

Analysis of polymorphisms of DNA repair genes in people exposed to residues of unutilized outdated pesticides of Almaty Region

P-06.3-13

B. Bekmanov^{I,II}, L. Skvortsova^I, I. Kiselev^{I,II}, K. Bespalova^{I,II}, G. Abylkasymova^I, A. Garshin^{I,II}, M. Begmanova^I, A. Seisenbayeva^I, A. Abyldasheva^{II}, N. Altynova^I, O. Cherednichenko^I, L. Djansugurova^{I,II}, E. Khussainova^I

^IInstitute of General Genetics and Cytology, Almaty, Kazakhstan, ^{II}al-Farabi Kazakh National University, Almaty, Kazakhstan

Environmental pollution by persistent organic pollutants (POPs) is one of the global environmental problems, which is closely related to health issues, as POPs adversely affect the human body, having a genotoxic, immunotoxic and carcinogenic effects, creating a real threat to the health of present and future generations. It is known that significant, constant and uniform pesticide contamination of agricultural areas significantly increases the frequency of chromosome aberrations (CA). There is evidence that mutations in DNA repair genes are directly proportional to the number of CA in lymphocytes. Our studies are aimed at analyzing the association between the number of chromosomal abnormalities and the polymorphism of DNA repair genes for pesticide toxicity. We examined 172 people living in close proximity to the centers of localization of unused pesticide reserves in rural areas of the Almaty Region (Kazakhstan). Based on our data on cytogenetic analysis, we divided people into a control group with a spontaneous level of CA (0-2% aberrations) and an experimental group - people with a CA level above 2%. DNA excision repair genes were selected as candidate genes XRCC1 Arg399Gln, XRCC1 Arg194Trp, XRCC3 Thr241Met, XPD Lys751Gln. The polymorphisms were examined by PCR-RFLP. Analysis of the distribution of alleles and genotypes of polymorphisms of the XRCC1Arg399Gln, XRCC3 Thr241Met, XPD Lys751Gln genes did not reveal statistically significant differences ($P > 0.05$). An exception is the XRCC1 gene polymorphism Arg194Trp. For this polymorphism, an increasing negative effect of the 194Trp allele was found in people with an increased level of CA. According to the dominant model of inheritance, people with a CA level above 2% show a 4-fold increase in the homozygous mutant allele (194Trp) genotype ($OR = 4.06, p = 0.02$), which indicates violations of the repair system in residents exposed to pesticides. The work was supported by Scientific Program: No. BR05236379.