and the Central Tuvinians, are characterized by the maximum range of haplogroups. More than a quarter of the Y-gene pool belonged to North Eurasian haplogroups Q-M242, the fifth part of the gene pool consists of West Eurasian haplogroup R1a1a-M198. Not only haplogroups N1b-P-43 and N1c1a-M178 are presented with frequencies from 2 to 10%, but also haplogroups C3-M217, C3c-M48, C3d-M407, and O3-M122. The genetic structure of the studied populations of Tuvinians and Todzhintsy was computed by the analysis of molecular variance (AMOVA), with Fst=0.085. The cluster analysis of the populations of Southern Siberia on the matrix of genetic distances (average d=0.4) has shown that all Tuvinians and Todzhintsy formed a united cluster together with Khakas-Sagaytsy. Our results indicate the general background in the origin of the populations of Tuvinians and the preservation of an ancient "Siberian" layer (N1b-P-43, N1c1a-M178, Q-M242) in the gene pool of Todzhintsy in the conditions of geographical isolation in mountain and taiga areas. It can be emphasized that the conditions formed a refugium, where the gene pool kept traces of the ancient population of Southern Siberia.

Key words: *Tuvinians, Todzhintsy, ethnogenesis, gene pool, haplogroups*

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INFLUENCE OF GENETIC POLYMORPHISM +1663A/G TNFR2 ON THE DEVELOPMENT OF CHRONIC TRUE ECZEMA

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Among the cases of chronic dermatosis, eczema makes 30 to 40%. The rise of sickness rate, the chronicity of the disease process, the frequent recurrence of its course, insufficient effect of the treatment methods make chronic eczema the most pressing problem in the modern dermatology. At present the leading pathogenic link of eczema development is considered to be a marked immunological disorders. The main role here is played by T-lymphocytes that bear specific receptors to the antigen and discharge a number of proinflammatory cytokines as well as the factors of tumor necrosis and their receptors. In connection with this, the object of this research work is the study of the role of genetic polymorphism +1663A/G TNFR2 in the development of chronic true eczema. 363 persons were examined (58 patients and 305 persons of the control group), all of Russian nationality, natives of the Central Chernozem region of the RF and having no blood relationship. The extraction of genome DNA from peripheral blood is made with the method of phenol-chlorophorm extraction. PCR was made on the amplifier IQ 5 (Bio-Rad) in the real time mode of operation with the use of DNA polymerases Thermus aquaticus and oligonucleotide primers and probes. Genotyping of DNA markers is made with the method of allele discrimination on the base of Tag Man probes. The results of the research revealed the following rates of genotypes among the patients with chronic true eczema: +1663 AA – 6.9%; +1663 AG – 63.8%; +1663GG – 29.3%, and the rates of alleles are as follows +1663A – 38.79%; +1663G – 61.21. The rates of the genotypes in the control group were the following: +1663AA – 21.64%; +1663 AG – 45.24%; +1663GG – 33.12% and the rates of alleles were: +1663A – 44.26%; +1663G – 55.74%. According to this comparative analysis, the statistical significant differences in the concentration of alleles and genotypes of this locus are not revealed in the group of patients and in the control group. This allows us to come to a conclusion that the polymorphism +1663A/G TNFR2 is not associated with the development of chronic true eczema.

Key words: *eczema, genetic polymorphism, natives of the Central Chernozem region of Russia*

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