

**A SINGLE NUCLEOTIDE POLYMORPHISM IN THE MATRIX METALLOPROTEINASE-1 PROMOTER IN BREAST CANCER**

**KAROLINA PRZYBYŁOWSKA<sup>1</sup>, JOANNA ZIELIŃSKA<sup>1</sup>, MAREK ZADROŻNY<sup>2</sup>, JAN RYKAŁA<sup>3</sup>, AGNIESZKA KOLACIŃSKA<sup>3</sup>, ZBIGNIEW MORAWIEC<sup>3</sup>, JÓZEF DRZEWÓSKI<sup>4</sup> and JANUSZ BŁASIAK<sup>1</sup>**

<sup>1</sup>Department of Molecular Genetics, University of Łódź, Łódź, Poland

<sup>2</sup>Polish Mother's Memorial Research Institute, Łódź, Poland, <sup>3</sup>Department of Oncological Surgery, N. Copernicus Hospital, Łódź, Poland, <sup>4</sup>Department of Clinical Pharmacology, Medical University of Łódź, Łódź, Poland

Matrix metalloproteinases (MMPs) may play an important role in tumour cell invasion and metastasis. These processes require the dissolution of the basement membrane and the invasion of the extracellular matrix (ECM). Matrix metalloproteinase-1 (MMP-1) is a member of the collagenases, a family of MMPs that degrades collagens type II, III, the main components of the interstitial stroma and I. Overexpression of MMP-1 has been demonstrated in tumour cell lines and tumour tissues. A guanine insertion/deletion polymorphism within the promoter region of *MMP-1* (the 1G/2G) polymorphism influences the transcription of this gene; i.e. the 2G (insertion type) promoter possesses greater transcription activity than the 1G (deletion type) promoter. In this study, we studied the distribution of genotypes and the frequency of alleles of the 1G/2G polymorphism in 75 subjects with node-negative and node-positive breast cancer in normal and cancer tissue samples. Blood samples derived from age-matched healthy individuals served as controls. The 1G/2G polymorphism was determined using the PCR method based on restriction endonuclease *XmnI* digestion. No differences were found between the genotypes of the 1G/2G polymorphism in the cancer tissue and normal tissue of each patient. The distribution of the genotypes in both groups under study did not differ significantly ( $p > 0.05$ ) from those predicted by the Hardy-Weinberg distribution. There were no differences in the genotype distribution and allele frequencies between node-positive and node-negative patients. Additionally, there were no differences in the frequencies of the 1G and 2G alleles between the patients and controls. Therefore, 1G/2G polymorphism may not be associated with the occurrence and/or progression of breast cancer.

Supported by grants: 6 P05A 045 21 from the State Committee of Scientific Research (KBN) and 505/431 from the University of Łódź.