





Molecular Design and Synthesis of Certain Quinoxaline Derivatives with Potential Anticancer Activity

Thesis Presented by

Mai Ibrahim Ibrahim Shahin

BSc. In Pharmaceutical Sciences (May 2009)
Instructor of Pharmaceutical Chemistry
Ain Shams University

Submitted for the partial fulfillment of the *Master Degree*In Pharmaceutical Chemistry

Under the supervision of

Prof. Dr. / Dalal A. Abou El Ella

Professor of Pharmaceutical Chemistry Faculty of pharmacy-Ain Shams University

Prof. Dr. / Khaled A. M. Abouzid

Professor of Pharmaceutical Chemistry & Vice Dean for the Educational & Student Affairs Faculty of pharmacy-Ain Shams University

Ass. Prof. Dr. /Nasser Saad Mohamed

Associate Professor of pharmaceutical Chemistry & Acting Head of Pharmaceutical Chemistry Department Faculty of pharmacy-Ain Shams University

Faculty of Pharmacy

Ain Shams University

Acknowledgements

I am profoundly indebted to **Professor Dr. Dalal Abdelrahman Abou El Ella,** Professor of Pharmaceutical Chemistry, for her kind supervision, innovative ideas, fruitful opinion, invaluable advices, precious suggestions, continuous encouragement and spiritual support.

I owe my deepest appreciation and truthful gratitude to **Professor Dr. Khaled Abouzid Mohamed Abouzid,** Professor of Pharmaceutical Chemistry and Vice Dean for Educational and Student Affairs, for his scientific supervision. I am really sincerely and profoundly indebted to him for his priceless guidance and endless support throughout the whole work and during writing this thesis. I truly thank him for his great efforts which allowed this thesis to appear in its final form.

I would like also to express my sincere thanks to **Dr. Nasser Saad Mohamed,** Assistant Professor in Pharmaceutical Chemistry & Acting Head of Pharmaceutical Chemistry Department for his kindness, continuous encouragement, indispensible assistance, valuable guidance and constant support throughout the whole work.

I acknowledge with thankfulness all my colleagues in Pharmaceutical Chemistry Department, for their friendly cooperation, support and their unconditional aid.

Also I would like to express my gratitude to the National Cancer Institute, Maryland, U.S.A for performing the in-vitro anticancer assay of the synthesized compounds.

I am profoundly indebted to my small family, my husband and my lovely kid (YOUSSEF). They have always been the source of pleasure for me. My husband, my colleague and my friend who always assisted me and was very considerable and helpful. My son, the source of pressure and pleasure at the same time who is always the only person who could make me laugh.

Finally, my big family, my parents and my brother. My father for his reasonable opinions, his constant spiritual support and providing me with some needed chemicals. He is always my source of inspiration. My mother, who helped me a lot in all issues and saved a lot of time for me to work. I would do nothing without her. I really appreciate their efforts and really thank them deep from my heart.

Contents

Acknowledgements	i
Contents	iii
List of figures:	vi
List of tables	
List of Abbreviations	
Abstract:	
1. Introduction	
1.1. Cancer	
1.1.1. Overview	1
1.1.2. Causes of cancer	1
1.1.3. Tumorigenesis: Formation of cancero	us cells2
	3
1.1.5. Treatment:	4
1.1.5.1. Traditional Treatments	4
1.1.5.1.1. Surgery	5
1.1.5.1.2. Radiotherapy	5
1.1.5.1.3. Chemotherapeutic drugs	5
1.1.5.1.3.1. Alkylating agents	6
1.1.5.1.3.2. Antimetabolites	7
1.1.5.1.3.2.1. Purine analogues:	7
1.1.5.1.3.2.2. Pyrimidine analogues:	7
1.1.5.1.3.2.3. Folic acid analogues:	
1.1.5.1.3.3. Antitumor antibiotics	
1.1.5.1.3.3.1. Anthracyclines	
1.1.5.1.3.3.2. Other anti-tumor antibiotics	
1.1.5.1.3.4. Topoisomerase inhibitors	
1.1.5.1.3.5. Mitotic inhibitors	

1.1.5.1.3.6. Corticosteroids	12
1.1.5.1.3.7. Other types of chemotherapeutic drugs	13
1.1.5.1.3.7.1. Differentiating agents	13
1.1.5.1.3.7.2. Hormone therapy	13
1.1.5.1.3.7.3. Immunotherapy	14
1.1.5.2. Targeted therapies	16
1.1.5.2.1. Targeting Protein kinases	19
1.1.5.2.1.1. Overview	19
1.1.5.2.1.2. Receptor tyrosine kinase structure	20
1.1.5.2.1.3. Receptor tyrosine kinase inhibition strategies	22
1.1.5.2.1.5. VEGFs and their receptors:	28
1.1.5.2.1.6. VEGFR-2 inhibition	31
2. Rationale and Design	34
2.1. Design process based on:	35
2.1.1. Structure Activity Relationship study (SAR)	35
2.1.2. Identification of the key interactions with the binding site of both ty II inhibitors	
2.2. Synthetic schemes adopted to prepare the target compounds	
3. Results and Discussion	
3.1. Chemistry	
3.2. Biological Evaluation	
3.2.1. In-vitro anticancer activity:	
3.2.2. Enzyme inhibition assay versus VEGFR-2:	
3.3. Molecular Modelling study:	
3.3.1. Docking study using Discovery Studio Module:	
3.3.2. Field alignment study using FieldAlign module:	
3.3.2.1. Principle of FieldAlign module	
3.3.2.2. Field alignment study:	
4. Conclusion	
5. Fxnerimental	88

