

Article-Human and Animal Health

In vitro, *in silico* and Pharmaco-toxicological Efficiencies of some Triazole Derivatives on Inhibition of Digestive Enzyme Alpha-amylase

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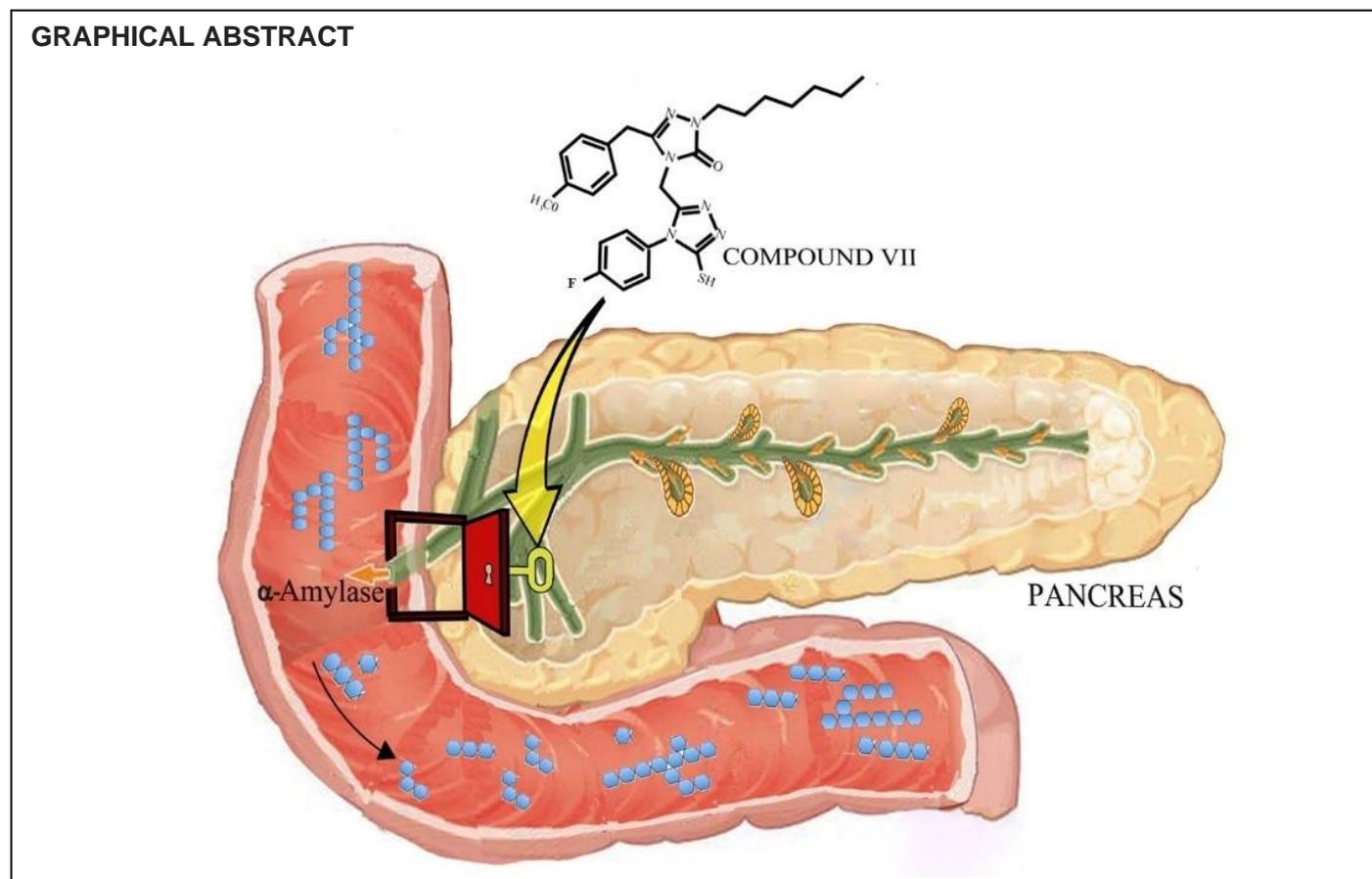
HIGHLIGHTS

- T2DM is increasing rapidly in the world and this brings a constant search for drugs.
- Compound VII showed the strongest inhibition on α -amylase activity with low IC₅₀ value.
- Compound VII, amylase inhibition activity was found to be strong on AR42J cells.
- Compound VII may play role an alternative and non-cytotoxic α -amylase inhibitor for T2DM.

Abstract: Obesity is one of the main health problems associated with a range of diseases. Genetic disposition is related to the risk for obesity but external conditions such lifestyle also increase the incidence. Current COVID-19 pandemic conditions around the globe have been reported to increase the cases of Type-2 diabetes mellitus (T2DM) due to prolonged sedentary life. Among the various treatment modalities, applications of α -amylase inhibitors are commonly used worldwide. Commercially available anti-diabetic drugs are potent inhibitors of α -amylase that reduce postprandial hyperglycemia. In this study, α -amylase inhibition efficiencies of some 1,2,4-triazole derivatives were evaluated. Furthermore, it has been attempted to determine the possible inhibition mechanism of the strongest inhibitor compound among the 8 candidate molecules for α -amylase. Compound VII showed the strongest inhibition on α -amylase activity with low IC₅₀ value (150 μ M). An inhibitory kinetic analysis on α -amylase activity by Compound VII was found to be reversible and uncompetitive. Furthermore, molecular docking studies with this molecule showed that it could bind to the catalytic site of the enzyme by performing weak interactions with Ser56, Tyr59, Tyr62, Asp176, Asp274 and Leu142 residues. Cytotoxic potential of Compound VII on amylase overexpressing AR42J

pancreatic cancer cells was also performed using trypan blue staining and the compound at the highest dose 10 μM was found to be cytotoxic, but effective for alpha amylase inhibition at non-cytotoxic doses. The results showed *in vitro* effect of Compound VII on alpha-amylase inhibition in cells. Here, we suggest an alternative and non-cytotoxic α -amylase inhibitor for T2DM.

