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Biosynthesis uses, and defensive mechanisms of *kauralexins* and *zealexins* against fungi that attack maize *(Zea mays)* crops - A Review

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Abstract, Fungal pathogens have a major impact on maize crops, leading to heavy losses in yield production globally. Secondary metabolites are biochemical compounds that play a crucial role in the stress and defense mechanism of plants. They control several biotic and abiotic stresses and their related side effects. Fungi cause high-impact diseases to bio-organisms such as plants, animals, and humans. Evidently, throughout the world, a notable feed and used industrial product source is "*Corn*". Earlier studies have shown diverse approaches in plant defense mechanisms for plant growth and development. Here, we can see a brief overview of the biosynthesis of phytoalexin derivatives, namely labdane-type diterpenoids *kauralexins* and acidic sesquiterpenoids *zealexins*, a mode of action against fungal pathogens in maize crops. Additionally, past and current trending approaches to plant-pathogen interactions have used bioinformatics and metabolomics tools for disease resistance, database tools of plant metabolomics, and especially focused on resource database tools of plant-fungus interactions. Furthermore, this review is to point out the antifungal defense mechanisms of bioactive diterpenoid compounds derived from *"Phytoalexins", kauralexins and zealexins*, in maize (*Z.mays*) crops.

Keywords: Phytoalexin, fungal disease, kauralexin biosynthesis, secondary metabolites, metabolomics, plant-fungus interaction.

Classification numbers ***:*** 1.5.3, 2.7.1, 2.7.2

1. INTRODUCTION

Fungal diseases are pre-eminent hazards to the most important crops on which humanity depends. Their effect on the globalized food system is spreading throughout the world which causes major epidemics that severely reduce the production. For example, *Ustilagomaydis*, the most significant fungal pathogen in corn smut for maize has spread to most places where maize are ingrown and can lead to at least 20 % crop loss [1]. Maize is the third most essential food crop in the world exceeded only by two other grains, rice and wheat [2]. Maize, also called corn, is accepted to have originated in central Mexico 7000 years ago from a wild grass. The native Americans revolutionized maize into a better source of food. Maize contains approximately 10 % protein, 72 % starch, and 4 % fat. It provides an energy density of 365 Kcal/100 g and is cultivated all over the world with the United States, China, and Brazil being the topmost three maize producing countries. These countries produce approximately 563 million tons out of 717 million metric tons/per year. Maize is found in several colours ranging from red to black to white to yellow. A diverse range of maize is grown throughout the world, with one paramount difference being colour only [3].

Exponential population growth followed by dietary habits and food style has made people realize the legitimate importance of a diet**.** A surge in worldwide demand for maize necessitates the increase in cultivation at an annual rate of 2 %. Recent advancements in technology and understanding the genetic traits will have a positive impact on cultivation on a large scale. According to an FAO survey report, world cereal production in 2019 was about 2.719 million tonnes, an increase of nearly 62 million tonnes, corresponding to an increase in output of 2.3 % compared to 2018 [4]. But, yet many factors like climate change, microbial pathogen *(fungal disease)* negatively impact maize cultivation. A drastic change in climatic conditions poses a greater risk to maize production, increasing market instability**.** Here, we focus on fungal diseases in maize crops. The plants have biotic stress caused by pathogens, insects, and nematodes. Naturally, the microorganisms cause several diseases in plants [5].

The phytopathogenic fungi classified as *necrotrophs, hemibiotrophic,* and *biotrophs* establish one of the leading infectious agents in plants, causing mutations during developmental stages including post-harvest [6]. To elaborate, the fungi are pint-sized, commonly microscopic, typically filamentous, eukaryotic, spore-bearing organisms that lack *chlorophyll*. Their cell walls are composed of *chitin* and *glucan* forming skeletal compartment and are fixed in a matrix of polysaccharides and glycoproteins. **"***Oomycota,* commonly known as oomycetes, were untill 1990 considered true fungi [5]. Under natural conditions, a vast array of secondary metabolites are generated in plants [7]. Plants and fungi are rich sources of thousands of secondary metabolites *(the number of compounds exceeds 100,000)* that are usually concerned as not crucial for life while their role is quite versatile [8, 9]. The secondary metabolites in plants are usually a part of their protective mechanism against phytopathogens. Plants form the secondary metabolites that can either be a part of the normal schedule of growth *(antifungal compounds performances),* or it can happen in response to an attack of pathogens *(antifungal compounds or phytoalexins are activated)* [10]. Here, we brief about one of the plant's secondary metabolites belonging to *Poaceae* family member maize crops that produce *diterpenoid* phytoalexins.

Other metabolites named *kauralexins* and acid *sesquiterpenoids* are known as *zealexins*. Compounds with low molecular weight and antimicrobial activity accumulate in these plants in response to pathogen attack [11]. For example, The synthesis of phytoalexins insoluble in *chitin* fragments released from fungal cell-wall through the action of plant *chitinases* was found to serve biotic elicitors related to defense mechanism responses [12]. Nowadays, plant pathologists have preferably relied on phenotypic and molecular assays to access protein interactions, gene expression, and symptoms of developments. To understand overall plant diseases, several advanced methodologies have been used, and studies using plant model organisms such as *Tomato, Arabidopsis thaliana*, and *Maize* have been carried out. To sum up, the studies of plant-pathogen are integrated by the observations of host metabolism that have bricked the way to a better understanding of plant disease mechanisms [13].

A good illustration of metabolomics has proven to be very fast and superior to any other post-genomics technology of biological samples pattern recognition analysis [14]. Metabolites perform divergent roles in *plant-pathogen interactions*, *pathogen attack scrutiny, enzyme regulation*, *signal transduction, cell-to-cell signalling,* and *anti-microbial activities* [13]. The pathogens may inhibit the production of defense compounds at many levels. Plants exactly monitor and adjust defense accumulation by integrating them directly into regulatory feedback loops allowing the biosynthesis of final steps [15]. So, in this review, we can focus on elaborate *metabolomics* and *bioinformatics tools* related approaches in plant-pathogen interactions, specifically in defense response role of *kauralexins* and *zealexins* compounds against fungal pathogens, a mode of active defense mechanism in diverse fungal pathogens in maize *(Zea mays)* crops. Next, we will see more on fungi and their maize diseases. In this review, the authors discuss defects caused by fungi in maize crops.

2. FUNGAL DISEASES *VS M*AIZE *(Z.MAYS)* CROPS

On the whole, around 19,000 fungal species have been identified worldwide, of which over 10,000 species can cause plant diseases. All plants are attacked by some varieties of fungi, and each pathogenic fungus can attack one or several kinds of plants. Some fungi are known to play a dual role as *obligate Parasites* or *biotrophs,* where they can grow and accumulate only by remaining, during their whole life, in cooperation with their host plants. *Non-obligate parasites* are those which can complete their life cycles on dead organic matter, or they can grow and proliferate on dead organic matter as well as on living plants [5, 16]. Plant diseases are occasionally grouped as per the symptoms they cause (*rusts, smuts, blights, leaf spots, wilts, root rots*) to plant organs (*stem, foliage, root diseases*), etc. [5]. It is well known that every plant is affected by two types of stresses like *biotic* and *abiotic*, some of which lead to the formation of diseases. *Abiotic* stress is caused by environmental factors, whereas *biotic* stress is due to plants being sessile in nature scrap numerous biotic agents, as well as *fungi, viruses, bacteriae, insects, nematodes*, and *protists*.

