QSAR and molecular docking modelling of anti-leishmanial activities of organic selenium and tellurium compounds

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Abstract

Leishmaniasis affects mainly rural areas and the poorest people in the world. A computational study of the antileishmanial activity of organic selenium and tellurium compounds was performed. The 3D structures of the compounds were optimized at the wb97xd/lanl2dz level and used in the quantitative structure-activity relationship (QSAR) analysis. The antileishmanial activity was measured by L. donovani β carbonic anhydrase inhibition (Ki) and the half-maximal inhibitory concentration (IC50) against L. infantum amastigotes. The dataset was divided into training (75%) and test sets (25%) by using a kmeans clustering algorithm. For pKi prediction, model M3 with seven 3D topographic descriptors was characterized by the following statistical parameters: r 2 = 0.879, Q 2 LOO = 0.822, and Q 2 ext = 0.840. For pIC50 prediction, model M12 with six attributes was characterized by the following statistical parameters: r 2 = 0.907, Q 2 LOO = 0.824, and Q 2 ext = 0.795. Both models met all the requirements of Tropsha´s test, which implies predictions of pIC50 and pKi activities with high accuracy. Concomitantly, favourable interactions of the sulphonamide group with the Zn atom in the protein were revealed by the docking analysis.

Keywords:

Leishmaniasis; QSAR; Docking analysis; Protozoan parasites; Organic selenium compounds