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Hit Identification Against Candida Albicans: Design, Synthesis, Molecular Docking and

Biological Evaluation of Hybrid Styryl-Quinoxaline Based Analogues.

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Abstract

The occurrence of invasive fungal infections (IFIs) and the incidence of resistant fungal pathogens have increased dramatically, leading to high morbidity and mortality especially with immune-compromised patients. Owing to their multifunctional pharmacological profiles, quinoxalines attract widespread attention being a part of several biologically and technologically relevant compounds. Herein, we report the design, synthesis, structural characterization, and biological screening of a series of new quinoxaline-based scaffolds. The antimicrobial activities of the synthesized compounds were assessed against a panel of bacterial species as well as representative fungi. Interestingly, *N*-(3-chlorophenyl)-2-(3-(2-hydroxystyryl)quinoxalin-2-yl) hydrazinecarboxamide (**3a**) displayed significant antifungal activity against *Candida albicans* (MIC₅₀ \leq **0.25 µg/mL**) compared to that of the reference drug fluconazole (MIC₅₀ =0.125 µg/mL). Molecular docking studies showed that the potency of our compounds could be attributed to the inhibition of fungal squalene epoxidase enzyme. Additionally, all synthesized compounds were almost neither toxic to human embryonic kidney cells (CC₅₀>32.0 µg/mL) nor to human red blood cells (HC₁₀>32.0 µg/mL). The above finding results suggested that compounds **3a** is a promising lead compound that merits further optimization and development as antifungal candidate.

Keywords: fungal infection; Candida albicans; quinoxaline; styryl; squalene epoxidase.

1. Introduction

Human race has been plagued by infectious diseases throughout history. Over the past decades, fungal infections have increased theatrically affecting over 150 million cases globally and resulting in approximately 1.7 million deaths per year [1]. The excessive use of antifungal agents is accountable for multi-resistance in several fungal strains. Fungal infections endorsed by these resistant fungal microorganisms often no respond to traditional treatment to Candida albicans. consequently increasing the severity of illness related to this fungal infection [2]. Candida albicans (C. albicans), Aspergillus fumigatus, and Cryptococcus neoformans (C. neoformans) are examples for opportunistic fungal pathogens affecting thousands of people every year. Candida spp. are accountable for the majority of human fungal infections [3]. Among all Candida spp., C. albicans is responsible for a high proportion

*Corresponding author e-mail: anewahie@msa.edu.eg.; (Aliya M. S. El Newahie). Received date 2023-04-11; revised date 2023-05-20; accepted date 2023-05-23 DOI: 10.21608/EJCHEM.2023.205360.7850 ©2023 National Information and Documentation Center (NIDOC) of candidiasis patients (70%~90% among all candidiasis-causing fungi) [4, 5], with mortality rate up to 43.6% due to candidemia. Among the versatile therapeutic antifungal agents (see Figure 1), azoles and allylamines were found to target the mevalonate pathway to block fungal sterol/ergosterol production. Azoles based antifungal agents target Erg11p/ Cyp51 and disrupt the biosynthesis of ergosterol in the lanosterol demethylation step [6] leading to the accumulation of toxic sterols on the fungal cell membranes and increased levels of endogenous reactive oxygen species [7], both of which promote fungal growth arrest. Whereas, allylamines targets squalene monooxygenase (Erg1p) that catalyzes squalene conversion to 2, 3-oxidosqualene, a ratelimiting step of fungal ergosterol biosynthesis [8]. [Figure 1 near Here]



Figure 1: The structures of some antifungal drugs.

Reduced fungal susceptibility to conventional antifungal agents and drug-resistant fungal infections poses a serious threat to continuing the treatment using conventional antifungal agents and warrants the search for new alternative molecules. In our quest for novel alternatives, we selected the styryl based quinoxaline scaffold for being reported as potential antifungal candidate in several studies. Quinoxaline-1,4-di-*N*-oxides are being identified as privileged structure in antifungal therapy with MIC₅₀ range between 2 to 4 μ g/mL [9]. Another series of quinoxaline 1.4-di-*N*-oxides possessing in vitro antifungal activity against C. albicans (I, II, MIC₅₀=7.8 µg/mL) and C. glabrata (I, II, MIC₅₀= $3.9 \,\mu$ g/mL) [10, 11], along with a series of 2,3-diphenylquinoxaline 1,4-di-N-oxides derivatives (III-V) that were useful *in-vitro* against C. albicans (III / IV / V, Zone of inhibition=15/11/10mm at 100 μ g/mL), which makes them candidates for subsequent biological studies [12]. Additionally, a series of 4-aminotetrazolo[1,5-a]quinoxaline based thiazolidinone & azetidinone derivatives (VI, VII) were reported by Kumar et al. [13], and have exhibited good antifungal activity against C. albicans (Zone of inhibition 7-10 mm at 50 μ g/mL) (see Figure 2). [Figure 2 near here]



Figure 2: The structures of several reported quinoxaline and styryl-based antifungal agent.

On the other hand styryl bearing compounds have been reported as potential antifungal agents such as styryl quinolines **VIII** [14-16], styryl quinazolines **IXa-c** (which is active against *C. albicans*, MIC₅₀=6 μ g/mL) [17], besides the styrylpyridinium derivatives **Xa**, **b** showed effective synergism with fluconazole, as well as good fungicidal activities against *C. albicans*.[18].

Our design strategy was relied on the previously mentioned antifungal properties of quinoxaline scaffolds and styryl moieties, in addition

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to several reported heterocyclic structures possessing superior antifungal activity against *C. albicans* bearing benzothiazole-amide-imidazole moiety [19], along with (E)-(3-(substituted-styryl)-7*H*-furo[2,3-f]chromen-2-yl)(phenyl)-methanone derivatives displaying remarkable antifungal activity against *C. albicans*. [20].

The aforementioned information and the allylamines antifungal agents' structure have inspired us to synthesize a hybrid molecule combining quinoxaline ring; instead of benzothiazole, furo chromen and napthyl rings in allylamines; with a styryl moiety in position 3 of quinoxaline along with attaching aliphatic, aromatic amines or urea chain to position Hence linking pharmacophoric 2. functionalities to different aryl moieties, promises to explore antifungal activities. For better understanding of the proposed mechanism of action of our synthesized compounds, they were docked into the active site of squalene epoxidase enzyme based on structure similarity with allylamines antifungal agents.

For the pursuit of discovering new candidates that may add a value in designing new, selective, and less toxic antimicrobial agents, herein we report the design, synthesis of novel series of functionalized quinoxaline and evaluation of their antimicrobial and cytotoxicity activities along with the discovery of a novel antifungal hit compound (3a), (see Figure 3) [Figure 3 near here].



Figure 3: The rationale design of our synthesized compounds.

