Abstract

Role of Gene Col3a1 Mutation with Expression of p53 in Menopausal Women with Uterine Prolapse

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Objective: Uterine prolapse is a condition that impaired women's quality of life. Multiple factors, mostly clinical, affect the course of uterine prolapse. The study aims to investigate the genetic variation in the form of HOXA11 and Col3a1 gene mutations in women with uterine prolapse. This study also aims to investigate different expression of HOXA11, COL3A1, COL1A1, MMP2, MMP9, TIMP, and p53 proteins in women with and without uterine prolapse, and to understand the risk factors associated with uterine prolapse.

Method: A total of 44 women were enrolled in this cross-sectional study, 22 of which with uterine prolapse and 22 others without uterine prolapse in RSUP dr Kariadi, Semarang. Demographic data including age, parity, BMI, and birth-weight were recorded. HOXA11 and COL3A1 gene sequencing, immunohistochemistry testing of uterosacral ligament were performed to assess HOXA11, COL1A1, COL3A1, MMP2, MMP9, TIMP, and p53 protein expressions.

Result: There was no mutation of HOXA11 gene found in the fragment from women with uterine prolapse used in DNA sequencing test. There was a mutation of COL3A1 gene from 10 subjects with uterine prolapse and 6 subjects without uterine prolapse ($p=0.719$) along the fragment used in DNA sequencing test. COL1A1, MMP-9, and p53 expression were found higher in group of women with uterine prolapse ($p<0.05$). The average of age, parity, and birth weight were found significantly difference in both groups.

Conclusions: On the fragment tested, there was no HOXA11 gene mutation found. However, this study found a mutation of COL3A1 gene from both group of women with and without uterine prolapse. It seems there is an internal factors taking a role in uterine prolapse beside various clinical risk factors. The external factors, such as age, birth weight, and parity also associate with uterine prolapse.