Keywords: α -Amylase inhibition; 1,2,4-triazole; Docking; Cytotoxicity; T2DM.



INTRODUCTION

Diabetes mellitus (DM) is one of the most common diseases in the world and the incidence increases during COVID-19 pandemic conditions [1]. It is estimated that 451 million adults around the world are diabetic and this disease will reach 693 million people by 2025 [2]. DM is a metabolic disorder of the endocrine system that caused by abnormal plasma blood glucose levels occurred with some complications including hyperglycemia, polyphagia, polydipsia, and polyuria. DM is concomitantly accompanied by various diseases such as neuropathy, nephropathy, angiopathy, cardiovascular diseases and retinopathy [3, 4]. Diabetes is a complex disease occurred by intrinsic and extrinsic conditions, and mainly classified as Type-1 and 2. Type-1 is more based on genetic background, but Type-2 is more related to personal eating habits and lifestyle. Type-2 diabet mellitus (T2DM) is the most common type of diabetes, accounting for 90-95% of cases [4]. One of the ways to control T2DM disease is to control hyperglycaemia after eating. Stabilization of blood glucose for diabetic patients is important, since it prevents the complexity relationship between hyperglycaemia and diabetes [3]. Amylase inhibition slows carbohydrate digestion and thus causes prolongation of overall time for carbohydrate digestion. As a result, the rate of glucose absorption in the metabolism decreases so that the postprandial plasma reduces glucose uptake [4].

Recent COVID-19 pandemic conditions experienced all over the world negatively affect people's lives in many ways. In addition, within the scope of the measures taken and compulsory to be followed in the world, many people have to live under heavy stress [5]. This situation has forced both a healthy and regular diet and a sedentary life. It is predicted that T2DM will be one of the global concerns at the end of the pandemic [6].

α -Amylases, α -1,4-glucan-4-hydrolase (EC 3.2.1.1) have activities on conversion of oligosaccharides and disaccharides into monosaccharides which can be easily absorbed. This suggests that amylases are

one of the key enzymes of the digestive system so that being a target for drug design studies [3]. Amylase inhibitors have been a prominent focus of attention due to their treatment potential for HIV infection, metastatic cancers, diseases with lysosomal storage abnormalities and specially diabetes [7-9]. The range of relevant diseases conditions suggests that α -amylase appears to be a target enzyme in the design of suitable drug molecules for therapies of diabetes, obesity and hyperlipidemia [3]. The inhibition of amylase may have profound effects on the mechanisms in controlling digestive system and glycoprotein release and may alter the process. Currently, different amylase inhibitors such as voglibose, acarbose and miglitol used as anti-HIV, anti-cancer, and anti-diabetic agents [10]. However, some side effects such as hepatotoxicity, diarrhea, stomach gas, and abdominal distension are observed in the use of these drugs [11]. Hence, it is important to alleviate the adverse effects resulting in serious disruptive impacts on the metabolism, with the application of anti-diabetic drugs or the discovery of new drugs.

Heterocyclic compounds are very important nuclei for drug discovery because they have a wide variety of binding interaction potentials [12]. These compounds are used as important building blocks in such many natural products, pharmaceuticals, and functional materials [3, 8, 13]. Triazole structures carry nitrogen atoms in their ring systems and act as key structural units in many pharmaceutical preparations [13]. The 1,2,4-triazole core is one of the most prominent heterocyclic structures and undoubtedly found a lot of natural products and bioactive molecules [7]. Triazole compounds, however, are promising heterocycles in the pharmaceutical industry. These are the most studied clinical entities in single and/or fused structures with different biologically active heterocyclic compounds [12]. The most remarkable isomers are 1*H*-[1,2,4]-triazoles which form a part of some biologically active pharmaceutical products [14]. It has been reported that heterocyclic compounds containing triazole derivatives have antimicrobial [15], antiviral [16], diuretic [12], anti-inflammatory [17], anticancer [18]. Also in addition COVID-19 associated is used as anti-fungal [19]. In the literature, triazoles have been reported as potent α -amylase inhibitors to control blood sugar levels in the diabetes mellitus [3, 20]. It has been reported that several triazole compounds exhibit a reversible and non-reversible inhibition on α -amylase [3, 21].

Regarding the importance of 1,2,4-triazole compounds for the treatment of T2DM by the inhibition of amylase, in this study, some novel 1,2,4-triazole derivatives were repurposed to be examined in terms of α -amylase inhibition potentials using in glass, *in silico* and *in vitro* approaches.

MATERIAL AND METHODS

Chemicals and reagents

α -Amylase enzyme (A6380), 3,5-dinitrosalicylic acid (DNS, D0550), acarbose (J61737), Roswell Park Memorial Institute-1640 Medium (RPMI-1640, Cat# R8758), Dulbecco's Modified Eagle's Medium (DMEM, Cat# D6429), trypan blue solution (Cat# T4049) and other reagents used in the inhibition studies were purchased from Sigma-Aldrich (St. Louis, MO, USA). In addition fetal bovine serum (FBS, Cat# 10270) and penicillin/streptomycin (Cat# 15140-122) were purchased from Gibco (CA, USA).

α -Amylase activity assay

α -Amylase activity was determined using with slight modifications of DNS method based on the calculation of the amount of released reducing sugars [1, 22]. Briefly, the reaction mixture containing 630 μ L pH 7.00 sodium phosphate buffer (0.05 M), 50 μ L of soluble starch solution (0.035%, by mass per volume) and 20 μ L of α -amylase solution (25 ng.mL⁻¹ in 0.05 M, pH 7.00 sodium phosphate buffer) was incubated at 40 °C for 15 min. The blank solution was free of enzymes. 700 μ L of 3,5-dinitrosalicylic acid (DNS) reagent was added to the samples and the reaction mixture was boiled for 10 min, the reactions were then stopped. Subsequently, the reaction mixture was kept at room temperature for 15 min for thermal stabilization. The absorbance was measured at 540 nm compared to blank (Perkin Elmer, Lambda 25). One unit of α -amylase activity was defined as 1 μ mol of reducing sugars that was released under optimum reaction conditions in 1 min reaction time at 40 °C [23].

