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Multi-Omics Investigation of Ferroptosis-Related Gene Expression in Ovarian Aging and the Impact of Nutritional Intervention

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Abstract : As women age, the quality of their oocytes deteriorates irreversibly, leading to reduced fertility. To better understand the role of Ferroptosis-related genes in ovarian aging, we employed a multi-omics analysis approach, including spatial transcriptomics, single-cell RNA sequencing, human ovarian pathology, and clinical biopsies. Our study identified excess lipid peroxide accumulation in aging germ cells, metal ion accumulation via oxidative reduction, and the interaction between ferroptosis and cellular energy metabolism. We used multi-histological prediction of ferroptosis key genes to evaluate 75 patients with ovarian aging insufficiency and then analyzed changes in hub genes after supplementing with DHEA, Ubiquinol CoQ10, and Cleo-20 T3 for two months. Our results demonstrated a significant increase in TFRC, GPX4, NCOA4, and SLC3A2, which were consistent with our multi-component prediction. We theorized that these supplements increase the mitochondrial tricarboxylic acid cycle (TCA) or electron transport chain (ETC), thereby increasing antioxidant enzyme GPX4 levels and reducing lipid peroxide accumulation and ferroptosis. Overall, our findings suggest that supplementation intervention significantly improves IVF outcomes in senescent cells by enhancing metal ion and energy metabolism and enhancing oocyte quality in aging women.

Keywords : multi-omics, nutrients, ferroptosis, ovarian aging
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