2. Material and Methods

2.1. Chemistry

All starting materials, reagents and solvents obtained from commercially available sources and used without purification. The reactions were monitored, and the purity of the compounds was checked by ascending thin layer chromatography (TLC) on silica gel-coated aluminum plates (Merck 60 F_{254} , 0.25 mm). Melting points were determined in open capillaries using Stuart (biocote) scientific melting point apparatus. IR spectra were determined as KBr discs using Shimadzu Infrared spectrometer (IR-435) and FT-IR 1650 (Perkin Elmer). ¹H NMR and ¹³C NMR spectra were recorded in δ scale given in ppm on а Bruker 400. 100 MHz spectrophotometer. Chemical shifts have been assessed relative to the internal standard TMS and are reported in δ ppm. The coupling constants (J) are expressed in hertz (Hz) and peak multiplicities are described as singlet (s), doublet (d), triplet (t), quartet (q) and multiplet (m). Mass spectra were recorded on Thermo Scientific ISQLT mass spectrometer.

2-Hydrazinyl-3-methylquinoxaline (1) was prepared according to the reported method [21].

N-(3-chlorophenyl)-2-(3-methylquinoxalin-2-yl) hydrazine carboxamide (2) to a hot solution of compound 1 (0.0012 mol, 0.2 g) in dry toluene (5mL), *m*-chloro phenyl isocyanate (0.0012 mol, 0.2 g) was added. The mixture was refluxed for 2 h till precipitation occurred. The precipitate was filtered while hot, washed with toluene and recrystallized from dry ethanol to afford the titled compound 2.

 $R_f = 0.6$ (Hexane: EtOAc 7:3). Creamy white solid (0.33g, 88%) ; m.p. 233 °C, ¹H NMR (400 MHz, **DMSO-** d_6) δ ppm: 9.02 (s, 2H, NH, D₂O) exchangeable), 8.42 (s, 1H, NH, D₂O exchangeable), 7.82 (d, J= 8 Hz, 1H, ArH), 7.72 (s, 1H, ArH), 7.64 (d, J= 9.6 Hz, 1H, ArH), 7.55 (t, J= 9.6, 7.2 Hz, 1H)ArH), 7.44-7.40 (m, 1H, ArH), 7.26 (t, J= 10.4, 6.4 Hz, 1H, ArH), 7.07 (t, J= 9.6, 10.8 Hz, 1H, ArH), 7.00 (d, J= 8 Hz, 1H, ArH), 2.62 (s, 3H, CH₃). ¹³C NMR (100 MHz, DMSO-d₆) δ ppm: 164.0, 151.5, 143.0, 141.0, 133.0, 132.4, 130.6, 129.3, 128.1, 126.3, 125.3, 122.0, 121.9, 119.0, 21.6. IR (KBr): 3334 (3 NH), 3088 (CH aromatic), 2947 (CH aliphatic), 1670 (C=O), 1589 (C=C aromatic) cm⁻¹. Anal. Calcd. for C₁₆H₁₄ClN₅O (327.77): C, 58.63; H, 4.31; N, 21.37 found: C, 58.91; H, 4.47; N, 21.09.

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Standard procedure for the preparation (*E*)-*N*-phenyl-2-(styryl) quinoxalin-2-yl) hydrazine carboxamide (3a-h) (Series A)

A mixture of intermediate 2 (0.005 mol), an appropriate aldehyde (0.005 mol, 1 eq.), glacial acetic acid (4.5 mL) and catalytic amount of conc. sulfuric acid (0.4 mL) was refluxed for 2 h. The reaction mixture was cooled to room temperature. The separated solids were filtered, washed with water, and recrystallized from dry ethanol to afford compounds 3a-h.

(*E*)-*N*-(3-chlorophenyl)-2-(3-(2-hydroxystyryl)quinoxalin-2-yl)hydrazine-

carboxamide (3a). $R_f = 0.6$ (Hexane : EtOAc 7:3). Olive green solid (0.4g, 93%); **m.p.** > 300 °C, ¹**H NMR** (400 MHz, DMSO-d₆) δ ppm : 9.15 (s, 1H, OH, D₂O exchangeable), 8.97 (s, 2H, NH, D₂O exchangeable), 8.75 (d, J=8 Hz, 1H, ArH), 8.69 (s, 1H, ArH), 8.57 (d, J=16 Hz, 1H, ArH), 7.88 (d, J=10 Hz, 1H, ArH), 7.71 (d, J=8 Hz, 1H, ArH), 7.62-7.37 (m, 5H, ArH), 7.24 (t, J=7.6, 6 Hz, 2H, ArH), 7.07-6.95 (m, 2H, CH=CH). ¹³C NMR (100 **MHz, DMSO-d₆**) δ ppm : 174.3, 157.0, 151.8, 148.9, 137.0, 136.5, 135.5, 135.2, 131.5, 130.8, 129.9, 129.1, 128.4, 126.8, 126.7, 122.8, 121.3, 120.1, 116.6, 115.4, 114.6, 113.4, 112.8. IR (KBr): 3300 (3 NH), 3500-3200 (OH), 3068 (CH aromatic), 2800 (CH aliphatic), 1675 (C=O), 1619-1598 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C23H18ClN5O2 (431.87): C, 63.96; H, 4.20; N, 16.22; found: C, 64.12; H, 4.36; N, 16.49.

(*E*)-*N*-(3-chlorophenyl)-2-(3-(4methoxystyryl) quinoxalin-2-yl) hydrazine-

carboxamide (3b). $R_f = 0.6$ (Hexane : EtOAc 7:3). Reddish brown solid (0.4g, 85%); m.p. 256-260 °C, ¹H NMR (400 MHz, DMSO- d_6) δ ppm: 13.04 (s, 2H, NH, D₂O exchangeable), 8.70 (d, J=8 Hz, 1H, ArH), 8.20 (d, J=16 Hz, 1H, ArH), 7.81 (d, J=8 Hz, 1H, ArH), 7.70 (d, J=8 Hz, 3H, ArH), 7.56 (t, J=8, 8 Hz, 2H, ArH), 7.48 (t, J=8, 8 Hz, 1H, ArH), 7.36 (d, J=13.6 Hz, 2H, CH=CH), 7.24 (s, 1H, ArH), 6.99 (d, J=9.2 Hz, 2H, ArH), 3.82 (s, 3H, OCH₃). ¹³C NMR (100 MHz, DMSO-d₆) δ ppm: 161.1, 154.6, 151.6, 148.4, 139.4, 136.3, 135.1, 134.1, 132.0, 131.0, 130.1, 129.9, 129.4, 129.1, 129.0, 128.4, 126.7, 119.5, 114.9, 114.6, 113.5, 55.7. IR (KBr): 3387 (3 NH), 3067 (CH aromatic), 2900 (CH aliphatic), 1670 (C=O), 1628-1573 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₄H₂₀ClN₅O₂ (445.90): C, 64.65; H, 4.52; N, 15.71; found: C, 64.51; H, 4.68; N, 15.95.