There are numerous studies showing that biotic agents remarkably reduce crop yields [1]. Here we describe some plant pathogens belonging to fungal species, mainly in the *phyla Ascomycota* and *Basidiomycota*. In the middle of ascomycetes, plant pathogens are in several classes such as the Sordariomycetes (*e.g. Magnaporthe spp.*), Dothideomycetes (*e.g. Cladosporium spp.*), or the Leotiomycetes (*e.g. Botrytis spp.*). There are two major plant pathogen groups in Basidiomycetes, namely the rusts (*Pucciniomycetes*) and the smuts (*subphylum of Ustilaginomycotoxins*) [17], which are responsible as a cause of several types of diseases in maize crops**.** Usually, fungi cause local or common *necrosis* of plant tissues and they often reduce the growth of plant organs or the whole plant’s excessive growth of infected plants or plant parts caused by similar fungi pathogens [5]. The characteristics of pathogenic fungal families such as morphology, reproduction, classification, ecology, dissemination, etc. have been largely predicted in previous research papers. So, we don’t need an elaborate view of this issue anymore.

Maize is one of the most crucial crops because of its affordability for food, feed, and biofuels. So, this crop is providing multibillion-dollar revenue annually. The classification of maize is based on the size and composition of the endosperm, arising in the artificial definition according to the type of kernel as follows: flint, dent flour, waxy, Indian, pop, sweet, and popcorn. Fungi may cause catastrophic diseases for plants. There are at least five reasons for that: (i) Spores produce a lot of inoculum, some of which sporulate prolifically and further infect plants, (ii) In the suppressed period, the infection and production of further infectious propagules, generally spores, during in-between time occur within only a few days, (iii) Wettable spores can spread on the water surface or form rain-splash droplets, while non-wettable spores can be carried long distances by wind, (iv) The destruction of the plant structure may produce phytotoxic compounds and/or a battery of enzymes, and (v) Plant production is economically beneficial because the part away from nutrients can attract pathogens. Moreover, the induction of production or growth regulators, such as cytokinin, depresses the yields [18]. Details of fungi and their rising diseases and symptoms are elaborated and illustrated in Figure 1. The criteria for distinction or classification are the amount of sugar or sweetness and the amount of enduring sugar, depending on when it is harvested and from which field it is cultivated. With this evidence of maize diversity, we can understand the importance of maize crops and their products [3].

Ultimately, maize and its agronomic emphasis have been the century’s milestone model organism plant for basic research [19]. Although there have been progressive advances in the understanding of disease etiology, the discovery and application of effective methods to protect crops and avoid symbolic losses continue till the present day). Nowadays, diseases have become a global problem and are a matter of great concern [20]. So, accurate diagnostic methods that can be used in-situ for diagnostic detection of plant diseases must be developed and tested on the essentials for data mining and analysis, where high-throughput bioinformatics, computational biology, and DNA sequencing biosensors are improving methods for effectively identifying fungal infections. Moreover, the approaches to fungal diseases are genetic investigations detecting pathogen sources and host resistance, RNA sequencing and double-stranded RNA setup, and fungal genetic biomarkers, etc. Additionally, the analysis of untargeted volatile organic compounds contributes to a broad view of the host biochemical organization, in which highly dissimilar volatile organic compounds must be detected and quantified rapidly and simultaneously [16]. Finally, over the past and current years research reports have demonstrated the plant's secondary metabolites defense mechanisms against fungal pathogens.

3. ROLE OF PLANT SECONDARY METABOLITES

Secondary metabolites, which are present in a huge amount and include a divergent array of organic compounds, are generated by plants and have no direct functions in the growth and development of plants. For example, the processes of photosynthesis, respiration, solute transport, translocation, assimilation, and differentiation of nutrients all demonstrate the role of metabolites [21]. In plants, secondary metabolites can be classified into several categories depending on their biosynthetic principles. A simple classification includes three main groups: (i) Terpenes: *monoterpenes, diterpenes, triterpenes, sesquiterpenes, polyterpenes and tertraterpenes, steroids, saponins, glycosides, and sterols*; (ii) Phenolics: *phenolic acids, lignans, coumarins, stilbenes, flavonoids, tannins, and lignins*; (iii) Nitrogen and sulfur-containing compounds: *GSH, GSL, phytoalexins, thionins, defensins, allinins, and alkaloids*, etc.

[10]. Interestingly, these secondary metabolites are active and offer defense to plants. Next, we will learn about secondary metabolite responses to stress and defense mechanisms in plants.

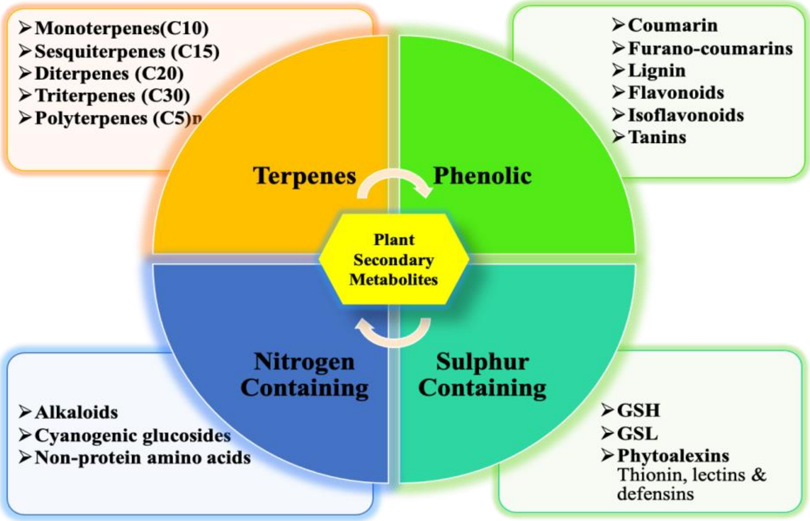

Figure 1. Plant secondary metabolites and their derivatives (*Terpenes, Phenolics, and Nitrogen and sulfur-containing compounds*)

3.1. Stress and Defense Mechanisms of Plant secondary metabolites

Naturally, plants have improved a complex defense system against pathogens and pests. The immune systems of a plant depend on their potential to recognize enemy molecules, transmit signals and respond defensively through pathways that are assumed to be rich in genes and their products [22]. Plants oppose several *abiotic* and *biotic* stresses in nature, but they have to adapt to diverse types of stress. Several types of plant secondary metabolites are presumed to be adaptations of central mechanisms. Secondary metabolites of biosynthetic pathways are entangled in adapting to environmental stresses. For example, the *phenylacetateflavonols* (saiginols) class plays a crucial role in adaptation to high UV-B irradiation, especially in northern latitude plants and the *Tryptophan-derived indoleglucosinolate* biosynthetic pathways involving most *Brassicaceae* species play an important role in plant-pathogen interactions with pathogenic and beneficial microbes [7]. The performance of plant defense mechanisms is demonstrated through bioactive compounds and these secondary metabolites can be *terpenes, phenolic compounds, alkaloids, sulfur and nitrogen compounds,* among others [23]. Several types of symbolic parasites (*fungi, bacteria, mites, insects*) in green plants, including our crops, are used by a host of consumers of virtually every kind to spread via herbivores (*mammals, snails, insects*).

A broad range of defense mechanisms allow plants to survive during their development. Defense mechanisms are predominantly based on avoidance, resistance, or tolerance. Avoidance utilizes before parasitic contacts between parasite and host are acclaimed and lessen the incidence frequency(The utilization of avoidance before parasitic contacts between parasite and host is acclaimed and helps lessen the incidence frequency). It's crucially active against animal parasites and builds such as several mechanisms as volatile repellents**(**It is crucially active against animal parasites and builds several mechanisms involving volatile repellents. Resistance is generally inherent to chemicals; little is known about tolerance, which is very difficult to measure and is of resistance [24]. In maize, genetic resistance is often divided into two major classes: *Qualitative* resistence, or major-gene resistance is high-level resistance, which is commonly race-specific and is based on single major-effect resistance genes (*R-genes*) associated with a swift cell death called hypersensitive response (*HR*). Generally, rapidly overcome when expanding in the field around the point of pathogen entryway.*Quantitative* resistance generally has a polygenic basis and typically remains at moderate levels of resistance that are not race-specific. For example, GWAS *(Genome-Wide Associated Studies)* have decoded important alleles that can be exploited to further develop disease-resistant crops [25]. Quantitative effects responsible for genome regions (or *loci*) are known as Quantitative trait loci (*QTL*). It is frequently effective against *biotrophic pathogens* (Pathogens that take nutrients from living host cells) and *necrotrophic pathogens* (Pathogens that take nutrients from dead cells), the mechanism of quantitative resistance has not been clearly determined but is likely to be fickle depending on the specific interaction [55]. Maize direct defenses against insects include physical defenses such as *lignin*, a primary component of plant cell walls.

