fungal growth and modeling

Both fungal growth and mycotoxin production fluctuate and are dependent on biological, agronomic, geographic and environmental factors (Li et al., 2023). Biological factors involve the living organisms and their interactions, such as insect damage and fungal species. Agronomic factors can include plant stresses, crop rotation, tillage methods and drying methods. Geographical location can be longitude and latitude, and also altitude. Environmental factors can include relative humidity, rainfall, temperature and droughts. The impact of these factors are different for each crop, fungi and mycotoxin. By monitoring and collecting field data, correlations between the factors and mycotoxin contamination can be found. For example, Klem et al. (2007) estimated that 48% of the variation of the content of the mycotoxin deoxynivalenol (DON) in wheat can be attributed to environmental effects (Klem et al., 2007). These correlations between influencing factors with the occurrence of the mycotoxin(s) can be collected into a predictive model, where agronomic, geographic and environmental factors act as inputs and mycotoxin contamination as output. Here the combined factors can give even more complete insights, for instance that warm, rainy and humid weather during flowering can increase the probability of DON accumulation in oat grains (Hjelkrem et al., 2017). Models can therefore offer insights in mycotoxin contamination, which is important for food safety and risk mitigation, agricultural management practice decision making and monitoring climate change effects (Damianidis et al., 2018; Medina et al., 2017).

Different types of models

Various types of predictive models exist. The main distinction between model types is mechanistic or empirical. Mechanistic models simulate the biological processes involved in fungal contamination, including plant interactions and mycotoxin formation (Liu et al., 2021). Empirical models use statistics and data analysis, a classic method used is logistic regression (Liu et al., 2018).



Each type of model has its benefits and drawbacks. In the case of a mechanistic model, the benefit is its ability to operate more easily in changing conditions, such as climate change, as compared to empirical models. However, to create a mechanistic model, extensive experimental data and research is required to develop the knowledge of the underlying biological processes (Liu et al., 2018). For empirical modeling a bias can arise from the low mycotoxin concentrations in field and monitoring data, which makes it difficult for the model to predict samples with high mycotoxin levels (Liu et al., 2021). Furthermore, empirical models need all the input data to be available, to be able to run the model, which are not always available. Recently, machine learning models have been making their debut in predictive mycology as well. Machine learning can bypass some of the drawbacks of the empirical model and even combine with mechanistic models (Liu et al., 2021).

Report aim

There has been a growing trend in developing models for predicting mycotoxin contamination. In this report currently available pre-harvest prediction models for fungal infection and mycotoxin production in grains and tomatoes are reviewed. The goal is to understand which predictive models have been created in order to combine or extend these models in the remaining of the project. To this end, a literature review has been performed to create an overview of the existing mycotoxin and fungal growth prediction models. We will end this report on a future outlook and advice for the next steps in the project.

Method

Literature search

Existing mycotoxin prediction models are identified via a literature review. The literature review is conducted in Scopus and Web of Science. Language and time period is not included as restriction. The search is conducted to identify prediction models for mycotoxin production in grains, tomatoes and other food products. The search string for Scopus is: TITLE-ABS-KEY("mycotoxin" AND "model" AND "food" AND "predict"). The search string for Web of Science is: TS=("mycotoxin" AND "model" AND "food" AND "predict"). No suitable synonyms are identified or used. The duplicates are removed and the records are screened based on the following exclusion criteria. Records are also removed for lack of predictive modeling, lack of detail and for being out of scope. The records that focused on toxicological and health aspects, non-food and cell or microbiological experiments or on post-harvest are considered out of scope.



Data extraction and organization

The final records kept in the scope are subject to full text screening and data extraction and organization. This involves capturing key characteristics of studies in a standardized form (Schmidt et al., 2021). In this report 12 characteristics are used for the records, which together create a structured and informative Excel sheet which enables effective comparison and analysis. These key characteristics are explained in the Table 2.

