Plasma Proteome Reveals Oxidative Stress As a Key Factor in Fibromyalgia

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Introduction

Fibromyalgia (FM) is a chronic disorder marked by widespread pain, fatigue, and cognitive difficulties. Oxidative stress plays a key role in its pathophysiology, linked to mitochondrial dysfunction, low-grade chronic inflammation, and heightened pain sensitivity. Mitochondrial imbalances lead to excessive production of reactive oxygen species (ROS) beyond the antioxidant system's capacity. This study investigates whether **oxidative stress processes are detectable in the plasma proteome** of FM patients compared to healthy volunteers

Methods

Whole blood was collected by venipuncture from a 200 FM patients cohort and healthy individuals. The plasma was obtained by centrifugation and analyzed by nLC-MS/MS proteomic method, using EvoSEP chromatograph

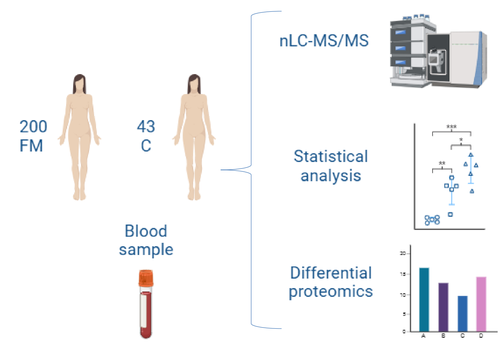

Figure 1. Study design and methodology.

Results

Among the 46 differentially expressed proteins, three were associated with **redox homeostasis**

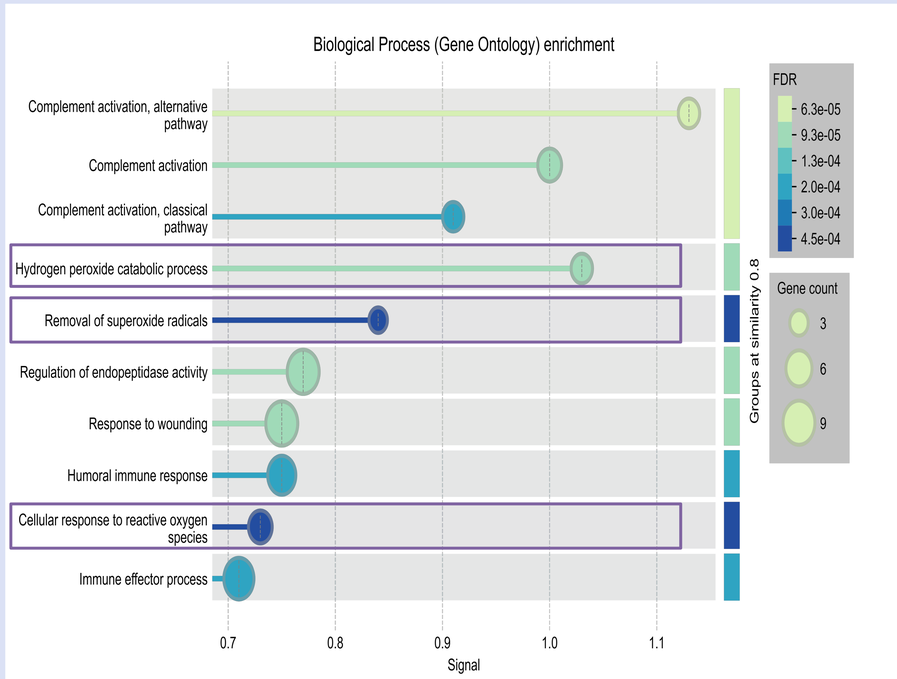

Figure 2. Functional enrichment of differentially expressed proteins.

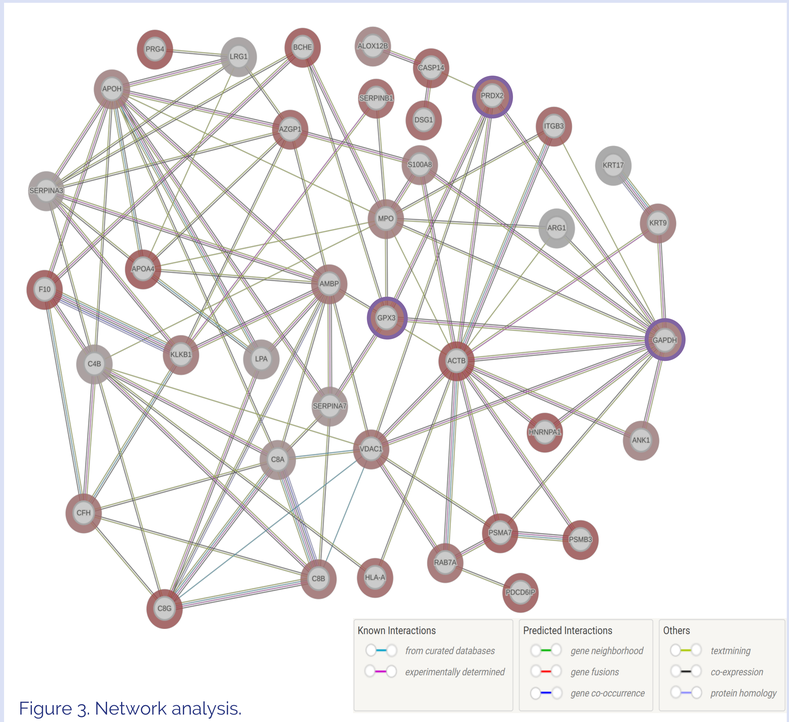

Figure 3. Network analysis.

Conclusion

Our study provides substantial insights into the molecular mechanisms underlying fibromyalgia, particularly highlighting the pivotal involvement of **oxidative stress pathways**. Notably, we identified myeloperoxidase, glutathione peroxidase 3, and peroxiredoxin-2 as key proteins differentially expressed in patients with fibromyalgia, underscoring their critical role in maintaining redox homeostasis and their potential contribution to the disease's pathophysiology

These findings emphasize the significance of oxidative stress dysregulation as a central feature of fibromyalgia. Consequently, our results advocate for the advancement of diagnostic methodologies capable of detecting oxidative stress biomarkers and support the implementation of therapeutic strategies specifically designed to modulate oxidative stress

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