Expanded *lignin* concentrations may be correlated with increased resistance against pathogens. For example, European corn borers and fall armyworms have been reported by many reseachers over the years. Another type of chemical defense mechanism in maize includes *protease* inhibitors, whose molecules inhibit protein digestion in the insect gut, and one more evidence is that *phytoalexins*, which are low molecular weight secondary metabolites, are active against a broad diversity of biotic stressors [26, 27]. For example, *cysteine protease, mir1-CP,* increases the resistance of plants against insects such as *aphids, S. frugiperda,* and *Diabrotica spp*. [27]. Additionally, *kauralexins*, which are specific phytoalexins, and *zealexins*, another family of phytoalexins, are active against pathogens [27, 28].

The role of information communication technology in biological research is very momentous. Recently, advances in omicstechnologies, e.g. *genomics*, *proteomics*, or *metabolomics* are allowing to elucidate fundamental relationships between host and pathogen through the pathogen genome sequencing and the plant host effect [28].

3.2. What is the important role of bioinformatics in plant-pathogen interactions?

Besides, the inclusion of plant pathologists in the global food security framework is also useful. In biotechnological studies on plant pathology, the 'concomitant' application stage of bioinformatics mostly occurs after a pathogen has been classified as a causative agent for a given plant host. A wide-ranging bioinformatics framework should also integrate with *interpretations/treatments and data/report* as soon as probable pathogen aggressions are encountered on a forestry or farm plot: Elements of the incursion, capturing *in real-time, sampling/survey, diagnostics, field/laboratory,* and *remedial treatments* have outstanding effects in developing new cultivars or resistance many diseases [28]. Currently, researchers search for all pieces of information collected from the internet. Databases available for biological research via the web have also become a significant platform. There are three types of biological databases that have established and developed: (i) Primary databases or community-specific databases that contain raw nucleotide sequences. For example, *Nucleic Acids Research (http://nar.oxfordjournals.org/), GenBank* for sequences, *EMBL*, and *DDBJ*, etc. [29]; ii) Secondary databases or large-scale public repositories containing highly annotated data, e.g., *SWISS-PROT and UniProt for Protein Information Resource*; and (iii) Specialized databases or project-specific databases included with particular organism and unique data e.g., *FlyBase*, *WormBase*, *TAIR*, *ArrayExpress,* and *Gene Expression Omnibus* [42] for microarray data [30].

The application of different tools of bioinformatics in biological research facilitates the retrieval, storage, analysis, visualization, and annotation of results and benefits a better understanding of biological systems in fullness. Several parts of the tools and application approaches are used in the growth and development of plants, such as *Sequence Analysis and Similarity Searching Tools*, *Genome Sequencing-Based Approaches*, *Transcriptome-Based Approach, Computational Proteomics Approaches, Metabolomics-Based Approach*, *Biological Database, and Genome Annotation*. This will help in plant well-being care-based disease diagnosis to improve the quality of plants [19]. Next, we can learn about one of the bioinformatics tools and the application of metabolomic approaches in fungal diseases of maize crops.

3.3. Role of Metabolomics-Based Approaches in Plant-pathogen Interactions

Metabolomics is one of the rising and delightful approaches of *"omics"* tools, which has now been broadly applied for crop improvement. It is crucial to study abiotic stress tolerance, robust ecotypes, pathogen resistance, and metabolically assisted breeding of crops [31]. This is one of the major disciplines in the so-called "omics" field in the animal, plant, and microbial sciences. It was a concession in the mid-1990s in the field of plant biology, using several studies for gene identification, in which metabolomics was reported [32]. Current years have endorsed massive developments in several *'Omics'* fields, namely *proteomics*, *genomics*, *epigenomics*, *transcriptomics*, *metabolomics*, and *phenomics*. [33]. The integration of metabolomics with current plant genomics tools, such as genome-wide genetic variants, genotype-based sequencing (GBS), and whole-genome sequencing, opens up breathtaking horizons for crop improvement.

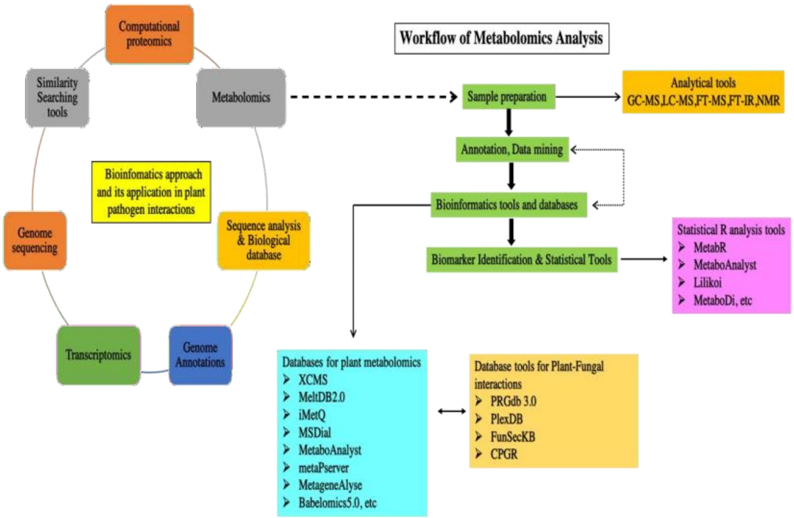

Figure 2. Role of bioinformatics tools and metabolomics approaches for plant growth and development.

The plant kingdom consists of a vast diversity of metabolites with approximately 200,000 compounds and the huge majority remains unknown. It is predicted that around 10,000 secondary metabolites have been discovered in plant species [31]. Metabolomics is a nearly novel approach aimed at enhanced understanding of these metabolic networks and the ensuing biochemical composition of plants and other biological organisms. It includes analytical tools within *GC-MS, LC-MS, FT-MS, FT-IR* and NMR spectroscopy that can account for the effects of time, nutritional status, stress, and environmental perturbations for hundreds of metabolites together resulting in massive complex data sets (Figure 2). It improves the functionality and productivity of plant areas such as stress tolerance, with the advantage of these techniques, and rising metabolic profile data for several crops [34, 35].

Bioinformatics Tools and Databases for plant metabolomics

Recent advances and ongoing challenges being made in four areas of computational informatics are essential to computational metabolomics: (i) *metabolomics LIMS* [29], (ii) *metabolomics databases*, (iii) *metabolic modeling*, and (iv) *spectral analysis tools for metabolomics* [31,36] For data processing, metabolomic data tools and the rest of the related metabolism software are in presented in S1.

