Computational Analisys of Hemoglobin Mutants in Hemoglobinopathies

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Most of the structural variants of hemoglobin molecule rise due to substitutions of amino acids, resulting from changes in sequences of nucleotides. Structural changes that cause changes in physical-chemical activities of the molecule vary with the extent of the mutational process and the places where these occur. Their structural similarities are based on the similarity of the composition of amino acids among the types of globin. Through works performed using X-ray diffraction or nuclear magnetic resonance, many mutations have been established experimentally, being 151 variants of alpha-Hb and 259 variants of beta-Hb. However, variants 38, 61, 117, 118, 119 belonging to the alpha chain, and variants 42 and 43 belonging to the beta chain do not have their structures experimentally determined. In order to three-dimensionally assess and determine the structures of these hemoglobin mutants, computer models were used. By using *in silico* analyses, three-dimensional differences of conformation between wild-type and hemoglobin mutants were investigated. For this purpose, three-dimensional theoretical models were created for hemoglobin mutants by homologous modeling using Geno3D. The predicted models, after being validated, were aligned with the wild-type structure placed in PDB using MATRAS software to compare 3D structures. According to the results obtained, hemoglobin mutants exhibited drastic structural changes, correlating the conformational change to loss of function found in hemoglobinopathies.