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FDX1, a Cuproptosis-Related Gene, Identified as a Potential Target for Human Ovarian Aging

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Abstract : Cuproptosis, a newly identified cell death mechanism, has attracted attention for its association with various diseases. However, the genetic interplay between cuproptosis and ovarian aging remains largely unexplored. This study aims to address this gap by analyzing datasets related to ovarian aging and cuproptosis. Spatial transcriptome analyses were conducted in the ovaries of both young and aged female mice to elucidate the role of FDX1. Comprehensive bioinformatics analyses, facilitated by R software, identified FDX1 as a potential cuproptosis-related gene with implications for ovarian aging. Clinical infertility biopsies were examined to validate these findings, showing consistent results in elderly infertile patients. Furthermore, pharmacogenomic analyses of ovarian cell lines explored the intricate association between FDX1 expression levels and sensitivity to specific small molecule drugs. Spatial transcriptome analyses revealed a significant reduction in FDX1 expression in aging ovaries, supported by consistent findings in biopsies from elderly infertile patients. Pharmacogenomic investigations indicated that modulating FDX1 could influence drug responses in ovarian-related therapies. This study pioneers the identification of FDX1 as a cuproptosis-related gene linked to ovarian aging. These findings not only contribute to understanding the mechanisms of ovarian aging but also position FDX1 as a potential diagnostic biomarker and therapeutic target. Further research may establish FDX1's pivotal role in advancing precision medicine and therapies for ovarian-related conditions.

Keywords : cuproptosis, FDX1, ovarian aging, biomarker
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