APOLIPOPROTEIN E AND ACE GENOTYPES MODULATE ALLOSTATIC LOAD

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Over a life span, both failed and successful responses to stressors promote physiological dysfunction, leading eventually to an allostatic load (AL). Adaptive and maladaptive stress responses depend on biology, culture, environment, and previous experience. Additionally, age, sex, occupation, sociocultural factors and self-perceptions affect physiological responses and structure predispositions to non-communicable diseases and mortality. Measurement of AL assesses physiological dysfunction secondary to lifelong responses to stressors. As yet, how genes modulate AL has not been examined. We examined associations of AL with apolipoprotein (Apo) E and H, ACE, and ANP genotypes in 284 American Samoans. AL was measured using seven secondary mediators of allostasis, along with aspects of body habitus and glucose metabolism. AL differed little by Apo H or ANP genotypes. However, significant differences in Al were observed across Apo E and ACE genotypes. Participants with the Apo E 3*2 genotype showed the lowest AL compared to 3*3 or 2*2 genotypes. Women showed the highest AL across all genotypes. Across ACE genotypes, AL was lower in those heterozygous (I/D), than those with the homozygous I/I genotype. Samoan women showed higher AL than men, along with stronger associations of AL with both Apo E genotypes. AL associates significantly with morbidity and mortality across multiple samples, our results suggest these relationships may depend in part on underlying genotypes.

Key words: *American Samoans, life span, stress, stressors, physiological dysfunction*

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GENETIC DIVERSITY OF INDEGENOUS POPULATIONS OF TUVA REPUBLIC ON SNP – HAPLOGROUPS OF Y-CHROMOSOME

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Studying of the genetic diversity of indigenous populations of the Altai-Sayan Mountains creates an additional historical source for reconstruction of ethnogenesis and ancient migratory ways of the populations of Southern Siberia. Polymorphism of the Y-chromosome in four indigenous populations of Tuva (N=333) was studied: Todzhintsy (N=87), Western (N=75), Central (N=81) and Southeast (N=90) Tuvinians. From 16 revealed haplogroups of Y-chromosomes the most frequent are North Eurasian haplogroups Q-M242, N1b-P43, N1c1a-M178, which have captured 60% of a gene pool of Tuvinians and more than 80% of a gene pool of Todzhintsy. At the western Tuvinians (so-called southern Siberian anthropological type) North Eurasian haplogroups N1b-P-43 and N1c1a-M178 prevail, and each of them cover about one-third of the Y-gene pool. Haplogroup Q-M242 is rare, while at Todzhintsy groups it makes half of the Y-gene pool, and at Southeast and Central Tuvinians groups it covers about a quarter of the Y-gene pool. Frequencies of East Eurasian haplogroup C3c-M48 and West Eurasian haplogroup R1a-M-198 at the western Tuvinians are approximately identical – everyone presents about 10% of the Y-gene pool. At the Northeast Tuvinians-Todzhintsy (so-called Katangsky variant of the Baikal anthropological type) after major haplogroup Q-M242, the second and third places are divided between haplogroups N1b-P-43 and N1c1a-M178 (overall about 40%). Other 10% are presented by West Eurasian haplogroups R1a1a-M198, R1b1a2-M269 and East Eurasian haplogroups C3c-M48 and O3-M122. Gene pools of Southeast Tuvinians (so-called Central Asian anthropological type)

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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