Optimization of enzyme activity

The variables used in the design of the inhibition studies were primarily optimized for the previously mentioned commercial amylase enzyme. For this, preliminary tests were performed, and activity curves were created to verify the minimum concentration and maximum activity of the amylase enzyme required for the experiments. A series of activity measurements (at enzyme concentration range of 0.09-250 ng.mL⁻¹) were

performed to determine suitable enzyme concentration for correctly measuring reaction velocity for α -amylase activity in the presence of constant soluble starch concentration as a substrate, at room temperature and pH 7.0 (50 mM phosphate buffer). The calculated enzyme activities were calculated by plotting the activity versus increasing enzyme concentration and continued in this way for further characterization and inhibition studies [24]. In order to determine the substrate concentration, a series of activity measurements were performed again by preparing reaction mixtures at constant enzyme concentration, temperature and pH in the presence of soluble starch as a substrate in the concentration range of 0.02-0.1%. Lineweaver-Burk graph was drawn to obtain K_m and V_{max} values [25]. To find the optimum pH value for the enzyme activity, 50 mM acetate buffer (pH 5.0), 50 mM phosphate buffer (pH 6.0-7.0) and 50 mM glycine-NaOH buffer (pH 8.0 -9.0) were used and pH-relative activity (%) graph was created [23]. Optimum temperature of the α -amylase activity was also determined by monitoring enzyme activities at different temperature between 10 °C and 90 °C and temperature-relative activity (%) graph was created [24].

Biological Activity Methods

Pretreatments

The stock solutions of organic molecules used in the experiments were prepared in absolute DMSO. Final solvent (DMSO) concentration in the reaction mixture was 1% [26]. Aliquots to be used in inhibition experiments were carried out by diluting in different concentrations in stock solutions of organic molecules performed on the day of the experiment.

α -Amylase inhibition studies

For inhibition studies, the reaction mixtures containing 20 μ L α -amylase enzyme solution, 10 μ L inhibitor solution was pre-incubated for 20 min in a water bath at 40 °C. This studies inhibitor molecules solutions in used were evaluated in different concentrations (Compound I: 0-540 μ M; Compound II: 0-9626 μ M, Compound III:0-1300 μ M; Compound IV: 0-417 μ M; Compound V: 0-1 mM; Compound VI:0-0.7 mM; Compound VII: 0-0.67 mM; Compound VII: 0-0.65 mM). Following this procedure, soluble starch solution and 50 mM phosphate buffer (pH 7.0) were added (final soluble starch concentration in the reaction mixture was 0.035%) to each reaction mixture and all reaction mixtures were kept for additional 15 min at same conditions. Subsequently, 700 μ L of DNS reagent was added to the samples and the reaction mixture was boiled for 10 min the reactions were stopped. Finally, all samples reached to thermal equilibrium were measured at 540 nm compared to blank by a spectrophotometer (Perkin Elmer, Lambda 25). After measuring enzyme activity, inhibitor concentrations were plotted against relative activities % to determine IC_{50} value which is the inhibitor concentration inhibits 50% of the enzyme activity representing inhibition efficiencies of each inhibitor molecules. The percentage inhibition effect was measured using the following Formula I as the effect on the amylase activity of each organic molecule:

$$\text{Formula I: Inhibition (\%)} = \left[\frac{(A_c - A_s)}{A_c} \right] \times 100$$

A_c : Absorbance of control, A_s : Absorbance of sample [27].

Determination the inhibition type and the K_i value of α -amylase inhibitory activities

To reveal the mechanism of enzyme inhibition, and determination of Michaelis Menten constant (K_m), V_{max} and inhibition constant (K_i) values, the Lineweaver-Burk graphics were plotted for different substrate concentrations at fixed Compound VII concentration using GraFit enzyme kinetical program (Version 7.0 Erithacus Software). K_i of Compound VII effect on amylase enzyme activity was calculated by employed Formula II using to uncompetitive inhibition model of the program.

$$\text{Formula II: } V = \frac{[V_{max} / (1 + [I]/K_i)]}{[K_m / (1 + [I]/K_i)]}$$

Where V is the reaction velocity; V_{max} is the limiting velocity; K_i is defined as the rate constant for kinetically binding inhibitor to the enzyme, the inhibition constant, K_m is the Michaelis constant; $[I]$ and $[S]$ are the concentration of inhibitor and substrate, respectively [9, 28].

α -Amylase molecular modeling study

The crystal structure of target protein, α -amylase (PDB ID: 1BAG) was obtained from Protein Data Bank (www.rcsb.org/pdb) [29]. Then, it was pre-processed, modified and refined using AutoDock Tools 1.5.6 and AutoDock Vina software for all compounds [30]. Ligand optimizations were performed by Gaussian 03 program. Discovery Studio 4.1 Visualizer was used to show binding interaction of molecules with the target site. After the calculation of docking scores were produced, the best fitted ligand to target protein were determined [31].

Cell culture

Mammalian pancreatic cancer (AR42J, Cat# 93100618) and mouse embryonic fibroblast cell lines (CF-1, Cat# SCRC-1040) were purchased from ECACC (UK, England) and ATCC (VA, USA), respectively. The cells were cultured in RPMI-1640 (for AR42J cells) or DMEM (for CF-1 cells) with 10% heat inactivated, 1% penicillin/streptomycin. Complete culture media were filtered by a 0.22 μm filter (Aisimo, London, England), and warmed at 37°C before use. Cells were incubated supplied at 37 °C humidified with 5% CO₂ [32].

Drug preparation and treatment

Acarbose and Compound VII were dissolved in DMSO. Acarbose, a standard α -amylase inhibitor, was used as a positive control [33] and was also included in cytotoxicity experiment. Final solvent (DMSO) concentrations were adjusted to 0.1% within the medium during cell culture [34].

