Integrated Multi-Omics Profiling to Define Anti-inflammatory Mechanisms of Fucoidan

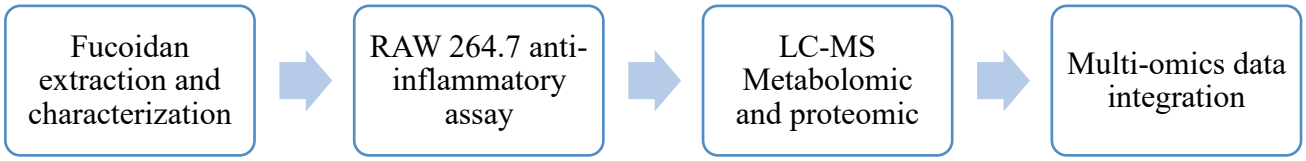
Background

Fucoidan, a bioactive sulphated polysaccharide derived from brown seaweeds, has shown significant anti-inflammatory potential in numerous studies. However, its mechanisms of action extend beyond the well-characterised NF-κB and MAPK pathways and remain incompletely understood. By integrating metabolomics and proteomics, this project aims to uncover novel molecular targets and provide a systems-level understanding of fucoidan-mediated regulation of inflammation.

Aim

To identify molecular targets and signalling pathways associated with the anti-inflammatory activity of fucoidan through the integration of metabolomics and proteomics.

Methodology



Results

Treatment with fucoidan significantly reduced nitric oxide (NO) production in LPS-stimulated RAW 264.7 macrophages (Fig. 1A), confirming its anti-inflammatory activity while maintaining high cell viability. Untargeted LC-MS proteomics (Fig. 1B) and metabolomics (Fig. 1C) revealed substantial alterations in several proteins and metabolic pathways following fucoidan treatment. Proteomics data revealed downregulation of pro-inflammatory mediators such as NF-κB and IL-1β and upregulation of anti-inflammatory mediators and antioxidant genes including Ifit2, Hmox1, Prdx5, and many more. Fucoidan acts as a dual metabolic and signaling regulator-directly intersecting with central oxidative stress networks and suppressing nitric oxide synthesis.

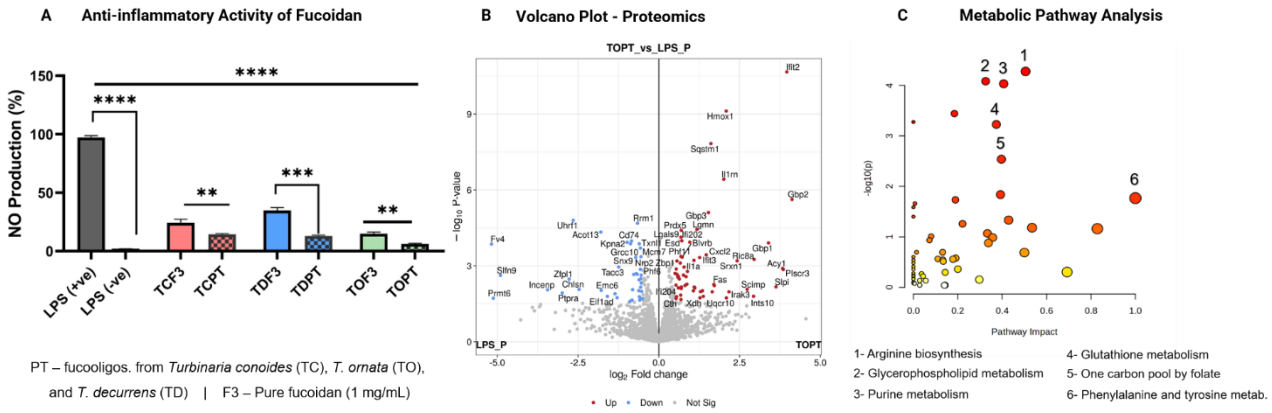


Figure 1. A – Effect of fucoidan on LPS-induced RAW 264.7 macrophages where n = 3 and ** p<0.01, ***p<0.001, and p<0.0001. B – Volcano plot showing differential abundant proteins between LPS and treated groups. C – Metabolic pathways altered in the macrophages

Conclusion

Preliminary multi-omics integration demonstrates that fucoidan does not rely on a single isolated receptor, but instead attenuates macrophage inflammatory responses by simultaneously tuning key proteomic signaling cascades and restoring metabolic redox balance.