Resourceful Database Tools For Plant-Fungus Interactions

Bioinformatics helps analyze fungal genomes and transcrtiptomes with the advent approaches of HiSeq and has enriched knowledge of the interplay between fungi and plants. Datebases including Phytopathogenic Fungi and Oomycete, EST Database [37], IntAct [38], Molecular Interaction Database (MINT) [39] and other related databases are presented in S2**.**

4. DEFENSE RESPONSES OF *KAURALEXINS* AND *ZEALEXINS* AGAINST FUNGAL PATHOGENS IN MAIZE *(Z.MAYS)* CROPS

4.1. Phytoalexins and Their Derivatives

Phytoalexins expose a huge diversity belonging to several chemical families such as *terpenoids, phenolics, sulfur-containing compounds, furanoacetylenes, steroid glycoalkaloids*, and *indoles* [21, 40, 41]. In this review, we can see about fungal diseases against defense mechanisms of *phytoalexins* and their derivatives in maize crops. Plants produced by *Phytoalexins* have low molecular weight antimicrobial compounds. They have a response to abiotic and biotic stresses. Such a sophisticated defence system can be involved in plants allowing control of invading microorganisms [40, 43]. Currently, there are about 30 plant families containing more than 350 phytoalexins that have been chemically characterized according to their families. It is reported that a large number of 130 phytoalexins have been characterized by the *Leguminosae* family. Mostly, the phytoalexins that generate the *Leguminosae* belong to six isoflavonoid classes: *isoflavones, isoflavones, pterocarpans, isoflavones, pterocarpenes, and coumestans.* The structure of phytoalexins depends upon the type of plant family, whose synthesis is sometimes entirely similar. For example, flavonoids are present in most legume phytoalexins, terpenoids in the *Solanaceae* family, and diterpenes in the *Poaceae* family.

The *Brassicaceae* family is the only one whose members are known to generate *indole* phytoalexins containing *sulphurous* phytoalexins [19, 41]. The types of phytoalexins identified in the same *Poaceae* family are *oryzalexins*, *momilactones*, *phytocassanes*, and *sakuranetin* from rice; *kauralexins* and *zealexins* from maize; and *3-deoxyanthocyanidins*, *luteolinidin,* and *apigeninidin* from sorghum [43, 44]. Maize, a member of the *Poaceae* family, generates large amounts of *diterpenoid* phytoalexins in response to a defense mechanism against fungal diseases [41]. Maize generates labdane-type *diterpenoid* phytoalexins named kauralexins and acidic *sesquiterpenoids* known as zealexins [44]. Biosynthetic features are linked to both eradication and up-regulation mechanisms for types of phytoalexins. This has resulted in several applications of maize *(Z.mays)* and sorghum *(Sorghum bicolour)* in the plant's disease resistance [40]. Moreover, these phytoalexins are known to exhibit noticeable antimicrobial activities against a broad array of pathogenic bacteria and fungi [44]. Next, we can see the detailed biosynthesis of terpenoid phytoalexins and associated products.

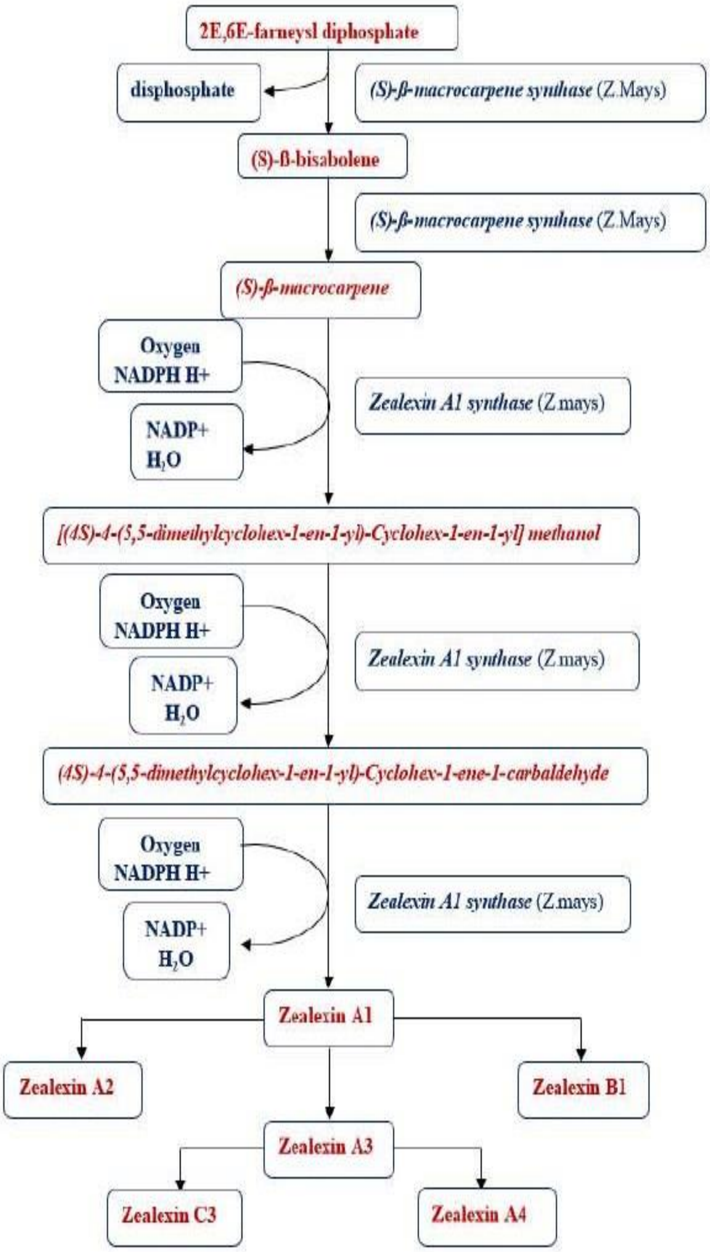

Figure 3. Biosynthetic pathways of zealexins.

Several secondary metabolites have regulated signalling activities of other cells and their control metabolic activities and co-ordinates of the whole plant development. It protects other substances such as colours of flowers that serve to communicate with pollinators or the plants are protected from feeding by animals or infections by generating specific phytoalexins after fungi infections, which inhibits the spreading of the fungi *mycelia* within the plant [19]. The complex defense system of plants against pathogens and pests, as well as the production of low molecular mass secondary metabolites with anti-microbial activity, which are *de novo* synthesized after stress and are accordingly known as "*Phytoalexins"* [11, 45]. The clarification of numerous biosynthetic pathways in *phytoalexins* also allows the use of microbiological tools. *Phytoalexins* belong to a diverse group of molecules with chemical structures, regulatory mechanisms, biological activities, and their enzyme biosynthetic pathways are controlled for pathogenic microbes in a broad range of plant disease resistance mechanisms [21, 43]. Especially, some *pterocarpan* phytoalexins are well known such as *Phaseollin, glyceollin, pisatin, maackiain*, and *medicarpin*. For example, the first phytoalexin *Pisatin* was isolated and characterized from the garden pea *Pisumsativum* [46, 19]. Several reports have proved aboutdemonstrated diverse chemical compounds belonging to the phytoalexin family. Here, we can focus on the *diterpenoid* phytoalexin types of *kauralexins* and *zealexins*, which provide defense responses against fungal pathogens of maize crops (Figure 3).

4.2. Terpenoid Phytoalexins biosynthesis in Maize (*Z.Mays*) Crops

Maize generates labdane-type diterpenoid phytoalexins named *kauralexins* and acidic sesquiterpenoids known as *zealexins* [44]. They are one of the sulphur-containing secondary metabolites which include *phytoalexins, GSH, GSL, thionins, defensins*, and *lectins*. In this part, we pinpoint the biosynthesis of phytoalexins in one of the maize crops of the *Poaceae* family [47]. The biosynthetic pathways of phytoalexins and involved enzymes are related to the knowledge and expression of plant responses to pathogen infections. For example, *terpenoid* phytoalexins survive in various species, such as sweet potato *(Ipomoea batatas)*, cotton *(Gossypiumhirsutum)*, etc. as well as in the family *Poaceae*, the genera *Oryza* (Rice) and *Zea mays* (Maize) [48]. The biosynthesis of terpenoid phytoalexins is included in the basic *5-carbon unit*, *isopentenyl diphosphate* (IPP), and its *allylic isomer dimethylallyl diphosphate* (DMAPP), the derivatives of isoprenoids. *Isopentenyl diphosphate* (IPP) is a series of sequences that shortens to DMAPP and yields a short chain of *geranyl diphosphate*, *farnesyl diphosphate*, and *isoprenoid* precursors. Finally, these are generally further metabolized by terpene*cyclases* and *oxidases* to provide 10-*carbon monoterpenes*, 15-*carbon sesquiterpenes*, and 20-*carbon diterpenes* as reported.