(E)-N-(3-chlorophenyl)-2-(3-(4chlorostyryl)quinoxalin-2-yl)hydrazine carboxamide (3c). R_i = 0.6 (Hexane: EtOAc 7:3). Brown solid (0.4 g, 83%) ; m.p. 240-244 °C, ¹H

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NMR (400 MHz, DMSO-d₆) δ ppm: 13.06 (s, 2H, NH, D₂O exchangeable), 8.71 (d, J=8 Hz, 1H, ArH), 8.19 (d, J=16 Hz, 1H, ArH), 7.83, 7.81 (dd, J=8 Hz, 2H, ArH), 7.78, 7.76 (dd, J=8 Hz, 2H, ArH), 7.58 (t, J=8, 8 Hz, 2H, ArH), 7.51 (d, J=13.6 Hz, 5H, ArH and CH=CH), 7.41 (s, 1H, ArH). ¹³C NMR (100 **MHz, DMSO-d**₆) δ ppm: 161.5, 150.1, 149.8, 148.8, 147.5, 137.8, 137.6, 136.6, 135.3, 134.3, 132.0, 131.4, 131.0, 130.5, 129.4, 129.0, 128.1, 126.0, 124.4, 122.6, 116.1. IR (KBr): 3350 (3 NH), 3029 (CH aromatic), 2949 (CH aliphatic), 168 (C=O), 1627-1591 (C=C aliphatic and aromatic) cm⁻ ¹. MS: m/z (%): 454.75 [M⁺+4, (8.23 %)], 452.34 [M⁺+2, (8.59 %)], 450.12 [M⁺, (12.64 %)], 279.43 (100%); Anal. Calcd. for C₂₃H₁₇Cl₂N₅O (450.32): C, 61.34; H, 3.81; N, 15.55; found: C, 61.53; H, 3.97; N, 15.82.

(*E*)-*N*-(3-chlorophenyl)-2-(3-(4-fluorostyryl)quinoxalin-2-yl)hydrazine-

carboxamide (3d). $R_f = 0.6$ (Hexane: EtOAc 7:3). Yellow solid (0.39, 85%) ; m.p. 235- 239 °C, ¹H NMR (400 MHz, DMSO-d₆) δ ppm: 13.07 (s, 2H, NH, D₂O exchangeable), 8.71, 8.68 (dd, J=12 Hz, 2H, ArH), 8.21 (d, J=16 Hz, 1H, ArH), 7.89-7.75 (m, 5H, ArH), 7.57 (t, J=8, 8 Hz, 1H, ArH), 7.48 (t, J=8, 8 Hz, 1H, ArH), 7.41 (d, J=20 Hz, 2H, CH=CH), 7.26 (t, J=8, 8 Hz, 2H, ArH). ¹³C NMR (100 MHz, DMSO-d₆) δ ppm: 188.0, 163.5, 159.5, 147.9, 142.8, 138.1, 136.3, 135.0, 132.4, 130.4, 129.5, 129.1, 126.8, 122.0, 121.9, 120.0, 116.6, 116.4, 116.0, 114.6, 107.6. IR (KBr): 3443 (3 NH), 3031-3071 (CH aromatic), 2907 (CH aliphatic), 1685 (C=O), 1627-1599 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₃H₁₇ClFN₅O (433.87): C, 63.67; H, 3.95; N, 16.14; found: C, 63.85; H, 4.13; N, 16.08.

(*E*)-*N*-(3-chlorophenyl)-2-(3-

(4(dimethylamino)styryl)quinoxaline-2-

yl)hydrazine carboxamide (3e). $R_f = 0.6$ (Hexane : EtOAc 7:3). Black solid (0.42g, 84%) ; m.p. 245-249 °C, ¹H NMR (400 MHz, DMSO- d_6) δ ppm : 8.73 (s, 2H, NH, D₂O exchangeable), 8.20 (d, J=13.6 Hz, 1H, ArH), 7.82 (d, J=8 Hz, 1H, ArH), 7.62 (d, J=8 Hz, 2H, ArH), 7.55 (t, J=8, 8 Hz, 2H, ArH), 7.49-7.46 (m, 3H, ArH), 7.37 (s, 1H, ArH), 7.25 (d, J=16 Hz, 2H, CH=CH), 6.78 (d, J=8 Hz, 2H, ArH), 3.02 (s, 6H, CH₃). ¹³C NMR (100 MHz, **DMSO-d₆**) δ ppm : 177.1, 158.0, 150.3,146.3, 145.0, 140.4, 137.0, 135.5, 133.0, 132.0, 130.0, 129.9, 127.2, 126.6, 125.0, 124.5, 122.0, 120.7, 118.5, 115.5, 111.7, 29.9. IR (KBr): 3200 (3 NH), 3148 (CH aromatic), 2890 (CH aliphatic), 1679 (C=O), 1642-1599 (C=C aliphatic and aromatic) cm⁻ **Anal. Calcd.** for $C_{25}H_{23}CIN_6O$ (458.94): C, 65.43; H, 5.05; N, 18.31; found: C, 65.19; H, 5.21; N, 18.47.

(E)-N-(3-chlorophenyl)-2-(3-(4-hydroxy-3methoxystyryl)quinoxalin-2-yl)hydrazine carboxamide (3f). R_f= 0.6 (Hexane: EtOAc 7:3). Yellowish brown solid (0.34g, 73%); m.p. 241-245 °C, ¹H NMR (400 MHz, DMSO-*d*₆) δ ppm: 9.04 (s, 1H, OH, D₂O exchangeable), 8.71 (s, 2H, NH, D₂O exchangeable), 7.81 (d, J=8 Hz, 1H, ArH), 7.72 (s, 2H, ArH), 7.56 (t, J=8, 8 Hz, 2H, ArH), 7.47-7.37 (m, 4H, ArH and CH=CH), 7.29 (t, J=8, 8 Hz, 2H, ArH), 7.03 (d, J=8 Hz, 2H, ArH), 3.75 (s, 3H, OCH₃). ¹³C NMR (100 MHz, DMSO- d_6) δ ppm: 160.4, 156.2, 145.1, 143.0, 141.4, 137.1, 135.5, 133.4, 132.5, 131.4, 130.7, 130.0, 129.7, 128.0, 126.5, 125.6, 124.0, 122.3, 120.5, 119.3, 118.0, 116.1, 105.0, 56.1. IR (KBr): 3301 (3 NH), 3300-3100 (OH), 3082 (CH aromatic), 2900 (CH aliphatic), 1680 (C=O), 1661-1599 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₄H₂₀ClN₅O₃ (461.90): C, 62.41; H, 4.36; N, 15.16; found: C, 62.65; H, 4.19; N, 15.42.