Measurement of cell viability

Cell viability was evaluated with trypan blue staining supplemented with fixative [35]. This method is based on the differences in cell membrane permeability between live and dead cells. Dead cells with disrupted membrane are seen dark blue/black under the brightfield tool of microscope due to the dye intake within the cell, whereas dye cannot diffuse into live cells with intact membrane. Briefly, 5x10³ of AR42J and CF-1 cells were seeded into each well of the sterile 96-well cell culture plates. Media was refreshed after overnight incubation followed by treatment with various concentrations of Compound VII (0,001-5 μM). Control cells were untreated. Subsequently, 0.4% trypan blue solution was added to each well for 10 min at room temperature, were washed with phosphate buffered saline (PBS) for three times. Cells were then treated with fresh 4% paraformaldehyde (PFA) for 30 min at room temperature. The fixative was washed with 1xPBS. The cells were visualized under Axio Vert inverted microscope (Carl Zeiss, Germany) and images for each treatment were captured. Dead/Live cells were analyzed using count tool of Adobe Photoshop software. Cell counts were transformed to percentages and viability (%) of treated and untreated cells was compared.

***In vitro* α -amylase inhibitory studies**

In vitro α -amylase inhibitory studies on AR42J cell line was performed using slight modifications on the microplate-based starch-iodine method [36]. The degraded amount of starch was used to estimate the activity of α -amylase. AR42J cells were cultured onto T25 flasks at the density of 5x10⁴ cells overnight. Cells were treated with Compound VII (0.05-4 μM) or acarbose (0.05-500 μM) for 48h). Following incubation, 0.5% soluble starch were added to the cells for 1 h. 100 μL samples taken from the flasks were added to sterile 96-well plates and 100 μL of iodine reagent (0.5% iodine and 5% potassium iodide) was then added. Finally, all samples were measured at 540 nm by a microplate reader (Molecular Devices Versamax, California, USA). After measuring *in vitro* α -amylase activity for reduce soluble starch digestion via Compound VII and acarbose was plotted against relative activities (%) to determine IC₅₀ value (the concentration inhibiting 50% of the enzyme activity). The percentage of inhibition was measured the Formula III as the effect on the amylase activity of Compound VII and acarbose as standard drug was using an online calculator (<https://www.aatbio.com/tools/ic50-calculator>) [37].

$$\text{Formula III: Inhibition (\%)} = \left[\frac{(A_c - A_s)}{A_c} \right] \times 100$$

Ac: absorbance of control, As: absorbance of sample.

Statistical analysis

All experiments were performed as at least three independent repeats and the results were given as arithmetic mean \pm standard deviations. Statistical analyzes were carried out using SPSS (Statistics Program for Social and Science) software (Version13.0.1). The suitability of the data to normal distribution was evaluated with the Kolmogorov-Smirnov test. One-Way ANOVA test was used for parametric data and then Post-hoc Tukey test for multiple comparisons between the groups. p value less than 0.05 was considered as statistically significant.

RESULTS AND DISCUSSION

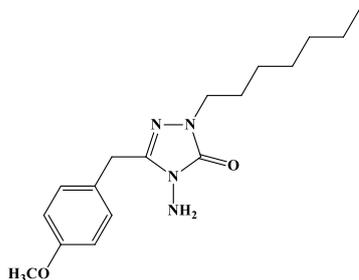
T2DM is one of the rapidly increasing diseases of our age. It is predicted that the measures taken and must be followed due to the COVID 19 pandemic will cause adverse effects especially on the young population and the rate of spread will come in the form of a Tsunami [6]. An effective treatment approach for treatment T2DM is to reduce food-related hyperglycemia by reducing the digestion of carbohydrates taken through the inhibition of carbohydrate-breaking enzymes [3]. The widely used component of many drugs are five-membered heterocyclic rings such as 1,2,4-triazole, 1,2,3-triazole derivatives. They have a wide spectrum of biological activities such as anti-cancer [18], anti-viral [11], anti-depressant [38], anti-bacterial [39], analgesic [40], anti-HIV [16], diuretic [12], anti-inflammatory [17], anti-tuberculosis [41] and COVID-19 associated anti-fungal [19]. Recent studies have shown that the easy synthesis of Schiff and Mannich base derivatives of 1,2,4-triazoles utilized their use in various applications, in particular biology and chemistry [42, 43].

α -Amylase inhibition activity

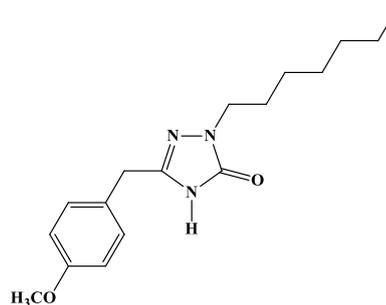
In this study, α -amylase inhibition potentials of some 1,2,4-triazole derivatives [44] (Table 1) were examined. Because of the different behavioral profile of hydrophobic groups in their structures of each organic molecule used in the study, the concentration ranges of inhibitor molecules were also different in the inhibition studies [45] (Table 2). Soluble starch (0.035%) was used as a substrate, and inhibition studies were performed at optimum pH (7.0) and temperature (40 °C) values for α -amylase activity. Relative activities were plotted against inhibitor concentrations and the inhibitor concentration at which 50% decrease in the activity was determined as the IC_{50} value (Table 2). Compound VII among the studied molecules had the lowest IC_{50} value as 150 μ M (Table 2). In the presence of other inhibitor molecules except of Compound VII, inhibition of α -amylase was observed in the range of 25-62% even at the highest inhibitor concentrations tested (Table 2). IC_{50} value of acarbose for α -amylase inhibition was determined as 235 μ M.