No.	Key characteristic	Description		
1	Type of article	This characteristic indicates the general category or type of the article		
2	Multiple models or datasets	Indicates whether the study involved multiple models or datasets		
3	Location of study	Specifies the geographic location where the study was conducted		
4	Type of study	Describes the nature and purpose of the study		
5	Amount of samples	Record the number of samples or data points included in the study		
6	Type of predictive modeling	Specifies the type of predictive modeling technique used		
7	Fungal species	Identifies the specific fungal species of interest		
8	Crop or food product	Indicates the crop that the study focuses on		
9	The modelled mycotoxin	Describes the specific mycotoxin being predicted		
10	Year range	Specify the range of years during which the study's data was collected		
11	Attributes included in model	Lists the attributes or variables included in the predictive model		
12	Future advice or implications	Capture recommendations, implications, or insights provided by authors		

Table 2. The 12 key characteristics for the data extraction and organization of the literature review records.

After carefully organizing the data using the 12 key characteristics, descriptive statistics of the relevant articles were used, such as to compare the different predictive fungal models in an understandable way. By using statistical tools, we're able to spot trends, differences, and similarities that show how different factors play a role in predicting mycotoxin contamination.

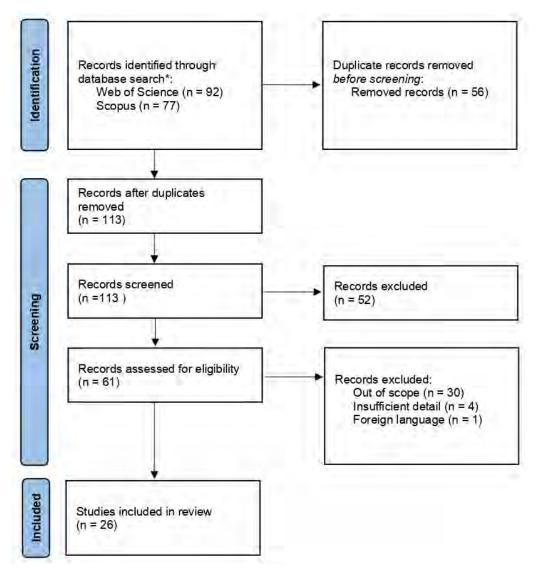


Results and discussion

Literature records

From the literature search 169 records are identified. Of these, 56 duplicates are removed. During the first screening a further 52 records are removed based on their title and abstract. The 61 remaining records are read in full and another 35 records are excluded based on the exclusion criteria. A final 26 records are kept for the data extraction and organization. This process is also depicted in the PRISMA flow diagram illustrated in Figure 1.

Figure 1. PRISMA flow diagram of the literature review record selection





Descriptive statistics

The records included from the review are read thoroughly and descriptive statistics are performed on the 12 key characteristics. The 26 records are a mix of articles (80.8%), reviews (15.4%) and one scientific report (3.8%). 38.4% of records have only one model or dataset, therefore primarily multiple models or datasets have been used in previous predictive modeling research. Figure 2 presents the geographic origin of the datasets or modeled countries. Three reviews included models from over the whole world and the other one review included models specific to the African continent.

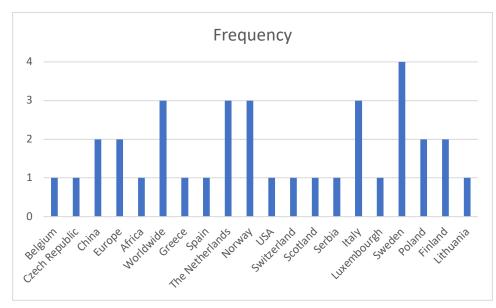


Figure 2. Frequency of geographic regions from records in literature review

The year ranges for data collection and modeling varied from the minimum year of 1977 and the maximum year of 2100. Certain models focused on the immediate future, while others are more focused on predicting decades into the future. These often look at climate change effects on mycotoxin contamination.

The amount of samples or data points included in the records ranged from 310 to 225400. The latter existing of geographical grid number multiplied by 100 years for future forecasting. This was a common variation in the records. Some of the records mentioned field data, while others referenced grid data which was mostly in the tens of thousands of data points. In some papers the mycotoxin concentration data was not or hardly described, making it difficult to understand what their data existed of and how it might introduce bias.

The records covered various fungal species and crops, as shown in Figure 3. Two records covered a broad array of fungal species and are therefore noted as "many", another two records did not



cover any crop but looked at the fungal growth regardless of crop and are therefore labelled at N/A. Tomatoes, feed products, and olives were tied in least frequently modelled commodities. This is an important consideration for this project, even though all crops are considered in the literature search, available predictive modeling of mycotoxins mostly focused on grains. So future research should focus on the other relevant affected commodities, such as tomatoes.