(*E*)-*N*-(3-chlorophenyl)-2-(3-(4nitrostyryl)quinoxalin-2-yl)hydrazine-

carboxamide (3g). $R_f= 0.85$ (Hexane : EtOAc 7:3). Brown solid (0.38g, 82%) ; m.p. 231-235 °C, ¹H NMR (400 MHz, DMSO-d₆) δ ppm : 8.83 (s, 2H, NH, D₂O exchangeable), 8.38-8.35 (m, 1H, ArH), 8.27, 8.25 (dd, J=8 Hz, 2H, ArH), 8.13-8.10 (m, 1H, ArH), 8.06, 8.04 (dd, J=8 Hz, 2H, ArH), 7.83 (d, J=8 Hz, 1H, ArH), 7.77-7.73 (m, 1H, ArH), 7.83 (d, J=17 Hz, 2H, CH=CH), 7.56 (t, J=8, 9 Hz, 1H, ArH), 3075 (CH aromatic), 2901 (CH aliphatic), 1681 (C=O), 1630-1598 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₃H₁₇ClN₆O₃ (460.87): C, 59.94; H, 3.72; N, 18.24; found: C, 60.12; H, 3.89; N, 18.45.

(E)-N-(3-chlorophenyl)-2-(3-(3nitrostyryl)quinoxalin-2-yl)hydrazine-

carboxamide (3h). R_f = 0.6 (Hexane : EtOAc 7:3). Red solid (0.11g, 78%) ; m.p. 255-257 °C, ¹H NMR (400 MHz, DMSO-d₆) δ ppm: 13.12 (s, 1H, NH, D₂O exchangeable), 12.97 (s, 1H, NH, D₂O exchangeable), 8.70-8.69 (m, 1H, ArH), 8.52 (s, 1H, ArH), 8.33- 8.23 (m, 2H, ArH), 8.10-7.86 (m, 3H, ArH), 7.73-7.40 (m, 4H, ArH), 7.36-6.53 (m, 3H, ArH and CH=CH). IR (KBr): 3397 (3 NH), 3031 (CH aromatic), 2899 (CH aliphatic), 1680 (C=O), 1632-1598 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₃H₁₇ClN₆O₃ (460.87): C, 59.94; H, 3.72; N, 18.24; found: C, 60.08; H, 3.95; N, 18.41.

3-Methylquinoxalin-2-(1*H*)-one (4) was prepared according to the reported method. [22]

(*E*)-3-Styrylquinoxalin-2(1H)-one derivatives (5a-d) were prepared according to the reported method. [23-29]

(E)-2-Chloro-3-styryl-1,2-

dihydroquinoxaline derivatives (6a-d) were prepared according to the reported method. [23, 26, 30]

Standard procedure for the synthesis of (E)-Nphenyl-3-styrylquinoxalin-2-amine final compounds 7a-c (Series B): To a hot solution of compounds 6a, b, c in ethanol (15 mL), equimolar amounts of aromatic amines (0.0056 mol, 0.77 g) and catalytic amount of potassium carbonate was added, then the reaction was heated under reflux for 12 h till precipitation. The contents were cooled at room temperature. The precipitates of the compound were filtered off, washed, and recrystallized from hexane yielding final compounds 7a-c.

(E)-N-(4-methoxyphenyl)-3-

styrylquinoxalin-2-amine (7a). R_i = 0.6 (Hexane: EtOAc 7:3). Orange solid (0.29g, 82%) ; m.p. 250-254 °C, ¹HNMR (400 MHz, DMSO-d₆) δ ppm: 8.70 (s, 1H, NH, D₂O exchangeable), 8.17 (t, J=4, 4 Hz, 1H, ArH), 7.98 (t, J=4, 4 Hz, 1H, ArH), 7.75-7.69 (m, 2H, ArH), 7.50 (t, J=4, 4 Hz, 2H, ArH), 7.41 (t, J=4, 4 Hz, 2H, ArH), 7.35 (d, J=8 Hz, 2H, ArH), 7.19 (s, 1H, ArH), 7.08 (d, J=8 Hz, 2H, ArH), 6.91-6.87 (m, 2H, CH=CH), 3.77 (s, 3H, OCH₃). **IR** (**KBr**): 3400 (NH), 3056 (CH aromatic), 2931 (CH aliphatic), 1608-1580 (C=C aliphatic and aromatic) cm⁻¹. **Anal. Calcd.** for C₂₃H₁₉N₃O (353.42): C, 78.16; H, 5.42; N, 11.89; found: C, 78.40; H, 5.66; N, 12.14.

(E)-3-((3-(4-chlorostyryl))quinoxalin-2-yl) amino) benzoic acid (7b). R_f= 0.6 (Hexane: EtOAc 7:3). Black solid (0.32g, 80%); m.p. 230-232 °C, ¹H NMR (400 MHz, DMSO-d₆) δ ppm: 10.00 (s, 1H, COOH, D₂O exchangeable), 9.00 (s, 1H, NH, D₂O exchangeable), 8.61-8.28 (m, 1H, ArH), 8.19-8.05 (m, 1H, ArH), 7.93-7.15 (m, 12H, ArH and CH=CH). IR (KBr): 3390 (NH), 3500-2400 (OH carboxylic), 3062 (CH aromatic), 2900 (CH aliphatic), 1696 (C=O), 1600-1541 (C=C aliphatic and aromatic) cm⁻¹. MS: m/z (%): 403.47 [M⁺+2, (4.41%)], 401.43 [M⁺, (10.98 %), 279.35 (100%); Anal. Calcd. for C₂₃H₁₆ClN₃O₂ (401.85): C, 68.74; H, 4.01; N, 10.46; found: C, 68.91; H, 4.18; N, 10.68.

(*E*)-3-(4-methoxystyryl)-*N*-(*m*-tolyl)

quinoxalin-2-amine (7c). R_{f} =0.6 (Hexane : EtOAc 8:2). Orange solid (0.29 g, 82%) ; **m.p.** 150-154 °C, ¹**HNMR (400 MHz, DMSO-***d*₆) δ **ppm :** 9.70 (*s*, 1H, NH, D₂O exchangeable), 8.09 (*d*, *J*=8*Hz*, 1H, ArH), 8.01-7.97 (*m*, 1H, ArH), 7.88-7.68 (*m*, 3H, ArH), 7.60 (*t*, *J*=8*Hz*, 2H, ArH), 7.33-7.31 (*m*, 1H, ArH), 7.21-7.07 (*m*, 3H, ArH), 7.02 (*d*, *J*=8*Hz*, 1H, ArH), 6.92-6.84 (*m*, 2H, CH=CH), 3.81 (*s*, 3H, OCH₃), 2.25 (*s*, 3H, CH₃). ¹³C NMR (100 MHz, DMSO-*d*₆) δ **ppm :** 161.1, 146.5, 140.7, 138.7,

132.2, 131.7, 131.4, 130.9, 130.8, 129.4, 129.1, 128.9, 128.6, 128.4, 128.2, 127.0, 125.2, 118.9, 114.9, 114.7, 55.6, 21.2. **IR** (**KBr**): 3425 (NH), 3061 (CH aromatic), 2960, 2834 (CH aliphatic), 1604-1572 (C=C aliphatic and aromatic) cm⁻¹. **Anal. Calcd.** For $C_{24}H_{21}N_{3}O$ (367.44): C, 78.45; H, 5.76; N, 11.44; found: C, 78.68; H, 5.89; N, 11.70.

