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## Declining menopausal estrogen levels effect expression of ERMs in epithelial cells

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Declining estrogen levels after the menopause lead to changes in many genes' expression resulting in myriad postmenopausal health problem such as vaginal dryness. ERM family (Ezrin-Moesin-Radixin) is among those protein families influenced by the estrogen decline. These proteins regulate many cellular functions especially in epithelial tissues such as lateral cellular specialization, functional complexes and membrane shape. Bioinformatics analysis has shown a very high level of similarity among members of the ERM family. We and others have shown that ERM family members influence cells in both normal and abnormal conditions. Until recently, it was believed that ERMs distribution and localization was tissue specific where ezrin was specific to epithelial tissues while moesin was present mainly in endothelial tissue. In this study, we analyze the expression of moesin and ezrin proteins in human vaginal epithelium at different age stages. Vaginal samples were collected from women during nonrelated surgical procedures. Samples from >30 patients at different ages were analyzed using immune-staining with anti-ezrin- and/or anti-moesin-specific antibodies. Our results indicated that both ezrin and moesin were expressed in vaginal tissues. However, these expression levels were both age and estrogen level specific. Ezrin expression increased with age while Moesin decreased with age. Samples from estrogen treated patients have shown the opposite expression patterns attesting to the fact that these proteins are estrogen dependent in vaginal epithelium.

## **Biography**

Ahmed Fadiel is a Molecular Biologist with extensive experience in Bioinformatics, Clinical Informatics, Genomics, and Proteomics. He has completed two Master degrees (MS, Cytogenetics; MS, Clinical Informatics) and a PhD in Molecular Genetics. He has years of research and teaching experience wherein he elucidates complex biological phenomena such as cancer initiation, progression and Fetal Growth Restriction. In addition, he explores protein folding and ligand-receptor interactions. He has also received extensive training in data analysis, mining, and processing and has gone on to develop numerous databases and whole genome analysis tools as well as participated in the development of several national and international research programs. He is a member of various societies and organizations, has won an assortment of national & international awards, sat on various editorial & organizing boards and been the invited speaker at numerous conferences.

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