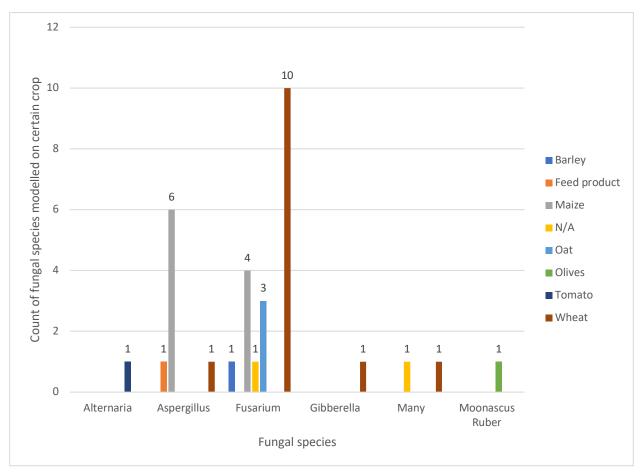


Figure 3. Bar chart of the count of fungal species and food products that were modelled.

Each study focused on mycotoxin contamination and some even considered multiple mycotoxins. The chart in Figure 4 presents the frequency of each mycotoxin covered by the predictive models included in the literature review. DON is the most frequent mycotoxin, with aflatoxin as second most frequently modelled mycotoxin in the records.



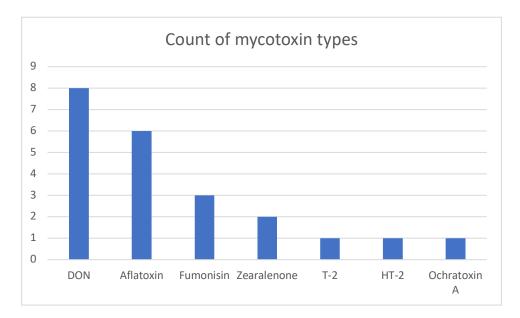


Figure 4. Frequency of mycotoxin types included in predictive models in the literature review records.

Comparison of models

There were many different types of modeling, with many of the included studies using more than one modeling technique. In Table 3 each model is listed and briefly explained. Furthermore, they are categorized as empirical (data driven models using observed patterns) or mechanistic (based on underlying biological processes). If the model is empirical, it is mentioned if it is machine learning technique. Here we can start comparing models and understand the different predictive tools available.

Table 3. Modeling techniques used in the available studies from the literature review. They are classified according to type and a brief description is given of the technique from the records.

Modeling Technique	Туре	Description		
Agro-Meteorological	Empirical	Incorporates weather radar data for agro-		
Model		meteorological predictions.		
Generalized Linear	Empirical	Links response variables to predictor		
Model (GLM)		variables for mycotoxin prediction.		
Logistic Regression	Empirical	Estimates likelihood of mycotoxin presence		
		based on input variables.		
Mixed Effect Logistic	Empirical	Combines fixed and random effects to		
Regression		account for interactions.		



Bayesian Network	Empirical, Machine learning	Models probabilistic dependencies among variables for mycotoxin presence prediction.		
Decision Trees	Empirical,	Hierarchical structures for classification and		
	Machine learning	regression based on conditions.		
Extreme Gradient	Empirical,	Utilizes boosting framework for enhanced		
Boosting (XGB)	Machine learning	predictive performance.		
Generalized Boosting	Empirical,	Combines weak learners to form strong		
Model (GBM)	Machine learning	predictive model.		
Maximum Entropy	Empirical,	Estimates uniform distribution for		
(MaxEnt)	Machine learning	presence-only data.		
Neural Network	Empirical,	Mimics human brain functions for pattern		
	Machine learning	recognition in mycotoxin prediction.		
Support Vector	Empirical,	Employs linear and nonlinear models for		
Machine (SVM)	Machine learning	classification and regression tasks.		
Dynamic Simulation	Empirical/Mechanistic	Forecasts mycotoxin risk by considering		
Model		weather, crop growth stages, and disease		
		observations.		
Mechanistic Logistic	Empirical/Mechanistic	Integrates mechanistic insights with logistic		
Regression Model		regression for mycotoxin prediction.		
Surface Range	Empirical/Mechanistic	Defines habitat suitability and spatial		
Envelope		distribution for species.		
Growth Kinetic Models	Mechanistic	Studies mycotoxin growth over time,		
		factoring in environmental influences.		