Table 1. 1,2,4-triazole derivatives were evaluated for *Bacillus subtilis* α -amylase inhibition¹⁵**Compound code/Nomenclature/ Formulas**

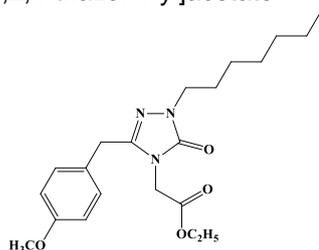
I. 4-amino-2-heptyl-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one



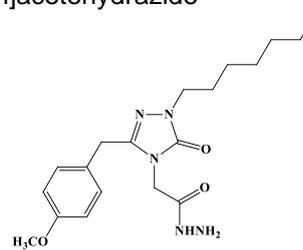
II. 2-heptyl-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one



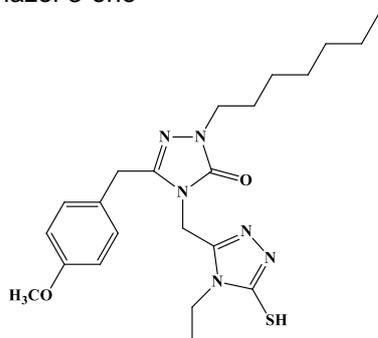
III. Ethyl [1-heptyl-3-(4-methoxybenzyl)-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl]acetate



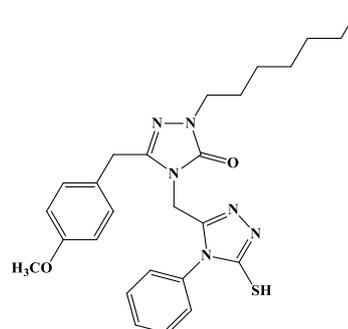
IV. 2-[1-heptyl-3-(4-methoxybenzyl)-5-oxo-1,5-dihydro-4*H*-1,2,4-triazol-4-yl]acetohydrazide



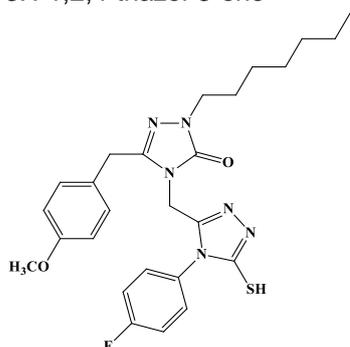
V. 4-[(4-ethyl-5-mercapto-4*H*-1,2,4-triazol-3-yl)methyl]-2-heptyl-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one



VI. 2-heptyl-4-[(5-mercapto-4-phenyl-4*H*-1,2,4-triazol-3-yl)methyl]-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one



VII. 4-[[4-(4-fluorophenyl)-5-mercapto-4*H*-1,2,4-triazol-3-yl]methyl]c-2-heptyl-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one



VIII. 4-[[4-(4-chlorophenyl)-5-mercapto-4*H*-1,2,4-triazol-3-yl]methyl]-2-heptyl-5-(4-methoxybenzyl)-2,4-dihydro-3*H*-1,2,4-triazol-3-one

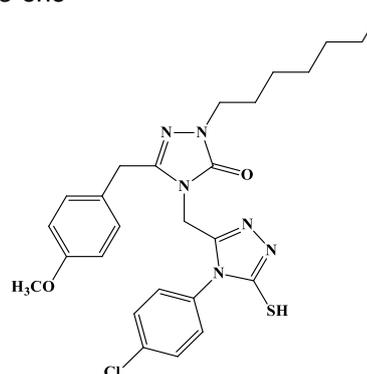


Table 2. α -Amylase inhibition potentials of evaluated organic compounds

Inhibitor Compounds	IC ₅₀ , μ M	Inhibition Level		Binding Affinity (Δ G, kcal.mol ⁻¹)
		%	[I] μ M	
I	>540	33.1 \pm 0.2	540	-7.4
II	>9625	45.0 \pm 0.1	9625	-7.3
III	>1300	29.0 \pm 0.1	1300	-6.7
IV	>415	25.2 \pm 0.1	415	-8.0
V	>1000	45.3 \pm 3.6	1000	-7.5
VI	>700	39.2 \pm 0.1	700	-7.9
VII	150	84.2 \pm 1.7	670	-8.2
VIII	163	62.1 \pm 0.2	650	-8.3
Acarbose	235	53.7 \pm 1.1	240	-

It is suggested that the Compounds VII and VIII are more potent than acarbose as α -amylase inhibitors. Gonzaga and coauthors observed α -glucosidase inhibition in the presence of 3 of 24 synthesized 1-phenyl-1*H*- and 2-phenyl-2*H*-1,2,3-triazole derivatives and IC₅₀ values of these three molecules was found as 145 μ M, 201 μ M and 281 μ M [45]. Nawaz and coauthors observed α -amylase inhibition for 5-amino-nicotinic acid derivatives with IC₅₀ values ranged 12.17 \pm 0.14 to 37.33 \pm 0.02 μ g.mL⁻¹ [8]. In studies conducted with wheat flour, Tu and coauthors defined a molecule with 37.58 μ g.mL⁻¹ IC₅₀ value for α -amylase activity [46]. On the other hand, IC₅₀ value for inhibition by acarbose was found between 16.7 μ M and 774 μ M [8, 21, 47].

Besides the synthetic organic compounds, some natural extracts *i.e.* from plants were frequently used for potential of amylase inhibition [21, 48, 49]. For instance, extracts from different species of *Cinnamomum zeylanicum* were shown to have IC₅₀ value 57 μ g.mL⁻¹ [48]. Although 1,2,4 triazole compounds have high potential as drug candidate, there is a limited understanding on their anti-diabetic potential. This study here presents a significant potential of the Compound VII to be used in controlling diabetes.

Kinetic study of α -amylase inhibition

To understand inhibition types, the mechanism of enzyme inhibition, and determination of Km, Vmax, and Ki values, the Lineweaver-Burk graphics were plotted for different substrate concentrations (50 μ M and 150 μ M) at fixed Compound VII concentration using GraFit enzyme kinetical program (Version 7.0 Erithacus Software) (Figure 1, Table 3). Previous studies have shown that molecules derived from similar starting molecules have similar inhibitory effects and mechanisms [50]. Activity measurements showed that Km and Vmax values were 0.68% and 0.66 μ mol min⁻¹, respectively when Compound VII was not included in the reaction mixture. However, in the presence of 50 μ M and 150 μ M Compound VII, the Km and Vmax values decreased to 0.07% and 0.12 μ mol.min⁻¹, and 0.03% and 0.04 μ mol.min⁻¹, respectively (Table 3). This indicates uncompetitive inhibition in which both Km and Vmax values decrease with increasing inhibitor concentration (Figure 1). According to this, it can be said that the Compound VII caused α -amylase inhibition by binding to a region rather than the active site of the enzyme, and the enzyme-substrate complex reversibly formed with some weak interactions. Ki value in the presence of Compound VII was also calculated as 6.43 \pm 0.12 μ M.

