

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) Tuvians. 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 Tuvians and more than 80% of a gene pool of Todzhintsy. At the western Tuvians (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 Tuvians 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 Tuvians are approximately identical – everyone presents about 10% of the Y-gene pool. At the Northeast Tuvians-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 Tuvians (so-called Central Asian anthropological type)