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Oestrogen regulated gene expression in normal and malignant endometrial tissue.

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OBJECTIVES: The aim of this study was to examine the expression of oestrogen regulated genes in premenopausal and postmenopausal normal and malignant endometrial specimens. The molecular mechanisms and the role of these genes in endometrial carcinogenesis are poorly understood. METHODS: Normal and malignant endometrial specimens were collected from patients undergoing hysterectomy. Real time TaqMan PCR was used to examine the mRNA expression levels of oestrogen receptor a (ERa) and b (ERb), progesterone receptor (PR), insulin like growth factor 1 (IGF-1) and vascular endothelial growth factor (VEGF). RESULTS: Expression analysis was carried out on 60 patients. ERa was more predominantly expressed in the endometrial samples than ERb, 28% of the specimens did not express ER. Normal pre and postmenopausal tissue expressed higher levels of ERa, PR and IGF-1 than malignant tissue. ERa and PR expression was significantly higher in the proliferative phase endometrium compared to the secretory phase ($P < 0.05$). PR mRNA expression was significantly correlated with ERa in all tissue types. CONCLUSIONS: ERa expression may play an important role in the regulation of PR in normal and malignant endometrium. Further work is needed to establish if IGF-1 plays a role in a subset of endometrial cancers and if isoforms of VEGF play a role in endometrial cancer.

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