Standard procedure for the synthesis of (*E*)-2-(4-Phenylpiperazin-1-yl)-3-styrylquinoxaline final compounds 8a, b, d (Series C): To hot solution of compounds 6a, b, d in isopropanol (15 mL), equimolar amounts of 1-phenyl piperazine (0.0056 mol, 0.77 g) and catalytic amount of triethylamine were added then the reaction was heated under reflux for 12 h till precipitation. The reaction was left to cool, and the resulted solid was filtered, washed with isopropanol, and recrystallized from benzene to give compounds 8a, b, d in a pure form.

(E)-2-(4-Phenylpiperazin-1-yl)-3-

styrylquinoxaline (8a). $R_f = 0.6$ (Hexane: EtOAc 7:3). Yellow solid (0.14g, 77%); **m.p.** > 300 °C, ¹H **NMR (400 MHz, DMSO-d₆) δ ppm:** 7.97-7.93 (m, 2H, ArH), 7.83-7.80 (m, 1H, ArH), 7.79 (d, J=8 Hz, 2H, ArH), 7.68 (t, J=8, 8 Hz, 1H, ArH), 7.61 (t, J=8, 8 Hz, 1H, ArH), 7.50-7.44 (m, 2H, ArH), 7.40-7.37 (m, 2H, CH=CH), 7.26 (t, J=8, 8 Hz, 2H, ArH), 7.05 (d, J=8 Hz, 2H, ArH), 6.83 (t, J=8, 8 Hz, 1H, ArH), 3.53 (s, 4H, aliphatic), 3.45 (s, 4H, aliphatic). ¹³C NMR (100 MHz, DMSO-d₆) δ ppm: 155.1, 151.3, 145.6, 141.0, 140.1, 138.8, 136.4, 135.7, 131.5, 130.5, 129.9, 129.6, 129.5, 129.4, 128.6, 127.9, 127.3, 123.7, 119.6, 116.1, 49.9, 48.4. IR (KBr): 3055 (CH aromatic), 2887 (CH aliphatic), 1629-1599 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₆H₂₄N₄ (392.50): C, 79.56; H, 6.16; N, 14.27; found: C, 79.42; H, 6.29; N, 14.44.

(E)-2-(4-Chlorostyryl)-3-(4-

phenylpiperazin-1-yl) quinoxaline (8b). $R_f=0.6$ (Hexane : EtOAc 7:3). Yellow solid (0.34g, 80%) ; m.p. 210-212 °C, ¹H NMR (400 MHz, DMSO-*d*₆) δ ppm: 7.97-7.90 (m, 2H, ArH), 7.82 (d, J=8 Hz, 2H, ArH), 7.67 (t, J=8, 4 Hz, 1H, ArH), 7.61 (t, J=8, 8 Hz, 1H, ArH), 7.51-7.45 (m, 2H, CH=CH), 7.26 (t, J=8, 8 Hz, 3H, ArH), 7.04-6.97 (m, 2H, ArH), 6.83 (t, J=5.6, 9.6 Hz, 2H, ArH), 3.52 (s, 4H, aliphatic), 3.43 (s, 4H, aliphatic). ¹³C NMR (100 MHz, **DMSO-d₆**) δ ppm: 155.1, 151.4, 145.4, 140.2, 138.8, 135.4, 134.3, 133.9, 130.0, 129.6, 129.4, 128.6, 127.6, 127.3, 124.6, 121.1, 119.6, 116.1, 50.0, 48.4. IR (KBr): 3056 (CH aromatic), 2911 (CH aliphatic), 1628-1597 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for $C_{26}H_{23}ClN_4$ (426.94): C, 73.14; H, 5.43; N, 13.12; found C, 73.38; H, 5.61; N, 13.40.

(*E*)-2-(4-Fluorostyryl)-3-(4phenylpiperazin-1-yl) quinoxaline (8d). $R_f=0.6$

(Hexane: EtOAc 7:3). Rose solid (0.15g, 75%); **m.p.** 206- 210 °C, ¹**H NMR** (400 MHz, DMSO-d₆) δ **ppm:** 7.97 (d, J=8 Hz, 2H, ArH), 7.87-7.80 (m, 2H, ArH), 7.68 (t, J=8.4, 10.8, 1H, ArH), 7.61 (t, J=7.6, 9.2 Hz, 1H, ArH), 7.44 (d, J= 16 Hz, 2H, CH=CH), 7.28, 7.26 (dd, J=10, 8 Hz, 4H, ArH), 7.05 (d, J=8 Hz, 2H, ArH), 6.83 (t, J=8, 8 Hz, 1H, ArH), 3.52 (s, 4H, aliphatic), 3.44 (s, 4H, aliphatic). ¹³C NMR (100 MHz, DMSO-d₆) δ ppm: 151.7, 129.4, 119.4, 115.9, 51.4, 48.8, 48.6, 45.2. IR (KBr): 3057 (CH aromatic), 2900 (CH aliphatic), 1635-1598 (C=C aliphatic and aromatic) cm⁻¹. Anal. Calcd. for C₂₆H₂₃FN₄ (410.49): C, 76.08; H, 5.65; N, 13.65; found: C, 75.87; H, 5.77; N, 13.89.

2.2. Biological activity

Sample Preparation

The antimicrobial screening tests on bacterial and fungal strains were performed at COADD (The Community for Antimicrobial Drug Discovery), funded by the Wellcome Trust (UK) and The University of Queensland (Australia). All tested compounds were dissolved and suspended in dimethyl sulfoxide (DMSO)/ water to attain a final testing concentration of 32 µg/ml or equivalent to 20 µM. The reconstituted compounds kept at 4 °C until testing. Different eight dilutions of the tested compounds achieved by serial dilutions of 1:2 folds. The antifungal and antibacterial assays performed in non-binding surface 384-well microtitration plates, while haemolysis and cytotoxicity assays performed in propylene 384-well plate and tissue culture plates treated by mammalian cell types, respectively. All assays were performed in duplicate where DMSO did not exceed 0.5%.

Antibacterial Assay

All assessed bacterial strains were cultivated in Cation-adjusted Mueller Hinton broth (CaMHB) at 37 °C overnight. Each culture was diluted in fresh medium and incubated at 37 °C for 1.5 - 3 hr. The mid-log phase cultures were then diluted to obtain a final cell density of $5x10^5$ CFU/mL in the final working volume of 50μ L containing the tested compound. The micro titration plates were then incubated at 37 °C for 18 h. The absorbance was measured at 600 nm (OD₆₀₀) to determine bacterial growth inhibition using Tecan M1000 Pro monochromator plate reader. The percentage of growth inhibition was calculated for each well by the

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aid of the negative control (media only) and positive control (media containing tested strain without inhibitor) on the same plate as references. The MIC_{50} was defined by an inhibition $\geq 80\%$. Hits were classified by $MIC_{50} \leq 16 \ \mu\text{g/mL}$ or $MIC_{50} \leq 10 \ \mu\text{M}$ in either replicate (n=2 on different plates).