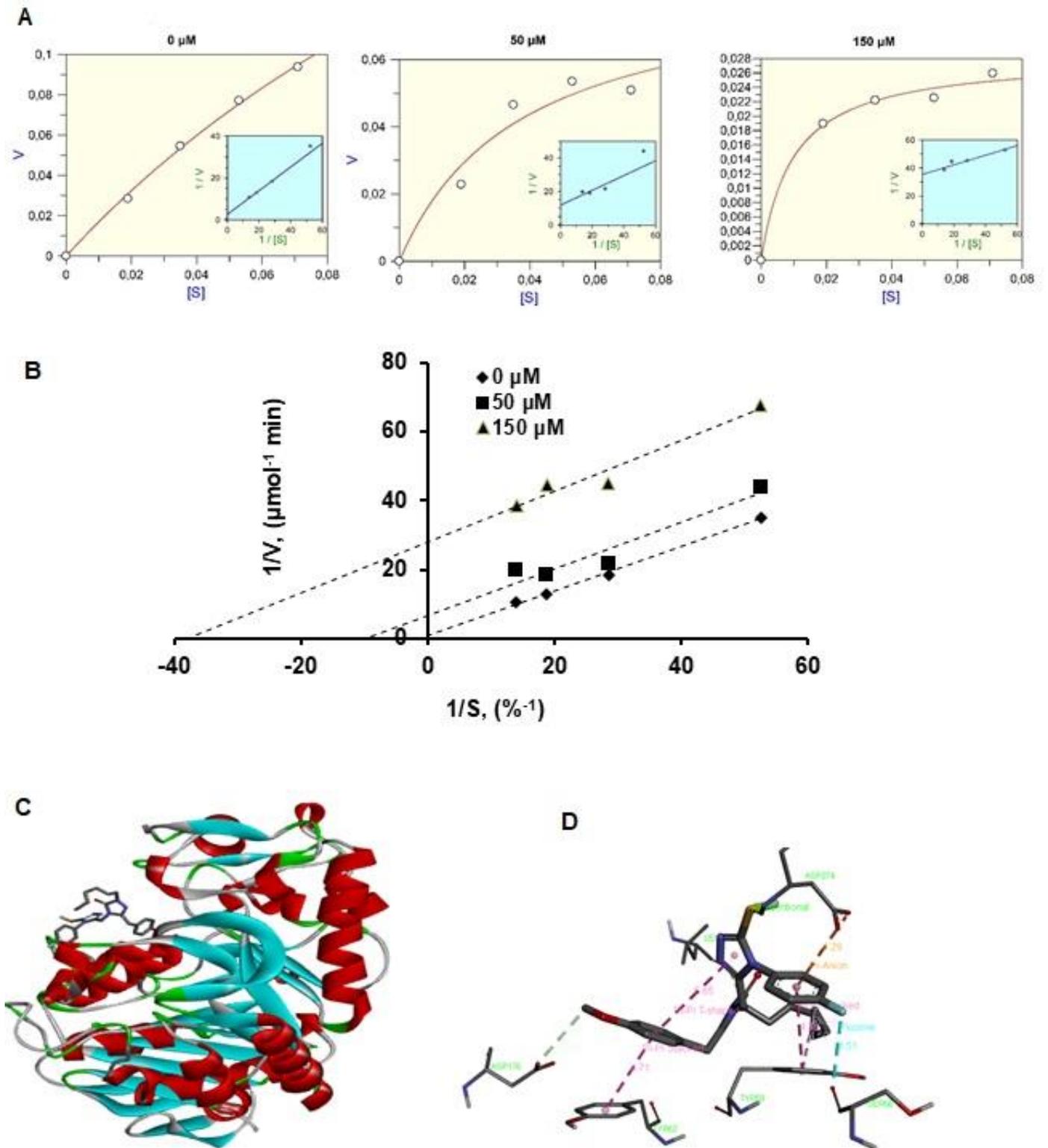


Figure 1. A) Lineweaver–Burk plots obtained with variable starch concentrations at fixed Compound VII concentration. B) Determination of α -amylase inhibition type in the presence of Compound VII. C) Predicted conformation of the Compound VII inside the binding pocket of *Bacillus subtilis* α -amylase. D) Micro environment which shows various types of interactions of the compounds atoms with the amino acid residues.

Table 3. The type of α -amylase inhibition in the presence of the Compound VII and the calculated kinetic parameters -

[Compound VII] (μM)	K_m (%)	V_{max} ($\mu\text{mol}\cdot\text{min}^{-1}$)	Type of inhibition	K_i (μM)
0	0.68	0.66		
50	0.07	0.12	Uncompetitive	6.43 \pm 0.12
150	0.03	0.04		

Dandekar and coauthors reported that they observed uncompetitive inhibition and K_i values of range of 2.49-47.60 μM for an α -amylase by dehydrodieugenol B isolated from *Ocimum tenuiflorum* [3]. Shahzad and coauthors observed competitive inhibition for an α -amylase in the presence of novel C-2 symmetric molecules with K_i value as 3.865 μM [1]. K_i value and inhibition type for α -amylase inhibition by wheat bran was reported to be as 17.24 $\mu\text{g}\cdot\text{mL}^{-1}$ and noncompetitive, respectively [46]. Balbaa and coauthors observed noncompetitive inhibition for an α -amylase in the presence of 4-amino-3-(D-gluco-pentyl-1-yl)-5-mercapto-1,2,4-triazoles and their 3-methyl analogues with K_i value 0.363 mM [51].

