Abstract

History: genotypes associated with allergy to cow's milk are unknown. They have not been replicated in independent populations, and could be responsible for the marked variability in individual clinical response to milk proteins.

Objective: To characterize haplogroups of the D-Loop region of mitochondrial DNA in a group of children allergic to cow's milk in order to arrive at a better understanding of biological and genetic heritability in the etiology of the disease.

Setting: Rio Cuarto, Cordoba, Argentina.

Design: Analysis of mutations or variants of the D-loop region of the mitochondrial genome.

Population: 41 children of both sexes aged 0-2 years old, 11 allergic to cow's milk and 30 healthy subjects (controls) living in the urban area of Rio Cuarto city.

Material and Methods: The D-Loop region HVI, II and III of the mitochondrial genome was amplified by Polymerase Chain Reaction (PCR), for which we used specific "primers".Phylogenetic analysis was calculated using the program CLUSTAL OMEGA, the Neighbor-Joining, BLOSUM62 with data studied and recorded by Jukes-Cantor and then with Kimura-2.

Results and Discussion: The degree of association of haplogroups with APLV children is not significant. The 42.8% of children who have the mutation T16519C were allergic to cow's milk (P = 6/14 = 0.428) CI: 95%, for the population (p = 6/41 = 0.146), this suggests to have this mutation, increases the probability of suffering APLV. In the development of the APLV, in addition to the mitocondrial DNA, other nuclear genes and epigenéticos factors, that make the phenome and perhaps the proteome, would be involved.

Key words: Cow´s milk allergy, haplogroups, children, mutation does not decipher, mitocondrial genome.