For inkauralexin, the biosynthetic pathway includes two different enzymes, *ent-kaurene* and *ent-isokaurene*, produced from the transformation process of *ent-CPP9 copalyldiphosphate* (CPP). For example, in maize, encoding a synthase of ent-copalyldiphosphate is a fungal-induced *An2* transcript accumulation leading to highly regional production of kauralexin [49,50]. It is also evident that the oxidation steps of ent-kaurene to gibberellin acid are catalyzed by cytochrome *P450 mono-oxygenases*, a process usually localized to the endoplasmic reticulum. The first three steps of the P450-mediated pathway, from *ent-kaurene* to *ent-kaurenoic acid*, are catalyzed by *ent-kaureneoxidase(AtKO1)* gene proteins. Remarkably, class I labdane-related *diterpene synthases* are shown to be stereo-specific isomers. *i.e. copalyldiphosphate* (CPP) specific enzymes [51]. So, in the pathways including cytochrome p450 enzymes and normal oxygen inputs, *NADPH cofactors* are present. In the catalyzed production of *alcohol* and then its transformation to an *aldehyde* and finally a *carboxylic acid* to give high efficiency to *kauralexin* A1 and *kauralexin* B1, a series of reactions are repeated on a diverse carbon atom to generate the first two (hidden) alcohols followed by aldehydes *kauralexin* A3 and *kauralexin* B3**.** Diterpenoid phytoalexins generate kauralexins as *ent-kaurane*-related downstream endproducts of the activity of *ent-copalyldiphosphate* synthase, whose types are *A1, A2, A3, B1, B2*, and *B3* [44].

The kauralexins A1 to A3, the metabolite series identified to date are: *ent-kauran-17-oic acid, ent-kauran-17,19-dioic acid,* and *ent-kaur-19-al-17-oic acid,* and kauralexin B includes *ent-kaur-15-en-17-oic acid, ent-kaur-15-en-17,19-dioic acid,* and *ent-kaur-15-en-19-al-17-oic acid,* named kauralexins B1, B2, and B3, respectively [44, 47, 52]. In maize, the biosynthetic pathway of zealexins includes a sequence of enzyme activities to increase the expression of genes encoding TPS11 and TERPENESYNTHASE6 (TPS6) that generate acidic sesquiterpenoids containing a hydrocarbon skeleton favourable for b-macrocarpene catalysis [49].

In maize, terpenoid phytoalexin biosynthesis requires the infusion of oxygen, seemingly catalyzed by *cytochrome 450* (CYPs), terpenoid phytoalexins identified to date are involved in the biosynthesis and suggest that each of the five sesquiterpene groups is a form of terpene synthase from farnesyldiphosphate [53]. For example, maize, CYP71Z18 from the >350 CYPs plays a role in zealexin biosynthesis, catalyzing multiple reactions for the transformation of carbon-15 (C15) in (S)-b-macrocarpenes [54]. The set of three reactions are catalyzed by cytochrome p450 enzyme and, on the basis of the predicted NADPH cofactor and oxygen input, this series of reactions further converts alcohols to aldehydes to carboxylic acids. Additionally, non-volatile sesquiterpenoid phytoalexins are generated from the bicyclic *olefin ß-macrocarpene*. The terpene synthases *TPS6* and *TPS11* are both duplicated to produce *ß-macrocarpene* from FPP and are anticipated to be responsible for the production of zealexins, but it has not yet been genetically confirmed. Furthermore, *zealexin* A1 can be modified by hydroxylation at the C1 or C8 position to form *zealexin* A2 and *zealexin* A3, respectively [44,47]**.** We can focus on this review to pinpoint the defense mechanisms of *kauralexins* and *zealexins* against several fungal pathogens in maize crops.

4.3. Mode of Action on defense mechanisms against fungal pathogens

Low molecular mass plant secondary metabolites are synthesized *de-novo* after stress and are accordingly known as phytoalexins. It is the biosynthesis of diterpenoid compounds of phytoalexins named *kauralexins* and acidic sesquiterpenoids known as *zealexins* that can fight pests and pathogens [11,48]. Generally, there are at least 6 different antifungal mechanisms of the fungal cell architecture, including *Inhibition of cell wall structure, Cell membrane disruption, fungal mitochondria Dysfunction, Inhibition of cell division, Inhibition of RNA/DNA synthesis* or *protein synthesis*, and *Inhibition of efflux pumps* [47]. Plants exhibit two types of defence or resistance responses: Specific *(Cultivar/pathogen)* resistance and non-specific *(non-host or general)* resistance [25,42]. Secondary metabolite compounds are biologically active forms or deposited as inactive precursors that are changed to their active forms by enzymes of hosts, its response to tissue damage or attacking pathogens [42]. Some fungal pathogens can cause severe diseases in maize such as *Aspergillusflavus, Aspergillussojae, Cochliobolusheterostrophus, Colletotrichumsublineolum, Fusarium graminearum, Ostrinianubilalis, Rhizopus microspores, Ustilagomaydis,* etc.

In this part, we discuss several defence mechanisms of *kauralexins* and *zealexins* in maize crops. Over the years, research reports [49 and others] have identified the *terpenoid* biosynthetic compounds of *kauralexins* and *zealexins* to defense maize crops against these fungal pathogens. We will further discuss the defense mechanisms of these two bioactive compounds against fungal diseases in maize crops (Figure 4). Naturally, plant pathogens have found plentiful strategies for obtaining nutritious materials from plants, which in turn serve as physical and chemical barriers and an immune system to combat the attack of pathogens [48].

Remarkably, the biosynthesis of kauralexins seems to be phytohormone-regulated for the application of a combination of *ethylene* and *jasmonic acid* (JA) to maize plants to induce tolerable kauralexin generations. The phytohormone-induced accumulation of *kauralexin* responses to plant defense is one of the factors that resist pathogen attack. The possible role of induced *oxylipins* as regulators of kauralexin production is that its treatment results in JA levels which are automatically greater than damage alone in just 4 h, so that *kauralexin* accumulation is anticipated to be detectable [49, 52].

The growth of those pathogens is inhibited by physiologically relevant concentrations of *kauralexins*. An accumulation of the fungal *kaurene synthase 2*(An2) inducible transcript predicts the appearance of a highly localized *kauralexin* product, and a combination of *ethylene* and JA *(Jasmonic acid)* application exhibits their symbiotic role in the regulation of *kauralexins*. The presence of *kauralexins* shows that maize stem attack by *Colletotrichumgraminicola* and *Rhizopusmicrosporus* induces diterpenoids related to the mutual accumulation of the six *ent-kauranes* [11]. Furthermore, *Zealexins* accumulate in *Fusarium graminearum* at very high levels, about 800 µg/g of infected maize [56]. Highly concentrated *zealexins* are also found in maize challenged by other fungal pathogens of *Rhizopusmicrosporus* and *Aspergillusflavus*. On the other hand, *zealexins* A1 and A3 (but not A2) inhibit the growth of *F. graminearum* and *A. flavus* in in-vitro toxicity tests shown, but A1 is also efficient against *R. microspores* [52].