Antifungal Assay

Fungal strains were cultivated on yeast extract-peptone dextrose (YPD) agar at 30 °C for 3 days. A yeast suspension of (1 x 10⁶) to (5 x 10⁶) CFU/mL, as determined by OD₅₃₀, was prepared from five colonies. The resultant suspension was diluted and added to each well of the compoundcontaining plates providing a final cell density of fungi suspension of 2.5 $\times 10^3$ CFU/mL and a total volume of 50 µL. Afterwards, all plates were covered and incubated at 35 °C for 36 h. The growth inhibition of C. albicans was determined by measuring the absorbance at 630 nm (OD₆₃₀), after the addition of resazurin (0.001% final concentration) and incubation at 35 °C for 2 h. The absorbance was measured using a Biotek Multiflo Synergy HTX plate reader. In both cases, the growth inhibition percentage was determined for each well, using the negative control (media only) and positive control (media containing tested strain without inhibitor) in the same plate. The MIC₅₀ was determined as the lowest concentration at which the growth was fully inhibited (inhibition $\geq 80\%$ for *C. albicans*). Hits were classified by MIC₅₀ \leq 16 µg/mL or MIC₅₀ \leq 10 μ M in either replicate (n=2 on different plates).

2.3. Molecular Docking

To evaluate the binding modes between compound 3a with the target enzyme (squalene epoxidase), the molecular docking was performed using the MOE program (Chemical Computing Group software, Canada). The molecular similarity between our compounds and common squalene epoxidase inhibitors (allylamines) was the basis to choose it as the molecular target. Other fungal targets have been excluded by the basis of the absence of structural requirements for their inhibition. For instance, inhibiting the $14-\alpha$ -demethylase enzyme requires interaction with the iron center in its heme moiety via azoles. [19] The geometry of the quinoxaline ring would not allow for binding with the nitrogen except in unfavorable conformations. The recently published crystal structure for the squalene epoxidase protein makes the docking experiment more reliable than relying on homology models [31]. The crystal structure (PDB ID: 6C6P) was loaded and prepared by MOE 2020.09 using the AMBER10EHT forcefield [32]. Databases with the compounds, along with the co-crystallized ligand, have been prepared using standard preparation tools in MOE. Rigid-body docking has been applied using default parameters in MOE. Visualization was also done using the MOE software [32].

2.4. Cytotoxicity and Hemolysis Assay

At first, HEK293 cells were counted manually using Neubauer hemocytometer, and then plated in the 384-well plates containing the compounds giving density of 5x10³ cells/ well in a final volume of 50 µL. DMEM supplemented with 10% FBS was used as growth media and the cells were incubated together with the compounds for 20 h at 37 °C in 5% CO₂. Cytotoxicity (or cell viability) was measured by fluorescence after addition of 5 μ L of 25 µg/mL resazurin (2.3 µg/mL final concentrations) and incubation for further 3 h at 37 °C in 5% CO₂. Tecan M1000 Pro monochromator plate reader was used to measure the fluorescence intensity with automatic gain calculation. CC50 values were calculated by curve fitting the inhibition values vs. log (concentration) using a sigmoidal doseresponse function. Cytotoxic samples were classified by $CC_{50} \leq 32 \ \mu g/mL$ or $CC_{50} \leq 10 \ \mu M$ in either replicate (n=2 on different plates).

Human whole blood was washed three times with 3 volumes of 0.9% saline and then suspended in saline to a concentration of 0.5×10^8 cells/ mL, as determined by manual cell count in a Neubauer hemocytometer. The washed cells were subsequently added to the 384 well compoundcontaining plates for a final volume of 50 µL followed by shaking on a plate shaker for 10 min. Afterwards, the plates were incubated for 1 h at 37 °C and centrifuged at 1000g for 10 min to pellet cells and debris, and then 25 µL of the supernatant was transferred to a polystyrene 384 well assay plate. Hemolysis was determined by measuring the supernatant absorbance at 405 mm (OD₄₀₅) using a Tecan M1000 Pro monochromator plate reader. HC₁₀ and HC₅₀, defined as concentration at 10% and 50% hemolysis and were calculated by curve fitting the inhibition values versus log (concentration) using a sigmoidal dose-response function. Hemolysis samples were classified by $HC_{10} \leq 32 \ \mu g/mL$ or HC_{10} $\leq 10 \ \mu$ M in either replicate (n=2 on different plates).

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3. Results

3.1. Chemistry

The synthetic routes of target compounds are illustrated in **Schemes 1**, **2**. Urea scaffold *N*-(3chlorophenyl)-2-(3-methylquinoxalin-2-yl) hydrazine carboxamide (**2**) has been obtained through the reaction of 2-hydrazinyl-3-methylquinoxaline (**1**) with *meta*-chlorophenyl isocyanate in dry toluene. In the present study, we planned to synthesize target styryl quinoxalines **3a-h**. For obtaining good yields of such compounds, treatment of the active methyl group of intermediate **2** with various aromatic aldehyde using acetic acid as a solvent and drops-ofconcentrated sulphuric acid as a catalyst [23] seemed to be the most convenient approach.



Chemical structure of all obtained compounds was elucidated based on spectral techniques and elemental analysis.



Scheme 1: The synthetic routes of intermediate **2** and finals **3a-h**. Reagents and conditions: (a) 3-chlorophenylisocyanate, dry toluene, reflux, 2 h, 88 %; (b) Aromatic aldehydes, AcOH, Conc.H₂SO₄, reflux, 2 h, 73-93 %.

In scheme 2, we used an alternative route to prepare styryl quinoxaline starting from the condensation of 3-methylquinoxalin-2(1H)-one (4) with different aromatic aldehydes at first to yield (E)-3-styrylquinoxalin-2(1H)-one (5a-d). Then chlorination of the resulted intermediates 5a-d using phosphorus oxychloride yielded the corresponding chloro compounds 6a-d in moderate yields and melting point as reported [23, 26, 30]. Those intermediates, 6a-d, were further utilized to obtain the corresponding substituted final series 7a, b, c and 8a, b, d in moderate yields through refluxing with various aromatic and aliphatic amines in different solvents (ethanol or isopropanol) using the appropriate catalysts.

Scheme 2: The synthetic routes of finals 7a, b, c and 8a, b, d. Reagents and conditions: (a) Aromatic aldehydes, AcOH, Conc.H₂SO₄, reflux, 2 h, 72-85 %; (b) POCl₃, reflux 1.5 h, 80-85 %; (c) Ethanol, aromatic amines, K_2CO_3 , 12 h, 80-82 %; (d) Isopropanol, *N*-phenylpiperazine, TEA, reflux, 12 h, 75-80 %.

