S4-1.11

Mode of Artemisinins' Action on Oxidative Stress, Genomic and G-quadruplex DNA

S.G. Ginosyan[1], G.V. Chilingaryan[2], H.V. Grabski[1], L.A. Ghulikyan[3], N.M. Ayvazyan[3], and S.G. Tiratsuyan[2]

[1] *Department of Medical Biochemistry and Biotechnology, Institute of Biomedicine and Pharmacy, Russian-Armenian University, Yerevan, Armenia*

[2] *Department of Bioinformatics, Bioengineering and Molecular Biology, Institute of Biomedicine and Pharmacy, Russian-Armenian University, Yerevan, Armenia*

[3] *Laboratory of Toxinology and Molecular Systematics, L.A. Orbeli Institute of Physiology NAS RA, Yerevan, Armenia*

The present study was conducted to evaluate the effect of artemisinins' on the level of lipid peroxidation (LPO), spontaneous chemiluminescence of the S-180 sarcoma homogenate and to study the nature of the interaction with canonical and non-canonical forms of DNA. Artemisinins are secondary metabolites of the medicinal plant *Artemisia annua* have anti-inflammatory, anticarcinogenic, immunomodulatory, antimicrobial, antihelminthic, antiviral, antioxidant and other properties. Our preliminary reverse virtual screening demonstrated that the ligand-binding domain of the human glucocorticoid receptor is the optimal target for artemisinin as well as for dexamethasone. However, the exact molecular targets and mechanisms of action of artemisinins are not well known. We have shown that the introduction of artemisinin leads to increase in LPO and chemiluminescence, which then causes apoptotic cell death in different ways without direct interaction with genomic DNA. We have also shown that artemisinin, dihydroartemisinin, and dimer of dihydroartemisinin interact with 2 sites of the G-quadruplex structure. Artemisinin and dimer of dihydroartemisinin are associated with a groove located between G15 and G21 while dihydroartemisinin binds to a groove located between guanine G5 and G23.