These models all required input variables. The inputs used in the models are combined and summarized in Table 4, showing which inputs are the most popular and often used in the existing predictive fungal modeling. This allows us to compare the input variables, and see which input variables should be considered in future models. Crop type and mycotoxin/fungal spp. are relevant for each model, making these basic input variables and therefore they have the highest frequency. For this same reason we look towards the next input variables. Temperature, relative humidity, preceding crop and rainfall are the four most mentioned input variables after the basic variables. Location is the only geographic input variable, but is almost as often used as the top four input variables previously listed.



Table 4. Input variables for predictive models, their frequency in the records of the literature review and the type of input variable it is. This can be agronomic, geographic or environmental/meteorological. Crop type and mycotoxin/fungal spp. are basic input variables.

Input variable	Frequency	Type of variable
Crop type	26	Agronomic
Mycotoxin/fungal spp.	26	Agronomic
Temperature	14	Environmental/Meteorological
Relative Humidity	12	Environmental/Meteorological
Preceding Crop	11	Agronomic
Rainfall	11	Environmental/Meteorological
Location	8	Geographic
Crop health	6	Agronomic
Crop Phenology	5	Agronomic
Pest and Disease Control Practices	4	Agronomic
Wind information	3	Environmental/Meteorological
Spore Dispersion Data	3	Environmental/Meteorological
Crop Variety Resistance	2	Agronomic
Air Pressure	2	Environmental/Meteorological
Sunshine Duration	2	Environmental/Meteorological
Flowering Date	2	Agronomic
Length of time between flowering-harvest	2	Agronomic
Grain Moisture	2	Agronomic
Kernel Moisture at Harvest	2	Agronomic
Cropping System Factors	2	Agronomic
CO2 Emissions	2	Environmental/Meteorological
Fertilization Type and Dose	2	Agronomic
Dew Point	1	Environmental/Meteorological
Frost	1	Environmental/Meteorological
Sowing and Harvest Week	1	Agronomic
Temperature Seasonality	1	Environmental/Meteorological
Water Activity	1	Environmental/Meteorological
pH Level	1	Environmental/Meteorological
Growing Days	1	Agronomic
Type of Soil	1	Agronomic
Type of Tillage	1	Agronomic
Plants per m ²	1	Agronomic
Number of Irrigation Interventions	1	Agronomic



Meteorological Models	1	Environmental/Meteorological
Sowing Date	1	Agronomic
Satellite Data (Netherlands)	1	Environmental/Meteorological

Future advice and implications

From each study we extracted any future advice and implications mentioned by the authors. This section discusses the main themes found. Four themes are found and are described in more detail below.

Data and Prediction:

Weather data is crucial for mycotoxin prediction models, especially before anthesis in case of *Fusarium spp*. (Marzec-Schmidt et al., 2021). Temperature and water activity significantly influence all types of fungal growth (Torelli et al., 2012). Just by using weather data, it is possible to achieve accurate predictive models (Panagou & Kodogiannis, 2009). Climate change will affect the weather, and therefore fungal growth and mycotoxin production (Ejaz et al., 2023). Especially aflatoxin contamination will likely increase with climate change (Battilani et al., 2016). Climate change can affect environmental inputs, such as increased temperatures and reduced annual rainfall. To this end, a drought index has been shown to predict aflatoxin contamination (Damianidis et al., 2018).

Agronomics was less often employed as input variable compared to weather data, besides the two basic input variables. In many of the included studies a call was made to also include agronomics in the future (Liu et al., 2021; Wang, Bouzembrak, et al., 2022). When agronomics was used, the most common were crop variety, mycotoxin/fungal spp., preceding crop, crop health and crop phenology (Klem et al., 2007; Li et al., 2023). Agronomics input require a lot of information from the agricultural setting the samples come from, making it a more intensive input to include.

Geographical data was often used, in the form of location. This could be only longitude and latitude, either in the form of grids or regions, and in some cases even altitude (Battilani et al., 2016; Skelsey & Newton, 2015). One record used geographic input in a different way, by using satellite imaging as input variable (Wang, Liu, et al., 2022). It was found that on its own it only leads to an average performing model and should be combined with environmental or agronomic inputs.