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3.2. Biological Screening

In Vitro antimicrobial activity

The antibacterial activity was examined against panel of representative Gram-negative bacteria (E. coli, K. pneumonia, A. baumannii, and P.aeruginosa) and Gram-positive bacteria [methicillin resistant S. aureus (MRSA)] at 32 µg/mL according to standard broth micro dilution assays [33]. Colistin and Vancomycin were used as positive bacterial inhibitor standards for Gramnegative and Gram-positive bacteria, respectively. The antifungal activity was performed against one fungal genera namely, C. albicans using fluconazole as a positive standard antifungal. From the obtained result, all synthesized compounds didn't exhibit any activity towards bacterial panel or C. albicans, however compound 3a revealed significant inhibitory activity (MIC₅₀ \leq 0.25 µg/mL) against *C. albicans* (see Table 1 & 2).

 Table 1: Results of antibacterial and antifungal activities of series (A) compounds.

Anti-microbial activity MIC ₅₀ (µg/mL)							
	Anti-bacterial					Anti- Fungal	
Compd.		A.baum annii	P.aereu ginosa.	S.aur.	E.col.	K.pne.	C.alb.
2	$\mathrm{Cl}_{N}^{N} \widetilde{\mathrm{L}}_{H}^{\tilde{\mathrm{L}}_{N}^{\tilde{\mathrm{L}}_{N}}} \mathrm{Cl}_{\mathrm{cl}}$	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
Series A							
	R:						
3a	2-OH	>32.0	>32.0	>32.0	>32.0	>32.0	≤0.25
3b	4-OCH ₃	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3c	4-C1	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3d	4-F	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3e	4-N(CH ₃) ₂	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3f	3-OCH ₃ , 4-OH	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3g	4-NO2	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
3h	3-NO ₂	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
Colistin		0.25	0.25		0.125	0.25	
Vancomycin				1			
Fluconazole							0.125

 Table 2: Results of antibacterial and antifungal activities of series (B) compounds.

Anti-microbial activity MIC ₅₀ (µg/mL)								
	Anti-bacterial					Anti- Fungal		
Compd.			A.baum annii	P.aereu ginosa.	S.aur.	E.col.	K.pne.	C.alb.
Series B	R							
7a	4-OCH ₃	Н	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
7ь	3-COOH	Cl	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
7c	CH_3	OCH ₃	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
Series C	x							
8a	н		>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
8b	4-0	1	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
8d	4-	F	>32.0	>32.0	>32.0	>32.0	>32.0	>32.0
Colistin			0.25	0.25		0.125	0.25	
Vancomycin					1			
Fluconazole								0.125

A.bau: Acinetobacter baumannii.
P.aer. Pseudomonas aeruginosa.
S.aur. Staphylococcus aureus.
E.col. Escherichia coli.
K.pne. Klebsiella pneumoniae.
C.alb. Candida albicans.

3.3. Molecular Docking

The docking study focused on compound 3a which showed considerable activity against Candida albicans. Compound **3a** shares a common pharmacophore with allylamine derivatives in terms of an aromatic center, a spacer containing H-bond acceptor, and a hydrophobic moiety. Since allylamines are known to work by the inhibition of fungal squalene epoxidase (SE), it has been chosen in this study as a possible target [34]. Although a reliable structure for the fungal SE has not been published, a recently resolved crystal structure for the human SE (PDB ID: 6C6P) can provide qualitative results on the possible binding mode of compound **3a**. Fortunately, as highlighted by Padyana *et al.* [31], the binding site of SE is highly conserved. The nonconserved region, which creates a difference between the binding sites in the corresponding human and fungal SE enzymes, is made up of three residues surrounding the aromatic side of the co-crystallized ligand, namely F166, I197 and L324 (see Figure 4).

Our aim is to compare the predicted binding pose of compound 3a to the binding pose of terbinafine, which is a famous example of SE inhibitors. To validate the docking protocol, redocking of the cocrystallized ligand has been performed at first where it generated a pose that is nearly congruent with the co-crystallized one (see Figure 4), with a docking score of -15 kcal/mol. Then, terbinafine and compound 3a were docked into the active site of human SE enzyme.



Figure 4: Overlay of the co-crystallized ligand in its original (grey) and its redocked (red) pose in the active site of squalene epoxidase (PDB ID: 6C6P). The non-conserved amino acids are shown in green lines.



Figure 5: 3D poses of the co-crystallized ligand (grey sticks) and terbinafine (cyan ball and sticks) in the active site of squalene epoxidase (PDB ID: 6C6P). The non-conserved amino acids are shown in green lines.



Figure 6: 3D poses of the co-crystallized ligand (grey sticks) and compound 3a (red ball and sticks) in the active site of squalene epoxidase (PDB ID: 6C6P).

3.4. Cytotoxicity against human embryonic

kidney cell line and hemolysis of human

red blood cells effect

To further investigate the safety profile of synthesized compounds; the final compounds were tested for their cytotoxicity against a human embryonic kidney cell line 293 (HEK293) and for hemolysis of human red blood corpuscles (RBCs) using tamoxifen and melittin as positive controls, respectively, the results were illustrated in **Table 3**. [**Table 3 near here**].

 Table 3: Cytotoxicity and haemolysis ability of the tested compounds.

Compd.	CC50(ug/mL)	HC10(ug/mL)
2	>32.0	>32.0
3a	>32.0	>32.0
3b	>32.0	>32.0
3c	>32.0	>32.0
3d	>32.0	>32.0
3e	>32.0	>32.0
3f	>32.0	>32.0
3g	>32.0	>32.0
3h	>32.0	>32.0
7a	>32.0	>32.0
7b	>32.0	>32.0
7c	>32.0	>32.0
8a	>32.0	>32.0
8b	>32.0	>32.0
8d	>32.0	>32.0
Tamoxifen	9	NA
Melittin	NA	2.7

 CC_{50} is the concentration at 50% cytotoxicity (cytotoxicity against a HEK293).

 HC_{10} is the concentration at 10% haemolysis (haemolysis of human RBCs).

NA, Not Applicable.

4. Discussion

4.1. Chemistry

¹H NMR spectrum of intermediate 2 displayed the appearance of two singlet signals at δ 9.02 and 8.42 ppm representing the D₂O exchangeable protons of the urea group. The additional aromatic protons were proved by the appearance of singlet signal at δ 7.72 ppm. IR spectrum revealed the disappearance of the forked peak of primary amino group (-NH₂) and the appearance of the amidic carbonyl group (C=O) at 1670 cm^{-1} . The resulting products **3a-h** were confirmed by ¹H and ¹³C NMR which revealed additional signals consistent to the introduced aromatic protons and carbons of the styryl moiety, and the disappearance of the singlet signals of aliphatic methyl (-CH₃) in ¹H NMR and ¹³C NMR. Compounds 3a, 3f, and 3h displayed the appearance of multiplet signals in the range of δ 7.47-6.53 ppm corresponding to the vinylic protons. Compounds **3b**, **3c**, **3d**, **3e** and **3g** showed doublet signals at δ 7.36, 7.51, 7.41, 7.25, and 7.71 ppm corresponding to the vinylic protons with J constant 13.6, 13.6, 20.0, 16.0, and 17.0 Hz respectively (indicating trans alkene).