The genetic, biosynthetic, and regulatory machines that control innate immunity is crucial for enhancing biochemical defenses and resistance of crop traits. In maize, antibiotic production is built on enzymes encoded by three *ZmCYP71Z-family genes* (Zx5 to Zx7) on chromosome 5 leading to multiple specific families of diterpenoids and sesquiterpenoids**.** The sole non-redundant pathway gene Zx10 represents and encodes ZmCYP81A39, which is responsible for the oxidation of ZX C8 to alcohol and the combined variants ZA3, ZB3, and ZC2. As the major product of ZX1 to ZX9 action, ZB1 exhibits symbolic antifungal activity at 25 µg.mL^{-1} against two key *Fusarium* pathogens in maize [57]. The combination of *kauralexins* and *zealexins* with other defense metabolites (JA, CA, SA, IAA, ABA, and 12-OPDA) reduces fungal growth. Statistical models demonstrated on maize stems show that kauralexins have a greater effect on the suppression of fungal growth than other classes of defence compounds, such as zealexin A4, which has forceful antimicrobial activity against *F.graminearum*. Direct defence metabolites infected with *F. graminearum* also elicit high levels of initial zealexins, specifically Z*A1* and Z*B1*, but the accumulation of ZA4 is forcefully reduced to levels equal to those elicited by *C. graminicola, Aspergillusflavus,* and *Rhizopusmicrospores* [58].

In the biosynthesis of hormone GA, a positional isomer is not used and thereby the need for direct production of *ent*-kaurene is avoided. Kauralexins are extensively developed from *ent*-isokaurene, a product of ZmKSL2. An independent pathway of GA with highly incongruent activities of ZmCYP71Z16/18 implements the committed production of kauralexins from both *ent-isokaurene* and *ent-kaurene* enzymes. It challenges ZmCYP71Z16/18-derived pathogens that can convert ZmKSL2-derived ent-kaurene and other *ent*-kaurene synthases into antibiotic defenses [59]. The pathogen of *CercosporaZeina* is a foliar pathogen and is responsible for maize *grey leaf spot* in southern Africa. *Zeina-resistant* RIL387 responded by accumulated transcripts is associated with cell wall modifications, including *auxin* signaling genes. The accumulation of *kauralexins* and *zealexins* is a response to both resistant and susceptible maize lines to *C. Zeina*. The association with ZmAn2 and ZmCPS3 was induced by *C. Zeina* and diversely expressed by RIL387 and RIL165 [60].

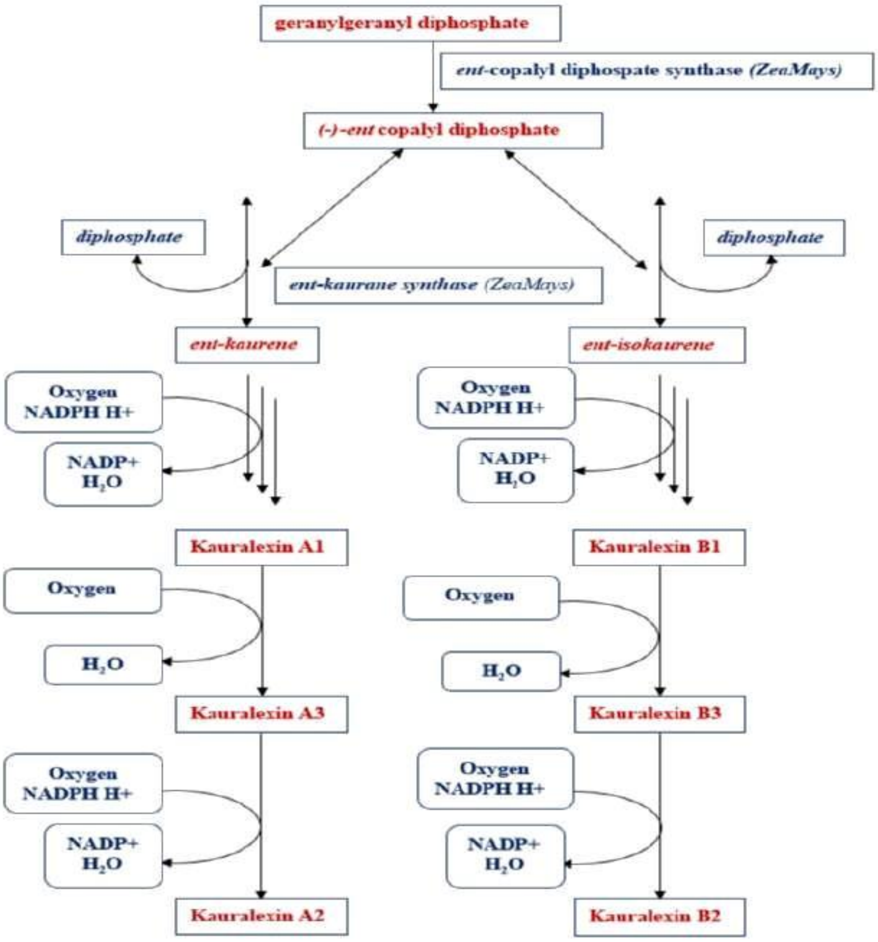

Figure 4. Kauralexins Biosynthetic Pathways.

5. CONCLUSION AND PROSPECTS

Globally, maize is a crucial food for humans and animals. Depending on the world population, the demand for cereals is increasing every year. Upon requirement, countries are changing their crop cultivation systems in agriculture worldwide. Currently, high-yielding food crops are affected by several diseases. In addition, due to global warming, plants are exposed to diverse effects from abiotic stress-related diseases. Moreover, biotic stress-related diseases are caused by *microorganisms*, *insects*, and *nematodes*, etc., thus leading to reduced yield in crop cultivation. Plant metabolites are natural defense players in plants. Secondary metabolite derivatives are chemically synthesized to generate key enzymes which react with pathogens. In previous years, so many secondary metabolites have been discovered by plant biologists, which help the plants relieve biotic and abiotic stresses. Recently, more improved methodologies and techniques have been facilitating the research. The plant secondary metabolites participate in the main role of plant physiology associated with its *biosynthetic reactions*, *defense mechanisms*, and *stress signal transductions*, etc. A number of studies have shown vast shreds of evidence on how they are involved in plant stress. Defence responses are concerned at the *subcellular level*, followed by their challenging and critical studies.

It is being a major crop plant that is widely suitable for cytogenetic studies, providing valuable insights into various facets of plant biology. In previous years, several studies have relatedly reported on maize plant defense mechanisms and disease control improvement. The role of maize phytoalexins, namely *kauralexins* and *zealexins* biosynthetic pathways, and their activities against the whole anti-fungal defense mechanisms have been somewhat elucidated but more detailed studies are still needed in the future. For example, to compare with compounds of *kauralexins* (labdane-type diterpenoids), *zealexins* (acidic sesquiterpenoids) require more extensive studies in the future. Also, the research on how plants react upon specific biotic stress and their pathogen interactions has given a strong approach that paves the way for further studies. Significantly, the studies on the effects of these phytoalexin derivative compounds on the control of *regulatory networks* and their pathogen *defense mechanisms* in specific plant tissues and development have provided extensive knowledge. So, it is necessary to elucidate the defence mechanisms of bioactive diterpenoid compounds namely *kauralexins* and *zealexins*, against pathogens as well as to improve the approaches of *proteomics*, *metabolomics*, *transcriptomics*, and their *database* tools. Not only that, in the future there needs to be more research on the disease control mechanisms of *kauralexins* and *zealexins* on maize crops.

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REFERENCES

1. Godfray H. C., Mason-D'Croz D., and Robinson S. - Food system consequences of a fungal disease epidemic in a major crop, Philos Trans R Soc. Lond B Biol. Sci. **371** (1709). https://doi.org/10.1098/rstb.2015.0467
2. Tyanova S., Temu T., and Cox J. - The MaxQuant computational platform for mass spectrometry-based shotgun proteomics, Nat. Protoc. **11** (12) (2016) 2301-2319. https://doi.org/10.1038/nprot.2016.136
3. Ranum P., Pena-Rosas J. P., and Garcia-Casal M. N. - Global maize production, utilization, and consumption, Ann. N. Y. Acad. Sci. **1312** (2014) 105-112. https://doi.org/10.1111/nyas.12396
4. FAO - Crop Prospects and Food Situation - Quarterly Global Report No. 1, March 2020. Rome. https://doi.org/10.4060/ca8032en
5. George N. Agrios - PlantPathology, Fifth Edition, Elsevier Academic Press, London, U.K., 2005.

