

Is the Expression of Elastin Metabolism-Related Proteins Site-Specific in Women with Pelvic Organ Prolapse?

Weng Chi Man, Yan Wen, Eric Sokol, Mary Lake Polan, and Bertha Chen

Department of Obstetrics and Gynecology, Stanford University School of Medicine, 300 Pasteur Drive, Room S363, Stanford, CA 94305

Phone: 650-723-9536 Fax: 650-723-7737 Email: weman@stanford.edu

PURPOSE: We sought to investigate whether the expression of alpha-1 antitrypsin (ATT), neutrophil elastase (NE) and lysyl oxidase-like protein 1 (LOXL-1) vary within the vagina in women with pelvic organ prolapse (POP).

METHODS: One cm² full-thickness vaginal wall biopsies were obtained from the vaginal apex, anterior, and posterior vaginal wall from 21 women undergoing surgery for pelvic organ prolapse. Patients with stage 2 or more prolapse and from whom we were able to biopsy at least two sites were included in this study. Based on the most prominent prolapse defect, the patients were further divided into 3 groups: mostly cystocele group, mostly rectocele group, and uterine prolapse plus cystocele group. Comparative quantitative real-time PCR and western blotting were performed to evaluate the level of mRNA and protein expression for all three proteins. An enzyme activity assay was performed for NE.

RESULTS: Within the same individual, the expression level of ATT, NE and LOXL-1 varied among different biopsy sites. However, no specific pattern was observed in the expression of ATT and NE. At the protein level, decreased LOXL-1 expression was noted in the most dependent site of the prolapse in the mostly cystocele (7 out of 10 patients), mostly rectocele group (3 out of 5 patients), and uterine prolapse and cystocele groups (4 out of 6 patients). These data correlated with clinical findings as assessed by POP-Q staging.

CONCLUSIONS: Given that the expression of elastin metabolism-related proteins may vary at different sites within the same individual, consistency in biopsy site is important in the design of future studies and when comparing data from different data sets. The decreased LOXL-1 expression in the most dependent site of the prolapse suggests that spatial orientation may be involved in its expression whereas the lack of site-specificity in the expression of ATT and NE is suggestive of their roles in a systemic connective tissue metabolism.

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