PP34. SYNTHESIS OF HETEROCYCLIC AMIDES OF THE 18βH-GLYCYRRHIZIC ACID

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Targeted orientation of physiologically active natural compounds which were obtained by the novel construction and structural forms of molecules with specific effects and low side effects are actual topic in bioorganic chemistry. It is known that these compounds will have biological and pharmacological properties, improved by adding new pharmacophore ligands to their structure. Plant triterpenoids, like Glycyrrhizin and its aglycone Glycyrrhetate, which are secondary metabolites, have more attention in recent years, because of they have anticancer, antiviral, anti-inflammatory, and antiulcer properties.

In this work it was synthesised novel Glycyrrhizin derivatives containing heterocyclic amines, analyzed some of their physical and chemical characteristics, chemical structures and investigated their biological activity. To isolate Glycyrrhizic acid, a commercial Glycyrrhizic acid, which is produced locally and has a primary material concentration of 32% HPLC, was used. Glycyrrhizic acid subjected to hydrolysis and removed its monoammonium salt. In a result yield was equal to 56% (95% HPLC purity). Glycyrrhizic acid derivatives were synthesized by activated ester method using EDCI and HOBT, as a solvent was used dry acetonitrile, 20% TEA was added and the amino derivative was taken in a two-fold molar ratio. The yield of the product was 85-90%. The synthesized Glycyrrhizic acid derivatives were analysed by HPLC and mass spectrometry, melting point and Rf were determined (petroleum ether: acetone 3/1). Molecular docking analysis by MOE 2014.0901 software of designed Glycyrrhizic acid derivatives was done to investigate the possible receptor-ligand complex binding types in the active cavity of $3CL^{pro}$. Among designed derivatives the structures of 6,22,36,48 in complex with $3CL^{pro}$ presented most docking scores (-7.16 to -7.67), lower RMSD values (1.74 Å to 2.04 Å), morehydrogen interactions with pocket amino acids. Overall, molecular docking data analysis results show, the aforementioned four structures might be an active inhibitor of SARS-CoV-2 $3CL^{pro}$ than the Glycyrrhizic acid.