Constitutional *BRCA1* promoter methylation and risk of ovarian cancer.

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Epigenetic mechanisms, including DNA methylation, play an important role in carcinogenesis. DNA methylation in promoter of a gene region can lead to inactivation of this gene by transcriptional silencing processes. Constitutional *BRCA1* promoter methylation has been shown to potentially correlate with the risk of ovarian cancer.

The aim of this study was to evaluate the association of *BRCA1* promoter methylation detected in blood-derived DNA with the risk of ovarian cancer.

The study group consisted of 649 unselected ovarian cancer patients and 795 healthy controls. All women were negative for 13 *BRCA1/2* germline mutations common in Polish population. Methylation status of *BRCA1/2* gene in ovarian cancer patients was assessed using methylation-sensitive high-resolution melting (MS-HRM), and classified as positive or negative. Statistical analysis was done using Fisher exact test.

We found that *BRCA1* promoter methylation was present in 10.3% of unselected ovarian cancer cases and in 6.5% of healthy controls, what corresponded to slightly (about 50%) increased risk of ovarian cancer (OR 1.65, 1.12-2.40, p = 0.01).

The results suggest that *BRCA1* promoter methylation can have a potential role in ovarian cancer susceptibility, but larger more in-depth studies are required.