Molecular docking calculation

The most rational and authentic approaches in the drug design and discovery are the investigation of the binding efficiencies and molecular interactions of the ligands with target proteins by molecular docking [1, 8, 43]. The docking analysis was performed with active site of amylase (PDB ID: 1BAG) and the results exhibited good binding interaction with receptor. Docking scores ranging from -8.3 to -6.7 can be seen in Table 2, and various interactions between target protein and ligands such as hydrogen bond, π - π stacking interaction and π -cation interaction were also mainly observed. The binding models (2D and 3D) of Compound VII with protein receptor are illustrated in Figure 1. The title compounds showed hydrogen bond interaction with six amino acids residues including SER 56, TYR 59, TYR 62, ASP 176, ASP 274, and LEU 142. Along with π - π stacking interaction with TYR 59 and TYR 62, it also displayed π -cation interaction with ASP 176. Thus, the docking studies show that multimerization enhances the binding affinity and occupies the highest docking score.

Cytotoxicity activity

Cytotoxic concentration of Compound VII on AR42J cells was first determined by the trypan blue method supplemented with fixative [35], and amylase inhibition studies were performed using non-cytotoxic conditions not to obtain false negative results (Figure 2). Thus, Figure 2 shows the amylase inhibition induced by the non-cytotoxic dose of Compound VII. Experiments were also performed for CF-1 cells, control cells which are not amylase overexpressing. Again, non-cytotoxic doses were used as well, and there was no significant difference in cell viability after treatment with Compound VII compared to untreated counterparts ($p < 0.05$) (Figure 2).

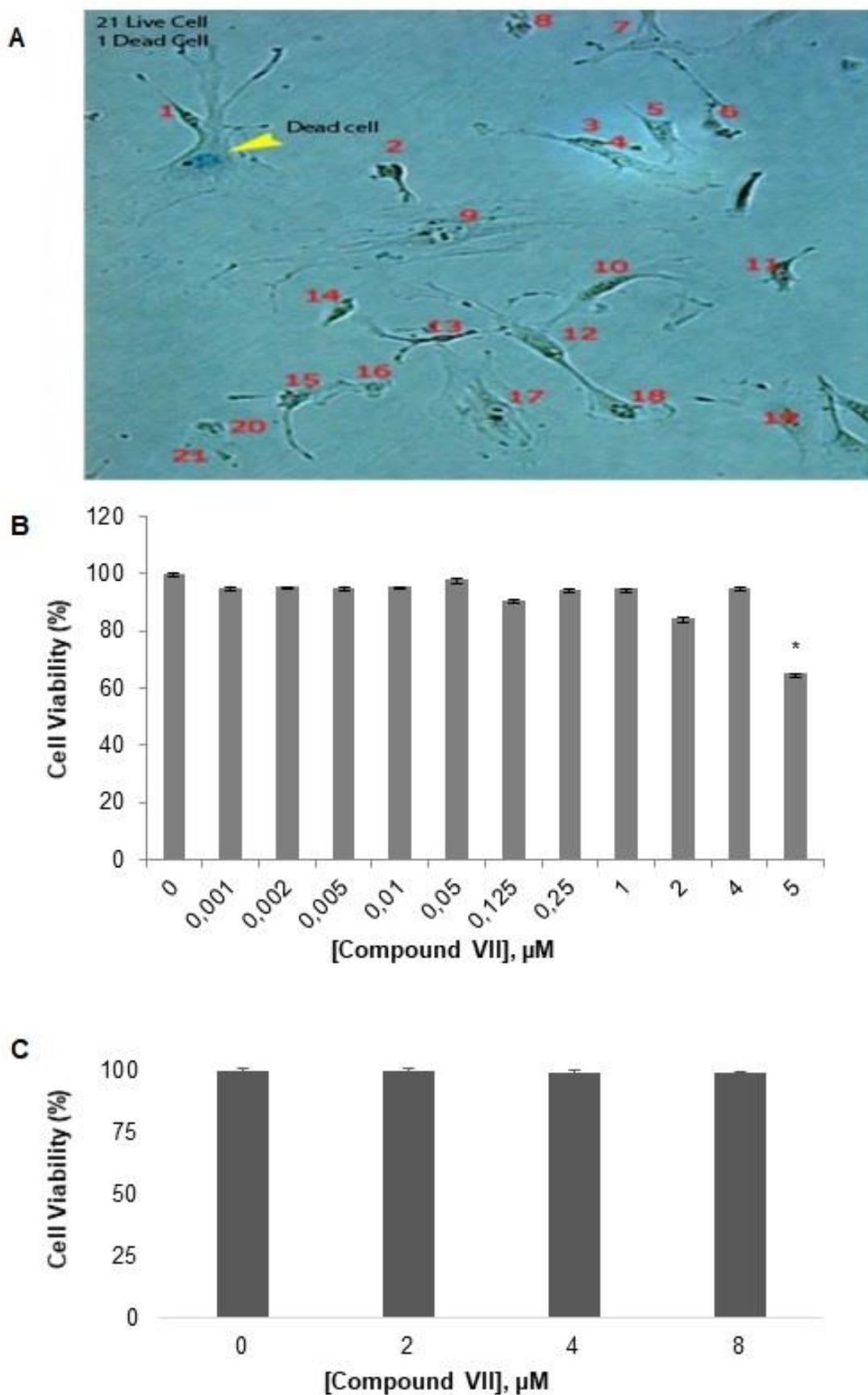


Figure 2. A) The concentrations of Compound VII using the Trypan blue staining supplemented with fixative. B) Cell viability (%) detected after treatment of Compound VII on AR42J cells. C) Cell viability (%) detected after treatment of Compound VII on CF-1 cells. *Statistically significant difference compared to untreated control cells ($p < 0.05$).