Modeling and machine learning:

One of the important themes for the future of the FoodSafeR project is data and modeling. Regression analysis are a classical approach and are still used today (Battilani et al., 2016; Pallez-



Barthel et al., 2021). However, machine learning is an up and coming field and is also starting to be used in prediction of mycotoxins (Castano-Duque et al., 2022). It was found that machine learning algorithms worked well in comparison to classic techniques (Liu et al., 2018; Wang, Bouzembrak, et al., 2022). Especially neural networks were found to be a promising approach to predict mycotoxin contamination of crops (Camardo Leggieri et al., 2021; Klem et al., 2007; Pallez-Barthel et al., 2021; Panagou & Kodogiannis, 2009). In the future, more mycotoxin prediction could be done with machine learning techniques, alone or in combination with other techniques, this would also allow for tailoring of the models on specific situations (Nji et al., 2022)

Integration

On both the input and the modeling side, there is a push to combine and integrate various types of data and methods. Mostly the integration is about environmental and agronomic input data into one model. Other inputs to be integrated are satellite imaging and genetic profiles of fungal species and or the food crops they contaminate. The input combinations are found to improve mycotoxin prediction accuracy. As one paper put it, the wider the range of inputs, the better the prediction (Battilani et al., 2008). On the modeling side, integration of models allows for reduction of bias, increase of accuracy and combining the strength of the various methods (Liu et al., 2018). Therefore, integration is an important theme, as it can give better decision making advice.

Fusarium spp. and Mycotoxin Behavior:

Fusarium spp. and its mycotoxins was the most modelled fungal species. Therefore, in this theme, a small overview of the most important findings relating to *Fusarium* spp. and its mycotoxins are given. A call is made to conduct yearly *Fusarium* spp. surveys or field trials to better understand their mycotoxins behavior (Landschoot et al., 2013). We already understand how DON contamination in wheat is influenced by weather conditions around flowering and close to harvest (Hjelkrem et al., 2017). For example wet years and a previous maize crops lead to higher concentrations of DON in wheat (Pallez-Barthel et al., 2021).

For the future, an integration recommendation is made to incorporate *Fusarium* spp. genetics into predictive models as there is great variation between *Fusarium* spp. (Pallez-Barthel et al., 2021). Another future advice is related to climate change. Climate change will also affect *Fusarium* spp. and its mycotoxin behavior, we should become more aware of this and prioritize research into *Fusarium* spp. behavior and mycotoxin formation (Ejaz et al., 2023; Liu & Van der Fels-Klerx, 2021; Van de Perre et al., 2015).



Conclusion

The goal of this report is to understand what predictive models have been created in order to combine and extend on these models in the future of the project. Currently available prediction models for fungal infection and mycotoxin production in grains and tomatoes were reviewed. This gave insights into the different types of predictive modeling for mycotoxin contamination and fungal growth pre-harvest. Most of the models are for wheat and/or maize, unfortunately only one model was created for tomatoes. In the future, more research should be done to understand mycotoxin contamination and fungal growth on tomatoes.

The main emphasis of the results is on data, modeling, integration and *Fusarium* spp. behavior. Furthermore, there was a strong push to consider climate change and how it might affect the future of food safety Of the models, many are empirical and some are machine learning models as well. This was found to give accurate predictions in the implications, especially when combining with mechanistic modeling and using agronomic, geographic and environmental factors integrated together. The top five most used input variables are temperature, relative humidity, preceding crop, rainfall and location, after the basic input variables of crop type and mycotoxin/fungal spp.

In the future, climate change should be considered more, tailor made models for crop, geography, fungal species and even stakeholders should be made. Long term data collection using field surveys is necessary, preferable with geolocation to allow for future use of satellite images to increase the performance of the predictive models. Also integration of agronomic, weather and geographic data should be emphasized for improved accuracy This integration is also relevant for modeling, different modeling approaches have their strengths and weaknesses; a combined approach shows to work well.

Currently the models for tomatoes are very limited, the major advice from this review is to conduct more research towards tomatoes, to collect dedicated data from field over multiple years, and to integrate modeling techniques and input variables.



