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Letter to the Editor

Advancing metabonomics in understanding immunological mechanisms of recurrent spontaneous abortion

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Dear Editor,

We read with great interest the recent paper by Devi et al. [1] on "Immunological insights into recurrent spontaneous abortions: The role of GATA3 and cytokine expression in maternal and placental tissues.". We are writing this article to highlight our interest in understanding the recent developments in metabonomics and its potential to elucidate the immunological mechanisms underlying recurrent spontaneous abortion (RSA). Despite comprehensive research, it remains unclear which pathophysiological factors precisely contribute to RSA, especially in terms of maternal-fetal immune tolerance and dysregulated metabolic pathways. Recent advances in metabonomics provide a promising approach to bridge these gaps by suggesting a comprehensive biochemical perspective of immunometabolic interactions involved in RSA [1–3].

Several studies have highlighted the potential role of metabolic reprogramming in immune cells, particularly T-helper (Th) cells, regulatory T cells (Tregs), and natural killer (NK) cells, which are critical for pregnancy maintenance [3, 4]. Metabonomics-based analyses have determined alterations in lipid metabolism, amino acid pathways, and oxidative stress indicators in women with RSA. This demonstrates that metabolic imbalances may make a contribution in immune dysfunction. Moreover, metabolomic profiling has revealed distinct biomarkers that distinguish successful pregnancies from those complicated by RSA, providing opportunities for potential diagnostic and therapeutic advances [2, 5].

Despite these promising findings, further research involving the integration of metabonomics data with immunophenotyping and transcriptomic analyses is required to elucidate causal relationships between metabolic changes and immune dysfunction in RSA. The application of high-throughput metabolomic technologies, such as nuclear magnetic resonance (NMR) and mass spectrometry (MS)-based approaches, will play a crucial role in the identification of new metabolic markers associated with pregnancy loss. In addition, longitudinal studies focusing on metabolic changes during early pregnancy could provide important information on early predictive markers for RSA.

Given the increasing interest in immunometabolism and reproductive immunology, we believe that a specific focus on metabonomics in RSA research would significantly enhance our understanding of its pathogenesis and inform targeted therapeutic strategies. We encourage the International Journal of Medical Biochemistry to further explore this emerging field, potentially through reviews or special issues, to foster interdisciplinary collaboration and accelerate translational applications.

Thank you for considering this perspective. We look forward to the journal's continued contributions to this vital area of research.

Sincerely.

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