6. Pusztahelyi T., Holb I. J., and Pocsi I. - Secondary metabolites in fungus-plant interactions, Front Plant Sci. **6** (2015) 573. https://doi.org/10.3389/fpls.2015.00573
7. Hiruma K. - Roles of Plant-Derived Secondary Metabolites during Interactions with Pathogenic and Beneficial Microbes under Conditions of Environmental Stress, Microorganisms **7** (9) (2019). https://doi.org/10.3390/microorganisms7090362
8. Pusztahelyi T., Holb I. J., and Pócsi I. - Plant-Fungal Interactions: Special Secondary Metabolites of the Biotrophic, Necrotrophic, and Other Specific Interactions, In: Fungal Metabolites (2016) 1-58. https://doi.org/10.1007/978-3-319-19456-1_39-1
9. Murphy K. M. and Zerbe P. - Specialized diterpenoid metabolism in monocot crops: Biosynthesis and chemical diversity, Phytochemistry **172** (2020) 112289. https://doi.org/10.1016/j.phytochem.2020.112289
10. Anna K., Jager S. H. F. - Correlation between Plant Secondary Metabolites and Their Antifungal Mechanisms A Review, Medicinal & Aromatic Plants **03** (02) (2014). https://doi.org/10.4172/2167-0412.1000154
11. Ahuja I., Kissen R., and Bones A. M. - Phytoalexins in defense against pathogens, Trends Plant Sci. **17** (2) (2012) 73-90. https://doi.org/10.1016/j.tplants.2011.11.002
12. Pusztahelyi T., Holb I. J., Pócsi I. - Plant-Fungal Interactions: Special Secondary Metabolites of the Biotrophic, Necrotrophic, and Other Specific Interactions, In: Mérillon JM., Ramawat K. (Eds.), Fungal Metabolites, Reference Series in Phytochemistry, Springer, Cham., 2017. https://doi.org/10.1007/978-3-319-25001-4_39
13. Castro-Moretti F. R., Gentzel I. N., Mackey D., and Alonso A. P. - Metabolomics as an Emerging Tool for the Study of Plant-Pathogen Interactions, Metabolites **10** (2) (2020). https://doi.org/10.3390/metabo10020052
14. Manoj *et.al.* - Chapter 8-Omics Technology: Role and Futurein Providing Biotic and Abiotic StressTolerance to PlantsA. Sharma (Ed.), Microbes and Signaling Biomolecules Against Plant Stress, Rhizosphere Biology, 2021, https://doi.org/10.1007/978-981-15-7094-0_8
15. Erb M. and Kliebenstein D. J. - Plant Secondary Metabolites as Defenses, Regulators, and Primary Metabolites: The Blurred Functional Trichotomy, Plant Physiol **184** (1) (2020) 39-52. https://doi.org/10.1104/pp.20.00433
16. Jain A., Sarsaiya S., Wu Q., Lu Y., and Shi J. - A review of plant leaf fungal diseases and its environment speciation, Bioengineered **10** (1) (2019) 409-424. https://doi.org/10.1080/21655979.2019.1649520
17. Redkar A., Matei A., and Doehlemann G. - Insights into Host Cell Modulation and Induction of New Cells by the Corn Smut Ustilago maydis, Front Plant Sci. **8** (2017) 899. https://doi.org/10.3389/fpls.2017.00899
18. Strange R. N. and Scott P. R. - Plant disease: a threat to global food security, Annu Rev. Phytopathol **43** (2005) 83116. https://doi.org/10.1146/annurev.phyto.43.113004.1338396
19. Singh R. and Chandrawat K. S. - Role of Phytoalexins in Plant Disease Resistance, International Journal of Current Microbiology and Applied Sciences **6** (1) (2017) 125-129. https://doi.org/10.20546/ijcmas.2017.601.016
20. Lee J., Hilgers F., Loeschke A., Jaeger K. E., and Feldbrugge M. - Ustilago maydis Serves as a Novel Production Host for the Synthesis of Plant and Fungal Sesquiterpenoids, Front Microbiol **11** (2020) 1655. https://doi.org/10.3389/fmicb.2020.01655

21. Mazid M., KhanT.A. and Mohammad F. (2011): Role of secondary metabolites in defense mechanismsof plants. Biology and Medicine3: 232-249.
22. Andersen E. J., Ali S., Byamukama E., Yen Y., and Nepal M. P. - Disease ResistanceMechanisms in Plants, Genes **9** (7) (2018) 339. https://doi.org/10.3390/genes9070339
23. Ramírez-Gómez S. X. N., Jiménez-García S., Beltrán Campos V., and Lourdes García Campos Ma. - Plant Metabolites in Plant Defense Against Pathogens, Intech Open (2020). doi: 10.5772/intechopen.87958
24. Soares M. B., Pontes-De-Carvalho L., and Ribeiro-Dos-Santos R. - The pathogenesis of Chagas' disease: when autoimmune and parasite-specific immune responses meet, Anais da Academia Brasileira de Ciencias **73** (4) (2001) 547-559. https://doi.org/10.1590/s0001-37652001000400008
25. Xiao Y., Liu H., Wu L., Warburton M., and Yan J. - Genome-wide Association Studies in Maize: Praise and Stargaze, Molecular plant **10** (3) (2017) 359-374. https://doi.org/10.1016/j.molp.2016.12.008
26. Schmelz E. A., Kaplan F., Huffaker A., Dafoe N. J., Vaughan M. M., Ni X., Rocca J. R., Alborn H. T., and Teal P. E. - Identity, regulation, and activity of inducible diterpenoid phytoalexins in maize, Proc. Nat. Acad Sci. USA **108** (13) (2011) 5455-5460. https://doi.org/10.1073/pnas.1014714108
27. Huffaker A., Kaplan F., Vaughan M. M., Dafoe N. J., Ni X., Rocca J. R., Alborn H. T., Teal P. E., and Schmelz E. A. - Novel acidic sesquiterpenoids constitute a dominant class of pathogen-induced phytoalexins in maize, Plant Physiol **156** (4) (2011) 2082-2097. https://doi.org/10.1104/pp.111.179457
28. Matthews D. E., Lazo G. R., Anderson O. D. - Plant and crop databases, Methods Mol. Biol. **513** (2009) 243-262. doi:10.1007/978-1-59745-427-8_13
29. Horai H., Arita M., Kanaya S., Nihei Y., Ikeda T., Suwa K., Ojima Y., Matsuura F., Soga T., Taguchi R., Saito K., and Nishioka T. - MassBank: a public repository for sharing mass spectral data for life sciences, J. Mass. Spectrom **45** (7) (2010) 703-714. https://doi.org/10.1002/jms.1777
30. Rahman, M., Shaheen, T., Rahman, M., Iqbal, M. A., & Zafar, Y. (2016). Bioinformatics: A Way Forward to Explore “Plant Omics”. InTech. doi: 10.5772/64043
31. Razzaq, A., Sadia, B., Raza, A., Khalid Hameed, M., & Saleem, F. (2019, Dec 14). Metabolomics: A Way Forward for Crop Improvement. *Metabolites, 9*(12). https://doi.org/10.3390/metabo9120303
32. Kusano M. and Saito K. - Role of Metabolomics in Crop Improvement, Journal of Plant Biochemistry and Biotechnology **21** (S1) (2012) 24-31. https://doi.org/10.1007/s13562-012-0131-4
33. Kumar R., Bohra A., Pandey A. K., Pandey M. K., and Kumar A. - Metabolomics for Plant Improvement: Status and Prospects, Front Plant Sci. 8 (2017) 1302. https://doi.org/10.3389/fpls.2017.01302
34. Dixon R. A., Gang D. R., Charlton A. J., Fiehn O., Kuiper H. A., Reynolds T. L., and Seiber J. N. - Applications of metabolomics in agriculture, Journal of agricultural and food chemistry **54** (24) (2006) 8984-8994.