Compound 3a and 3f exhibited D₂O exchangeable singlet signal corresponding to (OH) group at δ 9.15 and 9.04 ppm, in addition to the appearance of OH broad band in IR at (3500-3200) and (3300-3100) cm⁻¹ respectively. Compound **3b** showed the appearance of three methoxy protons (OCH₃) at δ 3.82 ppm in ¹H NMR and methoxy carbon at δ 55.7 ppm in ¹³ C NMR. Compounds **3c** and 3d showed the appearance of doublet of doublets signals at δ 7.83, 7.78 and 8.71 ppm respectively, corresponding to the aromatic protons of the introduced styryl moiety. Compound 3e showed the appearance of singlet signals at δ 3.02 ppm in ¹H NMR corresponding to six aliphatic protons (2 methyl groups) instead of 2.62 ppm representing one methyl group appeared with compound 2. Additionally, ¹³C NMR spectrum of compound 3e showed a signal at δ 29.9 ppm instead of 21.6 ppm (appeared with compound 2). A singlet signal appeared at δ 3.75 ppm in ¹H NMR corresponding to the three methoxy protons, in addition to a signal at δ 56.1 ppm appeared in ¹³C NMR spectrum corresponding to methoxy (OCH₃) carbon of compound 3f. Compound 3g showed the appearance of doublet of doublets signals at δ 8.27 and 8.06 ppm corresponding to the introduced aromatic protons of the styryl moiety.

As for compounds **7a-7c**, ¹H NMR spectra revealed the appearance of new singlet signal at the range of δ 9.70- 8.70 ppm corresponding to the D₂O exchangeable proton of the secondary amine (NH-) newly formed in compounds 7a-7c respectively, as well as the appearance of secondary amine (NH-) band in the range of 3425-3390 cm⁻¹ in IR spectrum. Compounds 7b showed the appearance of singlet signal at δ 10.00 ppm corresponding to the D₂O exchangeable proton of the newly formed carboxylic acid (-COOH). Whereas the IR spectrum of compounds **7b** showed the appearance of carboxylic band in the range of 3500-2400 cm⁻¹ as well as the presence of a band at 1696 cm⁻¹ corresponding to the carbonyl group of acid. Compounds 7a showed the appearance of multiplet signals at the range of δ 6.91-6.87 ppm, whereas compound **7c** displayed a doublet signal at δ 6.92-6.84 ppm corresponding to the deshielded olefinic protons. Compound **7a** and **7c** ¹H NMR spectra exhibited a singlet signal at δ 3.77, 3.81 ppm corresponding to methoxy (-OCH₃) group. Additionally, compound **7c** showed a singlet signal at δ 2.25 ppm corresponding to methyl (-CH₃) group.

Considering compounds **8a,b,d**, ¹H NMR spectrum showed the appearance of newly formed signals corresponding to the introduced aliphatic piperazinyl protons appeared as singlets in the range of δ 3.53, 3.45 ppm for **8a**, 3.52, 3.43 ppm for **8b** and 3.52, 3.44 ppm for **8d**. ¹³ C NMR spectra showed the presence of newly formed signals corresponding to the introduced aliphatic piperazinyl carbons appeared at δ 49.9 and 48.4 ppm for **8a**, 50.0 and 48.4 ppm for **8b**, 51.4 and 48.8 ppm for **8d**. Compounds **8a** and **8b** showed the appearance of multiplet signals at the range of δ 7.51-7.37 ppm, while compound **8d** showed the appearance of doublet signal at δ 7.44 ppm corresponding to the vinylic protons with *J* constant 16 *Hz* (indicating *trans* alkene).

4.2. Biological Screening

In Vitro antimicrobial activity

To interpret the biological results, series A emerging originally from compound **2** have been investigated. Replacement of hydrogen atom in the styryl ring with hydroxyl group in position 4 (as in compounds **3f**), methoxy group in position 4 or 3 (as in compounds **3b** and **3f**), chloro, floro or dimethyl amino in position 4 or 3 (as in compounds **3b** and **3f**), chloro, floro or dimethyl amino in position 4 or 3 (as in compounds **3g** and **3h**); didn't resulted in any promising activity against *C. albicans*, yet a promising candidate emerged through substitution at position 2 of the respective styryl ring with hydroxyl group possessing impressive MIC₅₀ against *C. albicans* (**MIC**₅₀ \leq **0.25 µg/mL**). Furthermore, series B where quinoxaline is attached

with different aliphatic and aromatic amines at position 2 along with a styryl moiety at position 3 also didn't develop any activity towards *C. albicans*. These results introduce compound **3a** as a promising lead compound and in the next section we shall explore its potential mechanism of action through molecular docking. [see **Table 1 & 2**].

4.3. Molecular Docking

The docking of terbinafine and compound 3a resulted in a docking score of -10 kcal/mol. As shown in Figure 5, terbinafine assumes a pose that is anchored by a H-bond between the conserved Tyr195 residue and its tertiary N atom. The pose in Figure 5 is in accordance with previous predictions by Padyana et al. [31]. Similarly, compound 3a assumes a pose that involves anchoring the quinoxaline ring via π - π stacking with Phe495 in addition to the interaction with Tyr195. Both interactions with Tyr195 are shown as dotted lines. Interestingly, both terbinafine and 3a do not extend in the region close to Phe166. This less extension might attribute to their decreased docking score compared to the cocrystallized ligand (-10 to -14 kcal/mol, respectively). This less binding of terbinafine to the human target, however, has been suggested to be the reason for its selectivity towards the fungal SE [31]. Based on the proposed pose for compound 3a, it is predicted to have the same selective property as terbinafine.

4.4. Cytotoxicity against human embryonic

kidney cell line and hemolysis of human

red blood cells effect

From the below results, the tested compounds showed $CC_{50} > 32 \ \mu g/mL$ against HEK293, which means that they are safe and non-cytotoxic compared to tamoxifen ($CC_{50}=9 \ \mu g/mL$). Additionally, the tested compounds exhibited HC_{10} more than 32 $\mu g/mL$, so they are considered as safe and non-toxic compounds). [see **Table 3**].

5. Conclusion

Summarizing, in the current study a series of styryl-based quinoxaline scaffolds bearing arylamino or arylurea moieties were designed and synthesized based on the structural similarities with allylamines and reported antifungal agents. Compound **3a** displayed significant antifungal activity against *C. albicans* (MIC₅₀ \leq **0.25 µg/mL**) compared to the reference drug fluconazole (MIC₅₀=0.125 µg/mL). Based on structure similarity with allylamines, the

predicated antifungal mechanism of compound **3a** is *via* inhibition of squalene epoxidase. The docking experiment showed similar binding modes and scores for compound **3a** and the well-known squalene epoxidase inhibitor terbinafine. Furthermore, all synthesized compounds were nearly safe to HEK293 cells ($CC_{50} > 32.0 \ \mu g/mL$) as well as to human RBCs ($HC_{10} > 32.0 \ \mu g/mL$). These results supported our design strategy and proudly introducing compound **3a** as a promising lead compound for the development of novel antifungal agents.

6. Conflict of Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

7. Formatting of funding sources

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