α -Amylase inhibitory activity *in vitro*

One of the group of chemicals in drug design for T2DM therapy is triazole-derived compounds so that a large scale of drug development studies currently focus on the design and synthesize these compounds due to their clinical importance [12, 14, 52]. This study reports that a heterocyclic molecule containing a triazole derivative the cytotoxic effect of Compound VII on AR42J cells above 5 μM , and amylase inhibition by Compound VII in a dose-dependent manner on AR42J cells. AR42J cell line is one of the best model for studies on amylase inhibition as it has been shown to overexpress amylase [53]. The Compound VII was also found to be more effective on α -amylase inhibition compared to acarbose as a positive control (Figure 3). Compound VII and acarbose were dissolved in DMSO before experiments and was used in a final concentration not exceeding 0.1% [34]. The prepared stock iodine solution was used diluted 1:100 (v/v) so that the final concentration of the starch solution was 0.125%. The IC_{50} value of Compound VII was found to be 4 μM but could not be calculated for acarbose even at 500 μM which was the highest concentration used for the Compound VII. There are a range of drugs developed chemically or using biotechnological tools. Ngoh and coauthors performed the α -amylase inhibition experiments on AR42J cells of the peptides they obtained by purifying from speckled beans on 2×10^4 cells and the IC_{50} value was calculated as 8 mM [54]. In addition, in amylase inhibition studies performed on AR42J cell line with limonoid derivatives obtained by purification, it has been reported that only 41.8% inhibition of Azadiradione can be observed at 3.5 μM [55]. It can be said that the studies conducted are meaningful compared to the other examples in the literature.

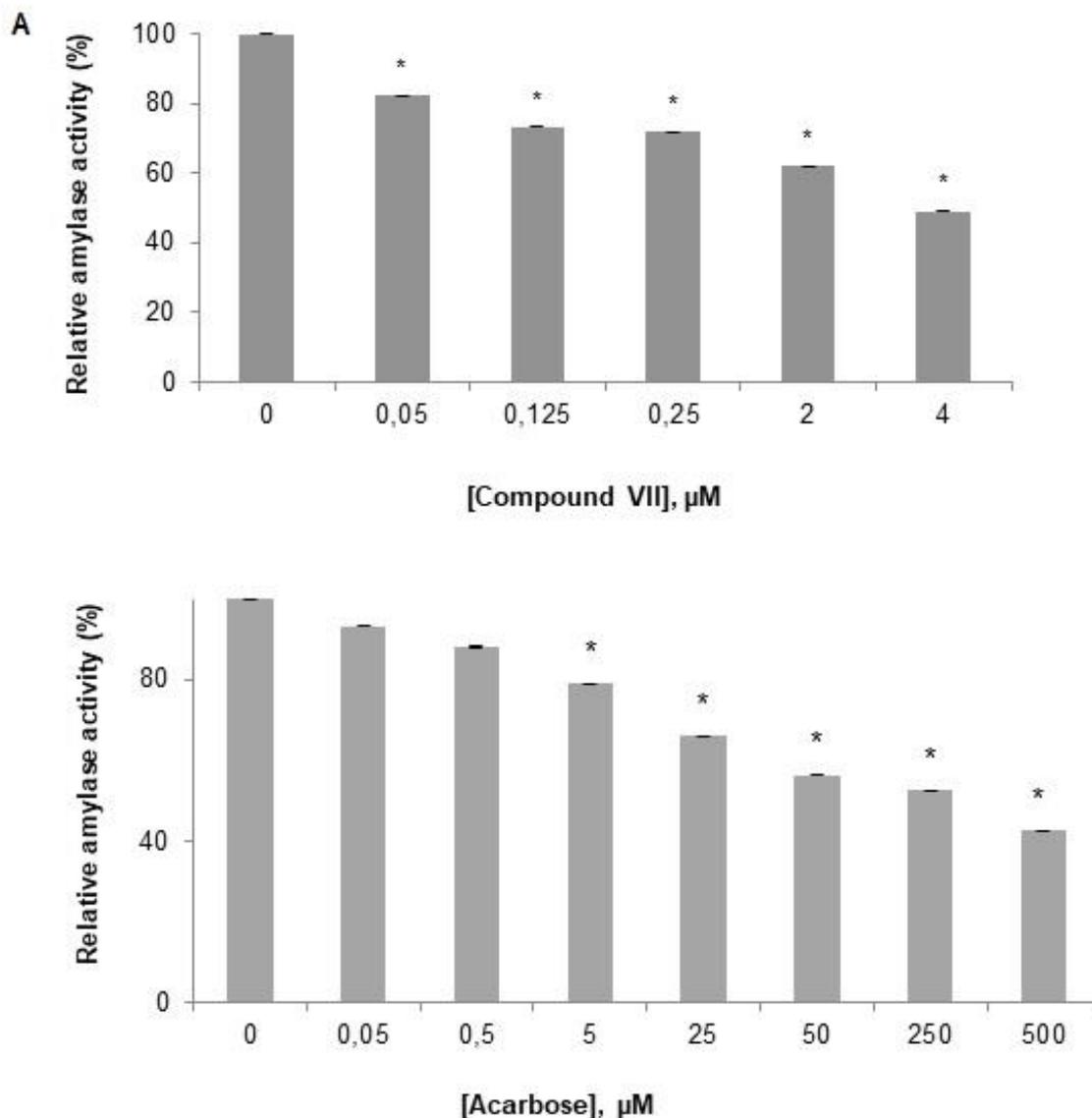


Figure 3. A) Amylase inhibition with compound VII on AR42J cells. B) Amylase inhibition with acarbose on AR42J cells. *Statistically significant difference compared to untreated control cells ($p < 0.05$).

CONCLUSION

Many triazole compounds are used as complementary supplies to current drug therapies, and some have been used for their inhibition of amylase activities in particular for the treatment of T2DM. AR42J cells are one of the precursor cells for T2DM, which is still used preclinically in the literature, and trials with 1,2,4 triazoles are not sufficient. In this study, eight triazole derivative compounds were examined for the first time to reveal their α -amylase inhibition potentials. Among the compounds, Compound VII was found to be the most potential (at micromolar level) for α -amylase inhibition *in silico* and *in vitro* studies. This study suggests a new drug candidate (Compound VII) for amylase inhibition, which is 2-Heptyl-4 - {[4- (4-fluorophenyl)-4,5-dihydro-5-thion-1*H*-1,2,4-triazol-3-yl] methyl}c-5-(4-methoxybenzyl)-2,4-dihydro-3*H* 1,2,4-triazol-3-one. But further biochemical and pharmacological tests should be performed for α -amylase inhibition under *in vivo* conditions for Compound VII.

Conflicts of Interest: The authors declare no conflicts of interest.

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