

ANTIOXIDANT GENE EXPRESSION OF PEROXIREDOXIN DECREASES IN GRANULOSE CELLS FROM OOCYTES OF YOUNG WOMEN WITH LOW OVARIAN RESERVE

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INTRODUCTION

Recent studies carried out by our team have shown that an increase in oxidative stress may have a negative impact on ovarian response.¹ Peroxiredoxins (PRDX), a family of peroxidases, are associated with various biological processes such as the detoxification of oxidants and cell apoptosis.² The latest studies have suggested that *PRDX2*, *PRDX3*, and *PRDX4* have the ability to protect against oxidative stress and apoptosis.³ *PRDX1* may play an important role in the regulation of cell signalling pathways induced by reactive oxygen species, whereas *PRDX5* would act as a scavenger.⁴ Nevertheless, little attention has been given to the role of *PRDX* in female infertility.

OBJECTIVE

The aim of this work was to investigate gene expression of *PRDX* (1-6) in granulosa cells (GC) and cumulus cells (CC) from peri-ovulatory follicles of young women who experienced a low response in controlled ovarian stimulation cycles (COH), when compared with fertile donors from the same age cohort.

MATERIALS AND METHODS

This prospective study compared the mRNA expression of *PRDX* (1-6) and caspase 3 in 56 oocyte-cumulus and 62 oocyte-granulosa complexes retrieved from six healthy, fertile oocyte donors and five patients (≤ 5 oocytes retrieved) after gonadotropin stimulation from July-December 2016. All study participants were < 35 years of age and stimulated with the same protocol (follicle-stimulating hormone receptor and triggering with gonadotropin-releasing hormone analogues). mRNA was extracted using the TaqMan® Gene Expression Cells-to-CT Kit (AM1729, Applied Biosystems, California, USA) and mRNA expression of *PRDX* genes and endogenous controls were measured by quantitative reverse transcription polymerase chain reaction (qRT-PCR) using TaqMan probes. No parametric tests were used to identify any significant differences between patients and healthy donors. Statistical significance was set at $p < 0.05$.

RESULTS

Following this study, we found that *PRDX1*, *PRDX2*, *PRDX3*, *PRDX4*, *PRDX5*, and *PRDX6* are expressed in GC and CC. The results obtained from comparative RT-PCR analysis revealed that the mean relative levels of mRNA coding for *PRDX2*, *PRDX3*, *PRDX4*, and *PRDX6* were significantly decreased in GC from women with low response in COH compared with healthy oocyte donors (*PRDX2* $p=0.03$; *PRDX3* $p=0.022$; *PRDX4* $p=0.014$; *PRDX6* $p=0.014$). mRNA expression of both *PRX1* and *PRX5* was much stronger in GC from the patient group compared with the expression observed in GC from the donor group (*PRDX1* $p=0.05$; *PRDX5*

$p=0.02$). Also, an increase of caspase-3 expression in GC ($p < 0.001$) was observed in the patient group, compared to the donor group. No significant differences were found in the levels of mRNA coding for *PRDX* (1-6) and caspase-3 in CC from young women with low response compared with oocyte donors.

CONCLUSIONS

From our study, we can conclude that *PRDX* are differentially expressed in GC and CC. Our results suggest a lower antioxidant capacity and increased apoptosis level in GC of women with low response to COH compared with fertile donors, as well as a role for *PRDX* in human GC function and in the pathogenesis of low ovarian reserve in women undergoing infertility treatment with COH-*in vitro* fertilisation (IVF). These results suggest that antioxidant capabilities are diminished during low

ovarian response, leading to an increase in oxidative damage in the ovary in a similar way to age-related oxidative damage. These findings could lead to the development of new therapeutic strategies for the treatment of low ovarian reserve.

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