Bibliography

- Battilani, P., Pietri, A., Barbano, C., Scandolara, A., Bertuzzi, T., & Marocco, A. (2008). Logistic Regression Modeling of Cropping Systems To Predict Fumonisin Contamination in Maize. *Journal of Agricultural and Food Chemistry*, *56*(21), 10433–10438. https://doi.org/10.1021/jf801809d
- Battilani, P., Toscano, P., Van der Fels-Klerx, H. J., Moretti, A., Camardo Leggieri, M., Brera, C., Rortais, A., Goumperis, T., & Robinson, T. (2016). Aflatoxin B1 contamination in maize in Europe increases due to climate change. *Scientific Reports*, 6(1), Article 1. https://doi.org/10.1038/srep24328
- Camardo Leggieri, M., Mazzoni, M., & Battilani, P. (2021). Machine Learning for Predicting Mycotoxin Occurrence in Maize. *Frontiers in Microbiology*, *12*. https://www.frontiersin.org/articles/10.3389/fmicb.2021.661132
- Castano-Duque, L., Vaughan, M., Lindsay, J., Barnett, K., & Rajasekaran, K. (2022). Gradient boosting and bayesian network machine learning models predict aflatoxin and fumonisin contamination of maize in Illinois – First USA case study. *Frontiers in Microbiology*, 13. https://www.frontiersin.org/articles/10.3389/fmicb.2022.1039947
- Damianidis, D., Ortiz, B. V., Windham, G. L., Bowen, K. L., Hoogenboom, G., Scully, B. T., Hagan, A., Knappenberger, T., Woli, P., & Williams, W. P. (2018). Evaluating a generic drought index as a predictive tool for aflatoxin contamination of corn: From plot to regional level. *Crop Protection*, *113*, 64–74. https://doi.org/10.1016/j.cropro.2018.07.013
- Ejaz, M. R., Jaoua, S., Ahmadi, M., & Shabani, F. (2023). An examination of how climate change could affect the future spread of Fusarium spp. Around the world, using correlative models to model the changes. *Environmental Technology & Innovation*, 31, 103177. https://doi.org/10.1016/j.eti.2023.103177
- El-Sayed, R. A., Jebur, A. B., Kang, W., & El-Demerdash, F. M. (2022). An overview on the major mycotoxins in food products: Characteristics, toxicity, and analysis. *Journal of Future Foods*, 2(2), 91–102. https://doi.org/10.1016/j.jfutfo.2022.03.002
- Hjelkrem, A.-G. R., Torp, T., Brodal, G., Aamot, H. U., Strand, E., Nordskog, B., Dill-Macky, R., Edwards, S. G., & Hofgaard, I. S. (2017). DON content in oat grains in Norway related to weather conditions at different growth stages. *EUROPEAN JOURNAL OF PLANT PATHOLOGY*, 148(3), 577–594. https://doi.org/10.1007/s10658-016-1113-5
- Klem, K., Vanova, M., Hajslova, J., Lancova, K., & Sehnalova, M. (2007). A neural network model for prediction of deoxynivalenol content in wheat grain based on weather data and preceding crop. *PLANT SOIL AND ENVIRONMENT*, *53*(10), 421–429. https://doi.org/10.17221/2200-PSE
- Landschoot, S., Waegeman, W., Audenaert, K., Van Damme, P., Vandepitte, J., De Baets, B., & Haesaert, G. (2013). A field-specific web tool for the prediction of Fusarium head blight



and deoxynivalenol content in Belgium. *Computers and Electronics in Agriculture, 93*, 140–148. https://doi.org/10.1016/j.compag.2013.02.011

- Li, S., Liu, N., Cai, D., Liu, C., Ye, J., Li, B., Wu, Y., Li, L., Wang, S., & van der Fels-Klerx, H. J. (2023). A predictive model on deoxynivalenol in harvested wheat in China: Revealing the impact of the environment and agronomic practicing. *Food Chemistry*, 405, 134727. https://doi.org/10.1016/j.foodchem.2022.134727
- Liu, C., Manstretta, V., Rossi, V., & Van der Fels-Klerx, H. J. (2018). Comparison of Three Modelling Approaches for Predicting Deoxynivalenol Contamination in Winter Wheat. *Toxins*, 10(7), Article 7. https://doi.org/10.3390/toxins10070267
- Liu, C., & Van der Fels-Klerx, H. J. (2021). Quantitative Modeling of Climate Change Impacts on Mycotoxins in Cereals: A Review. *Toxins*, 13(4), Article 4. https://doi.org/10.3390/toxins13040276
- Liu, N., Liu, C., Dudaš, T. N., Loc, M. Č., Bagi, F. F., & van der Fels-Klerx, H. J. (2021). Improved Aflatoxins and Fumonisins Forecasting Models for Maize (PREMA and PREFUM), Using Combined Mechanistic and Bayesian Network Modeling—Serbia as a Case Study. *Frontiers in Microbiology*, 12.

