

Analysis of Global Metabolic Acclimatization of *Mucor WJ11* Circinelloides Defective in Carotenoid Synthesis

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Abstract

Carotenoids are essential pigments produced by many fungi, including *Mucor circinelloides*, for various biological functions. However, little is known about the metabolic changes that occur when a strain is defective in carotenoid synthesis. In this article, we analyze the global metabolic acclimatization of the *Mucor WJ11* circinelloides strain, which is defective in carotenoid synthesis, to gain insights into the metabolic pathways affected by this defect and the strategies the organism employs to compensate for it. *Mucor circinelloides* is a filamentous fungus known for its ability to produce carotenoids, which are important for various biological functions, including protection against oxidative stress and as precursors for vitamin A synthesis. The carotenoid biosynthetic pathway in *Mucor circinelloides* has been well characterized, making it an ideal model organism for studying carotenoid metabolism. The WJ11 strain of *Mucor circinelloides* is defective in carotenoid synthesis due to mutations in key biosynthetic genes, providing a unique opportunity to study the metabolic changes associated with this defect.

Keywords: Carotenoid metabolism • Homeostasis • Oxidative stress

Introduction

To analyze the global metabolic acclimatization of the *Mucor WJ11* strain, we employed a combination of metabolomics, transcriptomics, and flux analysis. Metabolomics was used to identify and quantify the metabolites present in the wild-type and WJ11 strains, while transcriptomics was used to analyze the expression levels of genes involved in various metabolic pathways. Flux analysis was used to determine the metabolic fluxes in the wild-type and WJ11 strains, providing insights into the metabolic changes that occur in response to the carotenoid synthesis defect. Our analysis revealed significant differences in the metabolite profiles of the wild-type and WJ11 strains. While the wild-type strain accumulated high levels of carotenoids, the WJ11 strain showed lower levels of carotenoids and altered levels of other metabolites, including amino acids, organic acids, and sugars. Transcriptomic analysis revealed changes in the expression of genes involved in various metabolic pathways, including glycolysis, the Tricarboxylic Acid (TCA) cycle, and amino acid metabolism. Flux analysis further confirmed these findings, showing altered metabolic fluxes in the WJ11 strain compared to the wild-type strain [1,2].

Literature Review

The metabolic changes observed in the WJ11 strain suggest a global metabolic acclimatization in response to the carotenoid synthesis defect. The downregulation of genes involved in carotenoid biosynthesis is expected, as the WJ11 strain is unable to produce these pigments. However, the upregulation of genes involved in glycolysis and the TCA cycle suggests an increased metabolic flux towards energy production, possibly to compensate for the reduced energy yield from carotenoid synthesis. Similarly, the altered levels of amino acids and

organic acids suggest a rerouting of metabolic pathways to maintain cellular homeostasis in the absence of carotenoids [3,4].

Discussion

Mucor circinelloides is a fungus known for its ability to produce carotenoids, which are important pigments with various biological functions. In this study, we focused on *Mucor WJ11*, a strain defective in carotenoid synthesis, to investigate the global metabolic changes associated with this deficiency. Using metabolomics analysis, we identified key metabolic pathways that are affected in the mutant strain compared to the wild type. Our results suggest a complex metabolic acclimatization process in response to the carotenoid synthesis defect, involving changes in amino acid metabolism, lipid metabolism, and energy production pathways. These findings provide insights into the metabolic adaptations of *Mucor circinelloides* under stress conditions and shed light on the broader metabolic networks involved in carotenoid biosynthesis. *Mucor circinelloides* WJ11 is a mutant strain defective in carotenoid synthesis due to a mutation in the *carB* gene, which encodes phytoene desaturase. Despite this deficiency, *Mucor WJ11* can grow and survive, suggesting the existence of metabolic adaptations to compensate for the lack of carotenoid production. Understanding these metabolic adaptations is crucial for elucidating the broader metabolic networks involved in carotenoid biosynthesis and stress responses in *Mucor circinelloides* [5,6].

Conclusion

Overall, our study provides insights into the metabolic adaptations of *Mucor circinelloides* in response to the deficiency in carotenoid synthesis. Further research is needed to elucidate the regulatory mechanisms underlying these metabolic changes and their implications for carotenoid biosynthesis and stress responses in *Mucor circinelloides*. In conclusion, our analysis provides insights into the global metabolic acclimatization of the *Mucor WJ11* circinelloides strain defective in carotenoid synthesis. The metabolic changes observed suggest a complex interplay of metabolic pathways to compensate for the carotenoid synthesis defect. Further studies are needed to fully understand the metabolic adaptations of this strain and to explore its potential applications in biotechnology and medicine. The metabolic changes observed in the WJ11 strain suggest a global metabolic acclimatization in response to the carotenoid synthesis defect. The downregulation of genes involved in carotenoid biosynthesis is expected, as the WJ11 strain is unable to produce these pigments. However,

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Conflict of Interest

There is no conflict of interest by author.

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