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Virtual Conference | June 6 – 9, 2020



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E-P12.15 - Age depending prevalence of *RUNX3*, *BRCA1* genes comethylation among female breast cancer case

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June 6, 2020, 9:00 AM - 6:30 PM

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Disclosures

N. Medvedieva: None. **O. Lobanova:** None. **Z. Rossokha:** None. **V. Vershyhora:** None. **V. Cheshuk:** None. **R. Vereshchako:** None. **N. Gorovenko:** None.

Abstract

Introduction: Genes comethylation is important pathways of epigenetic mechanisms in the risk of breast cancer development. Hypermethylation of *RUNX3* and *BRCA1* genes is involved in disrupted oncosuppression process among breast cancer cases. But no so much known about their co-influences on breast cancer (BC) risk in different age. Aim of the study was to evaluate *RUNX3*, *BRCA1* genes age depending comethylation status. Materials and Methods: Tumor tissue of 52 BC female patients was obtained during surgery. Patients (mean age 53.05 ± 1.86) subdivided depending of age: Group 1 (25-44 years), Group 2 (45-60 years), Group 3 (61-85 years). Obtained tumor was tested for *BRCA1* and *RUNX3* gene methylation status. Tumor samples saved using DNA/RNA Shield. DNA extracted with Quick-DNA Miniprep Plus Kit. Bisulfide conversion was done by dint of EZ DNA Methylation-Gold Kit. Converted DNA with methyl-specific primers was used for PCR analysis. Results: No significant differences were found for *RUNX3* gene methylation. Patients of Group 1 had significantly higher methylation status (41.2%) in *BRCA1* gene compared to patients of Group 2 (25%) and Group 3 (26.6%), respectively. Comethylation of hypermethylated *BRCA1/RUNX3* was significantly prevalence also among Group 1 compared to others (Table). Conclusions: Higher hypermethylated *BRCA1/RUNX3* genes status was found among young patients (aged 25-44 years). Further careful studies are needed to understand comethylation effect of investigated genes on early breast cancer development.

Methylation status	<i>RUNX3</i> hypermethylation	<i>RUNX3</i> unmethylation
Group 1 (25-44 years) 17 patients		
<i>BRCA1</i> hypermethylation	41.2%	5.9%
<i>BRCA1</i> unmethylation	41.2%	11.7%
Group 2 (45-60 years) 20 patients		
<i>BRCA1</i> hypermethylation	25%	0
<i>BRCA1</i> unmethylation	60%	15%
Group 3 (61-85 years) 15 patients		
<i>BRCA1</i> hypermethylation	26.6%	6.7%
<i>BRCA1</i> unmethylation	60%	6.7%

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