https://www.frontiersin.org/articles/10.3389/fmicb.2021.643604

- Marzec-Schmidt, K., Börjesson, T., Suproniene, S., Jędryczka, M., Janavičienė, S., Góral, T., Karlsson, I., Kochiieru, Y., Ochodzki, P., Mankevičienė, A., & Piikki, K. (2021). Modelling the Effects of Weather Conditions on Cereal Grain Contamination with Deoxynivalenol in the Baltic Sea Region. *Toxins*, *13*(11), Article 11. https://doi.org/10.3390/toxins13110737
- Medina, Á., González-Jartín, J. M., & Sainz, M. J. (2017). Impact of global warming on mycotoxins. *Current Opinion in Food Science*, 18, 76–81. https://doi.org/10.1016/j.cofs.2017.11.009
- Nji, Q. N., Babalola, O. O., & Mwanza, M. (2022). Aflatoxins in Maize: Can Their Occurrence Be Effectively Managed in Africa in the Face of Climate Change and Food Insecurity? *TOXINS*, 14(8), 574. https://doi.org/10.3390/toxins14080574
- Pallez-Barthel, M., Cocco, E., Vogelgsang, S., & Beyer, M. (2021). Frequency of Deoxynivalenol Concentrations above the Maximum Limit in Raw Winter Wheat Grain during a 12-Year Multi-Site Survey. AGRONOMY-BASEL, 11(5), 960. https://doi.org/10.3390/agronomy11050960
- Panagou, E. Z., & Kodogiannis, V. S. (2009). Application of neural networks as a non-linear modelling technique in food mycology. *Expert Systems with Applications*, 36(1), 121– 131. https://doi.org/10.1016/j.eswa.2007.09.022
- Schmidt, L., Olorisade, B. K., McGuinness, L. A., Thomas, J., & Higgins, J. P. T. (2021). Data extraction methods for systematic review (semi)automation: A living systematic review. *F1000Research*, 10, 401. https://doi.org/10.12688/f1000research.51117.1



- Skelsey, P., & Newton, A. C. (2015). Future environmental and geographic risks of Fusarium head blight of wheat in Scotland. EUROPEAN JOURNAL OF PLANT PATHOLOGY, 142(1), 133–147. https://doi.org/10.1007/s10658-015-0598-7
- Torelli, E., Firrao, G., Bianchi, G., Saccardo, F., & Locci, R. (2012). The influence of local factors on the prediction of fumonisin contamination in maize. *Journal of the Science of Food and Agriculture*, *92*(8), 1808–1814. Scopus. https://doi.org/10.1002/jsfa.5551
- Van de Perre, E., Jacxsens, L., Liu, C., Devlieghere, F., & De Meulenaer, B. (2015). Climate impact on Alternaria moulds and their mycotoxins in fresh produce: The case of the tomato chain. *Food Research International*, 68, 41–46. https://doi.org/10.1016/j.foodres.2014.10.014
- Wang, X., Bouzembrak, Y., Oude Lansink, A. G. J. M., & van der Fels-Klerx, H. J. (2022). Designing a monitoring program for aflatoxin B1 in feed products using machine learning. *Npj Science of Food*, 6(1). Scopus. https://doi.org/10.1038/s41538-022-00154-2
- Wang, X., Liu, C., & van der Fels-Klerx, H. J. (2022). Regional prediction of multi-mycotoxin contamination of wheat in Europe using machine learning. *Food Research International*, 159, 111588. https://doi.org/10.1016/j.foodres.2022.111588
- World Health Organization, & Nations, F. and A. O. of the U. (2006). *Food safety risk analysis: A guide for national food safety authorities*. World Health Organization. https://apps.who.int/iris/handle/10665/43718
- Yin, S., Liu, X., Fan, L., & Hu, H. (2018). Mechanisms of cell death induction by food-borne mycotoxins. Critical Reviews in Food Science and Nutrition, 58(8), 1406–1417. https://doi.org/10.1080/10408398.2016.1260526