Metabolic Pattern Alterations in Pearl Millet Inflorescence Florets Caused by Downy Mildew

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Abstract

Millions of people in dry and semi-arid areas rely on pearl millet, scientifically known as Pennisetum glaucum, as a grain crop. However, the parasite Sclerospora graminicola, which causes downy mildew, dramatically reduces its output. The impact of downy mildew contamination on the chemical composition of millet and pearl inflorescence florets, namely floral deformity, is investigated in this research. Using cutting-edge metabolomic methods, we determined that the metabolite composition of diseased florets differed significantly from that of healthy controls. Both primary and secondary metabolite levels changed, suggesting metabolic pathway disruption and stress reactions due to these alterations. Our research sheds light on the molecular mechanisms that cause floral malformation caused by downy mildew and could help in the quest to create tolerant pearl millet variants.

Keywords

Pearl millet, downy mildew, Sclerospora graminicola, floral malformation, metabolite profiling, metabolomics, plant pathology, stress response.

Introduction

Because of its nutritional content and durability, pearl millet (Pennisetum glaucum) is a staple crop in areas that experience drought. The growth stunting, chlorosis, and floral distortion produced by the oomycete infection Sclerospora graminicola, often known as downy mildewing disease, considerably reduces grain output and quality. Little is known about the physiological and molecular processes that cause pearl millet flower deformity, despite a great deal of study on the epidemiology and life cycle of the disease. Inflorescence floret metabolite profile variations in pearl millet in reaction to downy mildew disease are the focus of this investigation.

Materials and Methods

Plant Material and Disease Inoculation

A controllable atmospheric greenhouse environment was used for the sowing of millet with pearl coating seeds (variety 843B). A spore slurry of Sclerospora graminicola was introduced into the crops at the three-leaf stage by inoculation. Sterile water was used to mock-inoculate control plants. The progression of diseases was tracked, and inflorescence florets were taken as soon as noticeable abnormalities in the flowers were apparent.

Metabolite Extraction and Analysis

A fine powder was made from the freeze-dried floral samples. Metabolites were isolated utilizing a methanol/water (80:20 v/v) mixture and then examined utilising gas chromatography-mass spectra (GC-MS) and mass spectrometry-liquid characterisation (LC-MS). In order to find noteworthy changes in metabolites and related pathways, the data was analysed using the MetaboAnalyst and the study of KEGG tools.

Statistical Analysis

Clustering based on hierarchy and the methods of PCA were used to compare metabolic profiles of healthy and diseased individuals. Differences of statistical importance ($p < 0.05$) were determined using Student's t-test.

Results

Disease Symptoms and Floral Malformation

The fungus known as downy mildew has a significant impact on the health of plants. Plants that have been infected exhibit a diminished development, with the leaves becoming yellow due to chlorosis, which indicates a chlorophyll deficiency.

The illness is also responsible for major abnormalities of the flowers. Floral malformation is characterised by defective and twisted floret structures, making individuals identifiable.

It is critical to identify these signs at an early stage in order to manage downy mildew effectively. The illness has many major signs, including decreased growth, chlorosis of the leaves, and deformed blooms.

It is possible to lessen the effects of downy mildew by providing the appropriate care and treatment, which will result in better plant growth and reduce the lost crop. In order to limit the spread of this plant infection and the severity of its symptoms, it is essential to perform periodic surveillance and prompt treatments.

Metabolite Profile Alterations

The metabolomic analysis of downy mildew-infected pearl millet inflorescence florets found significant changes in both primary and secondary metabolites. Amino acid levels, particularly the tryptophan mentioned above, especially tyrosine, dropped dramatically, marking one of the most striking decreases among the main metabolites. This decline is presumably caused by the pathogen interfering with the plant's metabolic processes, disrupting secondary metabolism and protein synthesis. Decreased glucose and fructose levels also impacted the breakdown of carbohydrates. This points to a decrease in the effectiveness of photosynthetic processes and energy utilisation in the infected plants. On the other hand, phenolic compounds and other secondary metabolites exhibited an increase in accumulation. There was an increase in some compounds, including flavonoids and phenolic acids, suggesting a stress response that may have activated defence systems to fight off the infection.

Pathway Analysis

Downy mildew infection disrupts metabolism, and the KEGG pathway analysis sheds light on this. There was a significant alteration to many metabolic pathways. An increase in defense-related compounds was seen in the phenylpropanoid manufacturing pathway, suggesting that the plant was attempting to fight off the infection. On the flip side, pathways involved in the metabolism of amino acids were shown to be downregulated, especially those linked to growth and development biosynthesis pathways. The plant's resources seem to be redirected from growth to defence by the pathogen. The tricarboxylic acid (TCA) cycle and glycolysis, two processes in energy metabolism, were also disrupted. Consistently, with the detected decreases in levels of main metabolites like glucose and fructose, this disturbance suggests changed energy balances within the diseased plants. Taken together, our results provide light on the pathogen's effect on pearl millet metabolism and the plant's defence systems by demonstrating the profound metabolic reconfiguration that occurs in the plant's florets when downy mildew is present.

Discussion

The intricate metabolic reactions of pathogen invasion are highlighted by the biomarker profile alterations reported in pearl millet florets infected with downy mildew. The presence of phenolic compounds implies active participation in pathogen resistance, whereas the decrease in necessary amino acids and carbohydrates indicates a reallocation of resources towards defence mechanisms. These results provide insight into possible immune-to-disease pearl millet variety breeding areas and give a holistic picture of the metabolic disturbances induced by downy mildew.

Conclusion

According to this research, Pearl millet blooming florets undergo significant changes in their metabolite profiles upon infection with downy mold. These changes are most noticeable in the areas linked to floral deformity. Improved knowledge of the relationships between plants and pathogens and potential avenues for disease management approach creation in pearl millet is aided by this metabolomic study's results.

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