P467

ASSOCIATION BETWEEN SIX GENE POLYMORPHISMS AND POSTMENOPAUSAL OSTEOPOROSIS IN BELARUSIAN AND LITHUANIAN WOMEN

P. M. Marozik[1], M. Tamulaitiene[2], I. B. Mosse[1], V. Alekna[2], E. V. Rudenka[3], V. Strazdiene[4], M. D. Ameliyanovich[1], A. V. Rudenka[3], O. V. Samakhavets[3], K. V. Zhur[1]

[1]Institute of Genetics & Cytology NAS Belarus, Minsk, Belarus, [2]Faculty of Medicine, Vilnius University, Vilnius, Lithuania, [3]Belarusian Medical Academy of Postgraduate Education, Minsk, Belarus, [4]National Osteoporosis Center, Vilnius, Lithuania

Objective: Genetic factors play an essential role in bone mass regulation and predisposition to osteoporosis. Identification of genetic determinants of osteoporosis will help clinicians of various specialties to evaluate the risk of this disease in various populations and to perform preventive measures. We analyzed the frequency of six polymorphisms in three candidate genes to reveal their contribution into development of postmenopausal osteoporosis (PMO) in Belarusians and Lithuanians.

Materials and methods: Case group included women with severe PMO (54 Belarusians, average age 58.3±6.2 years, and 28 Lithuanians, aged 74.1±1.2 years), the control group comprised postmenopausal women with the BMD T-score of> −2.5 and without previous fragility fractures (77 Belarusians,

56.7±7.42 years and 45 Lithuanians, 72.9±0.9 years, $p>0.05$). DNA was extracted from bloodspots dried on special cards (Macherey-Nagel, Germany). Polymorphic sites in candidate genes (osteoporosis predisposition genes, ApaI, BsmI, TaqI and Cdx2 polymorphisms of VDR gene, G2046T polymorphism of COL1A1 gene and T-13910C polymorphism of LCT gene) were determined using PCR analysis. Significance was assessed using $\chi 2$ test. The differences were considered significant at $p<0.05$.

Results: The analysis of samples from Belarusian postmenopausal women revealed association of VDR ApaI, BsmI with PMO. The risk of osteoporosis was 3.3 times higher for the bearers of AA-genotype of VDR ApaI gene polymorphism and 2.6 times higher for B-allele bearers of VDR BsmI, compared to controls ($p<0.05$). The genotyping of Lithuanian women showed that the total frequency of unfavorable risk alleles (predisposing to PMO) in case group (52.1 %) was higher comparing to controls (48.6 %). No statistically significant difference was found between Lithuanian women with PMO and control group. Observed insufficient statistical power may be due to small number of genotyped subjects.

Conclusion: The findings of this study suggest that at least the ApaI and BsmI polymorphisms of the VDR gene are associated with the risk of PMO in Belarusian women. Screening of these genetic markers may enable early identification of risk groups to perform preventive measures and avoid osteoporotic fractures.