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An Influence of Aryloxy-/Arylthio-ethyl Fragment on 5-HT_{1A}/5-HT₇ Receptor Selectivity in a Group of Quinolinesulfonamide Derivatives of Aryloxyethyl- and Arylthioethyl- Piperidines.

<u>Katarzyna Grychowska</u>, ¹ Krzysztof Marciniec, ² Michał Szymiec, ¹ Grzegorz Satała, ³ Andrzej J. Bojarski, ³ Andrzej Maślankiewicz. ² Maciej Pawłowski, ¹ Paweł Zajdel ¹

Department of Medicinal Chemistry, Jagiellonian University Medical College, 9 Medyczna, 30-688 Kraków, Poland
Department of Organic Chemistry, Medical University of Silesia, 4 Jagiellońska, 41-200 Sosnowiec, Poland
Department of Medicinal Chemistry, Institute of Pharmacology, Polish Academy of Sciences, 12 Smętna, 31-343 Kraków, Poland e-mail: k.grychowska@gmail.com

Employing a parallel solid-phase synthesis integrated with virtual combinatorial library design, and followed by multistep virtual screening procedure, allowed us to replace arylpiperazine moieties of LCAP with their flexible biomimetics [1]. In this series of compounds, arylpiperazine moiety was changed into a flexible aryloxy-/arylthio-ethyl fragment, while in the part corresponding to the alkylene spacer of LCAP, different, partially rigidified amines – 3-aminopyrrolidine, 4-aminopiperidine, 4-aminomethylpiperidine were introduced. It was further presented, that the affinity of compounds for the tested monoamine receptors (5-HT_{1A}, 5-HT₆, 5-HT₇, D₂) depended upon a kind of a substituent in the aryloxy-/arylthio- ethyl fragments, a distance between the basic nitrogen atom and amide/sulfonamide moiety, and finally a kind of amide/sulfonamide fragment [1].

Now we report on the design, synthesis, and biological evaluation for 5-HT_{1A} , 5-HT_{6} , and 5-HT_{7} receptors of a new series of quinolinesulfonamide derivatives of aryl(heteroaryl)oxy-/heteroarylthioethyl 4-aminomethylpiperidines. The structural modifications comprised introduction of different quinoline sulfamoyl fragments, to further extend exploration in a group of azinesulfonamides (I), variation of different substituents in the phenyl ring of aryloxy-/arylthio- ethyl fragment, as well as a replacement of the central phenyl ring of the aryloxy-/arylthioethyl fragment with five-membered heteroaromatic system. We chose 4-aminomethylpiperidine central core to maintain a distance between tertiary nitrogen atom and sulfonamide bond, corresponding to the four-methylene linker present in the previously reported azinesulfonamide derivatives of LCAP [2]. In particular, we determined an influence of aryl(heteroaryl)oxy-/heteroarylthio- fragment on 5-HT_{1A} and 5-HT_{7} receptor binding profile.

[1] Zajdel P., et al.: Eur. Med. Chem. 2012 (accepted)

[2] Zajdel P., et al.: Bioorg. Med. Chem. 20 (2012), 1545–1556.

The study was supported by the Funds for Statutory Activity of Jagiellonian University Medical College.