INTERACTION OF GENETIC, CLINICAL AND BIOCHEMICAL MARKERS OF BONE REMODELING IN SEVERE POSTMENOPAUSAL OSTEOPOROSIS

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Osteoporosis is a systemic metabolic disease of the skeleton is a disease of bones that leads to an increased risk of fracture. In osteoporosis the bone mineral density is reduced, bone microarchitecture is deteriorating, and the amount and variety of proteins in bone is altered. Frequency of the disease is linked with age. Around the ages of 50-55 among women, osteoporosis occurs with a frequency of 6-8%, and after 85 years - 58%. The risk of osteopenia at the age of 65 years is 37-45%. Thus, more than 50% of women at the age of 65 have a decreased indexes of bone mass. The social impact of the issue consists of disability and increased mortality due to the vertebrae and proximal femur fractures. Variability analysis of the bone tissue mineral density has shown the strong impact of genetic factors between 60-90% among adult individuals.

Osteoporosis is a multifactorial disease, which is determined by mutual effects of environmental and genetic factors. The widespread distribution and strong negative impact of osteoporosis on human health and life quality as well as significant costs for treatment cause high priority of the investigations in the field of pathogenetic mechanisms of regulation of bone metabolism and methods for early detection and prevention of osteoporosis.

There are at least 30 genes associated with the development of osteoporosis. Among the genes involved in the regulation of bone metabolism, Vitamin D receptor (VDR), lactase (LCT) and α1 chain of type I collagen (COL1A1) genes are of special importance.

Associations of osteoporosis development with different polymorphisms of these genes were revealed. Such associations are often population-dependent. Moreover, it is important to study the effects of not separate genes, but their complex effects. Analysis of osteoporosis predisposition genes in Belarus and Lithuania populations will help to reveal and compare the susceptibility and risk of fractures in these populations.

To determine the osteoporosis predisposition genes, a new method designed in Laboratory of Human Genetics IGC NASB was used, which is 3-5 times cheaper compared to imported diagnostic kits. Blood samples were dried and stored on special blanks, which allows to send them by post and keep at room temperature for years.

As a source of biological material instead of fresh venous blood used in dry spots of capillary blood on specially designed templates, which proved to be cheaper, allowing to store the samples even at room temperature, to post, etc.

The case group consisted of people with severe postmenopausal osteoporosis, and included "mother - daughter" patients. Control group consisted of women without osteoporosis diagnostically detected. Clinical examination of patients has been performed and biochemical markers identified.

Analysis of COL1A1 (-441 G> T), VDR (BsmI, CdxI, ApaI, TagI) and LCT (13910T> C) polymorphisms was performed to determine the genetic predisposition to osteoporosis.

It was revealed an association of predisposition genes with bone mineral density level. Results of the study contribute to the understanding of the molecular genetic mechanisms of osteoporosis and contribute to the algorithm of early prevention of osteoporotic fractures in high genetic risk.