



Book of abstracts

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Correlation between mRNA expression of IL-1 β , IL-8, TNF α , IL-6 and IL-10 in PBMCs and redox status parameters in GDM

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Abstract

Gestational diabetes mellitus (GDM) is characterized by chronic low-level inflammation and oxidative stress, both of which contribute to disease pathogenesis. Cytokines expressed in peripheral blood mononuclear cells (PBMCs) may reflect the inflammatory status associated with redox alterations. This study aimed to investigate the correlations between the expression of IL-1 β , IL-8, TNF α , IL-6 and IL-10 in PBMCs and selected oxidative stress parameters in women with GDM. Redox status was assessed by measuring the activities of the antioxidant enzymes glutathione reductase (GR), superoxide dismutase (SOD) and catalase (CAT), serum thiol content, expression of NRF2, as well as protein carbonyl (PCO) levels and TBARS as markers of oxidative biomacromolecular damage. Expression of IL-1 β , IL-8, TNF α , IL-6 and IL-10 mRNA in PBMC of GDM patients (n=50) and a matching number of controls was measured by qPCR. Expression of IL-1 β showed a negative correlation with SOD activity, while IL-8 expression was negatively correlated with SOD activity and positively correlated with protein carbonyl levels. TNF α expression demonstrated negative correlations with both SOD and CAT activities. In contrast, IL-10 expression was positively correlated with protein carbonyl levels. All these correlations were absent in the control group. Increased expression of proinflammatory cytokines was associated with reduced antioxidant enzyme activity, whereas elevated IL-8 and IL-10 expression correlated with increased oxidative protein damage. These findings support the involvement of redox imbalance in the regulation of inflammatory responses in GDM and highlight the potential value of combining inflammatory and oxidative stress biomarkers for a better understanding of disease pathophysiology.

Keywords: Cytokines, redox status, GDM, SOD, protein carbonyl levels

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