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Synthesis, docking and *in vitro* activity of thiosemicarbazones and acylthiazolidones against *Trypanosoma cruzi*

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Introduction

Chagas' disease is a serious health problem that affects around 20 million people in Central and South America, and results in 50,000 yearly deaths. Development of new anti-chagasic drugs is a must. Cruzain is the major cysteine protease of T. cruzi and appears to have potential for new antitrypanosomal chemotherapy. Some derivatives with thiosecarbazones scaffolds have been related for their ability to interaction with cruzain. These data suggest a promising direction for the development of new antitrypanosome chemotherapy. Here we report here the synthesis of thiosemicarbazones and acylthiazolidone and the in vitro evaluation of their ability inhibit the growth of epimastigote to and trypomastigote forms of T. cruzi, as well as a docking analysis under Trypanosoma cruzi cruzain (TCC). The compounds designed were thus analyzed as potential ligands for cruzain¹.

Results and Discussion

The novel compounds were prepared as described in reference 2 and showed below.



These compounds were tested at noncytotoxic concentrations on the epimastigote form of Y strain. The free energy of binding (\(\Delta G)\) values for complexes (most stable docking solutions) between compounds and target (TCC) are presented in Table, along with the pIC_{50} (equals $-log IC_{50}$ of the Y strain epimastigotes) values. In the case of acylthiazolidones derivatives, the compound 5c (a proline derivative) was more active than analogues 5a and 5b, however, inactive against the Colombian strain (data not shown). With regard to the aryl-thiazolinhydrazones series, biological analyses revealed that 10b (in racemic form), was the least cytotoxic and the most active against the Colombian strain in a high concentration (data not shown). Yet compound 10a was the most active at the concentrations tested. This compound possesses a chlorine substituent in

the phenyl ring system and has shown itself to be active against epimastigote, when compared with benznidazole.

Table: Biological and Docking results.

Comp.	Y epimastigote		plC ₅₀ ^c	? G ^d (kcal/mol)
50	(%)	72 /	1 12	5 27
Ja	0.0	73.4	4.15	-3.21
5b	8.7	83.3	4.08	-6.88
5c	65.2	30.5	4.52	-7.01
10a	89.0	31.9	4.50	-6.92 (R) and -7.10
10b	100.0	128.4	3.89	-7.02 (R) and -7.01
10c	92.3	45.0	4.35	-6.67

 a (%) growth inhibition, ${}^b\!\mu\text{mol/L},\,{}^c\text{-log IC}_{50}$ with IC_{50} in mol/L, d is free energy of binding values.

The docking analysis was carried out using the AutoDockTools (ADT) v1.1 and Autodock v3.0.5 programs. The active site was treated as a rigid molecule, whereas the ligands were treated as flexible, which means that all non-ring torsions were maintained (active). The compound that produced the best result (i.e. the most stable complex) in docking analysis, the S enantiomer of molecule **10a**, was analyzed in details. Important interactions found include three hydrogen bonds and also hydrophobic interactions between ligand and target residues (see figure).



HB distances in Å (blue) and residues names (yellow).

Conclusions

In summary, some derivatives exhibit significant in vitro activity against epimastigote T. cruzi, particularly compounds **5c** and **10a**. These results confirm that the thiosemicarbazone scaffold is a potential anti-T. cruzi agent.

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