35. Upadhyay J., Joshi R., Singh B., Bohra A., Vijayan R., Bhatt M., ... and Wani S. H. - Application of bioinformatics in understanding of plant stress tolerance, Plant Bioinformatics: Decoding the Phyta (2017) 347-374.
36. Wishart D. S. - Current progress in computational metabolomics, Brief Bioinform **8** (5) (2007) 279-293. https://doi.org/10.1093/bib/bbm030
37. Srivastava M., Malviya N., and Dandekar T. - Application of Biotechnology and Bioinformatics Tools in Plant–Fungus Interactions, In: Plant Biology and Biotechnology, 2015, pp. 49-64. https://doi.org/10.1007/978-81-322-2283-5_3
38. Orchard S., Ammari M., Aranda B., Breuza L., Briganti L., Iannuccelli M., Jagannathan S., Jimenez Cesareni G., and Hermjakob H. - The MIntAct project--IntAct as a common curation platform for 11 molecular interaction databases, Nucleic Acids Res. **42** (Database issue) (2014) D358-363. https://doi.org/10.1093/nar/gkt1115
39. Licata L., Briganti L., Peluso D., Perfetto L., Iannuccelli M., Galeota E., Sacco F., Palma A., Nardozza A. P., Santonico E., Castagnoli L., and Cesareni G. - MINT, the molecular interaction database: 2012 update, Nucleic Acids Res. **40** (Database issue) (2012) D857-861. https://doi.org/10.1093/nar/gkr930
40. Jeandet P. - Phytoalexins: Current Progress and Future Prospects, Molecules **20** (2) (2015) 2770-2774. https://doi.org/10.3390/molecules20022770
41. Bizuneh G. K. - The chemical diversity and biological activities of phytoalexins, Adv. Tradit Med. (ADTM) **21** (2021) 31-43. https://doi.org/10.1007/s13596-020-00442-w
42. Onaga G. and Wydra K. - Advances in Plant Tolerance to Biotic Stresses, In: Plant Genomics, 2016. https://doi.org/10.5772/64351
43. Jeandet P., Hébrard C., Deville M. A., Cordelier S., Dorey S., Aziz A., and Crouzet J. - Deciphering the role of phytoalexins in plant-microorganism interactions and human health, Molecules, Basel, Switzerland, **19** (11) (2014) 18033-18056. https://doi.org/10.3390/molecules191118033
44. Ejike C. E. C. C., Gong M., and Udenigwe C. C. - Phytoalexins from the Poaceae: Biosynthesis, function and prospects in food preservation, Food Research International **52** (1) (2013) 167-177. https://doi.org/10.1016/j.foodres.2013.03.012
45. Zaynab M., Fatima M., Abbas S., Sharif Y., Umair M., Zafar M. H., and Bahadar K. - Role of secondary metabolites in plant defense against pathogens, Microb Pathog **124** (2018) 198-202. https://doi.org/10.1016/j.micpath.2018.08.034
46. Cruickshank I. A. M. and Perrin D. R. - Isolation of a phytoalexin from Pisum sativum L, Nature **187** (1960) 799-800.
47. Anna K., Jager S. H. F. - Correlation between Plant Secondary Metabolites and Their Antifungal Mechanisms A Review, Medicinal & Aromatic Plants **03** (02) (2014). https://doi.org/10.4172/2167-0412.1000154
48. Arruda R. L., Paz A. T. S., Bara M. T. F., Côrtes M. V. D. C. B., Filippi M. C. C. D., and Conceição E. C. D. - An approach on phytoalexins: function, characterization and biosynthesis in plants of the family Poaceae, Ciência Rural **46** (2016) 1206-1216.
49. Huffaker A., Kaplan F., Vaughan M. M., Dafoe N. J., Ni X., Rocca J. R., Alborn H. T., Teal P. E., and Schmelz E. A. - Novel acidic sesquiterpenoids constitute a dominant class of pathogen-induced phytoalexins in maize, Plant Physiol **156** (4) (2011) 2082-2097. https://doi.org/10.1104/pp.111.179457

50. Lambarey H., Moola N., Veenstra A., Murray S., and Suhail Rafudeen M. - Transcriptomic Analysis of a Susceptible African Maize Line to Fusarium verticillioides Infection, Plants (Basel) **9** (9) (2020). https://doi.org/10.3390/plants9091112
51. Xu M., Wilderman P. R., Morrone D., Xu J., Roy A., Margis-Pinheiro M., Upadhyaya N. M., Coates R. M., and Peters R. J. - Functional characterization of the rice kaurene synthase-like gene family, Phytochemistry **68** (3) (2007) 312-326. https://doi.org/10.1016/j.phytochem.2006.10.016
52. Poloni A. and Schirawski J. - Red card for pathogens: phytoalexins in sorghum and maize, Molecules **19** (7) (2014) 9114-9133. https://doi.org/10.3390/molecules19079114
53. Schnee C., Kollner T. G., Held M., Turlings T. C., Gershenzon J., and Degenhardt J. - The products of a single maize sesquiterpene synthase form a volatile defense signal that attracts natural enemies of maize herbivores, Proc. Natl. Acad. Sci. USA **103** (4) (2006) 1129-1134. https://doi.org/10.1073/pnas.0508027103
54. Mao H., Liu J., Ren F., Peters R. J., and Wang Q. - Characterization of CYP71Z18 indicates a role in maize zealexin biosynthesis, Phytochemistry **121** (2016) 4-10. https://doi.org/10.1016/j.phytochem.2015.10.003
55. Peters R. J. - Uncovering the complex metabolic network underlying diterpenoid phytoalexin biosynthesis in rice and other cereal crop plants, Phytochemistry **67** (21) (2006) 2307-2317. https://doi.org/10.1016/j.phytochem.2006.08.009
56. Schmelz E. A., Kaplan F., Huffaker A., Dafoe N. J., Vaughan M. M., Ni X., Rocca J. R., Alborn H. T., and Teal P. E. - Identity, regulation, and activity of inducible diterpenoid phytoalexins in maize, Proceedings of the National Academy of Sciences of the United States of America **108** (13) (2011) 5455-5460. https://doi.org/10.1073/pnas.1014714108
57. Ding Y., Weckwerth P. R., Poretsky E., Murphy K. M., Sims J., Saldivar E., ... and Huffaker A. - Genetic elucidation of interconnected antibiotic pathways mediating maize innate immunity, Nature plants **6** (11) (2020) 1375-1388.
58. Christensen S. A., Huffaker A., Sims J., Hunter C. T., Block A., Vaughan M. M., Willett D., Romero M., Mylroie J. E., Williams W. P., and Schmelz E. A. - Fungal and herbivore elicitation of the novel maize sesquiterpenoid, zealexin A4, is attenuated by elevated CO_2, Planta **247** (4) (2018b) 863-873. https://doi.org/10.1007/s00425-017-2830-5
59. Block A. K., Vaughan M. M., Schmelz E. A., and Christensen S. A. - Biosynthesis and function of terpenoid defense compounds in maize (Zea mays), Planta **249** (2019) 21-30.
60. Meyer J., Berger D. K., Christensen S. A., and Murray S. L. - RNA-Seq analysis of resistant and susceptible sub-tropical maize lines reveals a role for kauralexins in resistance to grey leaf spot disease, caused by Cercospora zeina, BMC Plant Biol. **17** (1) (2017) 197. https://doi.org/10.1186/s12870-017-1137-9