6. References	122
5.3.2.4. Processing	121
5.3.2.3. Load excluded volume:	121
5.3.2.2. Add database molecules:	121
5.3.2.1. Add reference molecule:	121
5.3.2. Field alignment (using Fieldalign Software):	121
5.3.1.3. Docking process:	120
5.3.1.2. Ligands preparation for docking:	
5.3.1.1. Protein preparation for docking:	120
5.3.1. Docking study (using Gold 4.1 software in the interface of Accelry's di studio 2.5):	•
5.3. Molecular modeling study:	120
5.2.2. Enzyme inhibition assay:	
5.2.1. In-vitro anticancer activity	117
5.2. Biological evaluation:	117
5.1.2. Synthesis	89
5.1.1. Materials and instrumentation	88
5.1. Chemistry	88

List of figures:

Figure 1. The Main Hallmarks of Cancer4
Figure 2. Therapeutic Targeting of the Cancer Hallmarks
Figure 3 . Targeted therapy approaches
Figure 4. Consensus model structure of summarizing the human Protein Kinase family. The
model structure of human Protein Kinase, shows the basic two-lobe kinase fold, with the N-
and C-terminal (green and orange respectively) lobes joined by a hinge region (magenta).
Substrate recognition is through interaction with the activation segment (blue), a region in
the C-terminal lobe. ATP binds at a site between the two lobes (yellow)21
Figure 5. Mechanisms of targeted therapies. The molecular targets in this figure are not
$over expressed\ in\ a\ single\ cell\ type,\ but\ rather\ on\ various\ malignant\ and\ normal\ tissues.\ .\ 23$
Figure 6. Schematic representation of the equilibrium between active, inactive
conformations with type I and II inhibitors
Figure 7. Schematic illustration of the expression patterns, ligand specificity and
cellular/physiological effects of each of the vascular endothelial growth factor receptors
(VEGFRs)
Figure 8. Tumor angiogenesis and inhibitors of VEGFR-2 signaling
$\textbf{Figure 9}. \ \textbf{Structures of some VEGFR kinase inhibitors' with the first line representing type I}$
inhibitors and the second one for type II inhibitors
Figure 10. Binding modes of kinase inhibitors. (a) Schematic representation of the ATP
binding site divided into subregions. (b) Schematic representation of the allosteric binding
site. (c) Ribbon diagram of ATP binding site with a DFG-in activation-loop conformation
(active conformation). (d) Ribbon diagram of a representative of type II binding mode
showing the DFG-out activation-loop conformation (inactive conformation) 36
Figure 11 . Origins of the first-generation type II kinase inhibitors Gleevec®, BIRB796 and
Nexavar®
Figure 12. Fitness of the essential features of three type II inhibitors on our designed
compounds revealing the green left side that presents the main scaffold adopting the active
site. Also, the urea, amide or sulfonamide core was presented in yellow color and finally the
extra moiety occupying the allosteric site was given in pink color39

Figure 13. Acid catalyzed quinoxaline scaffold synthesis
Figure 14. Mean graph produced from NCI 60 cell line screening program of compound
VIIc. Colour codes are given for each cell line
Figure 15. Mean graph produced from NCI 60 cell line screening program of compound
VIIe
Figure 16. Mean graph produced from NCI 60 cell line screening program of compound
VIIIb
Figure 17 . Mean graph produced from NCI 60 cell line screening program of compound X
Figure 18 . Mean graph produced from NCI 60 cell line screening program of compound XVId
Figure 19 . Mean graph produced from NCI 60 cell line screening program of compound XVIIb
Figure 20 . (a) and (b) showing the matching of the negative field (hydrogen bond acceptor) with Sorafenib in both compounds XVIc , VIIa . (c) Compound VIId shows the negative field in the totally opposite directions (d) Compound XVIb showing no negative
field around that of Sorafenib.
Figure 21. XVId and Sorafenib negative fields in comparison to each other
List of tables
Table 1. NCI percentage growth of the 60 cell lines for the 6 elected compounds. 62
Table 2. VEGFR-2 inhibition results of the twenty final compounds
Table 3. Molecular modeling investigational study

List of Abbreviations

5-FU: 5-Fluorouuracil

6-MP: 6-Mercaptopurine

ATP: Adenosine triphosphate

BC: Before Christ

DFG: Aspartate- Phenylalanine- Glycine

DMF: Dimethyl formamide

DNA: Deoxyribo Neucleic Acid

EC: Endothelial cells

FDA: Food and Drug Administration

FGFR: Fibroblast growth factor receptor

FT-IR: Fourier transform-Infrared

GIST: gastrointestinal stromal tumors

GOLD: Genetic optimization of ligand docking

HUVEC: Human umbilical vein endothelial cell

IBX: 2-Iodoxybenzoic acid

KDa: Kilodalton

KDR: Kinase insert domain

MHz: Mega hertz

MS: Mass spectroscopy

NCI: National Cancer Institute.

NMR: Nuclear magnetic resonance

NRTK: Non- receptor tyrosine kinase

PDGFR: Platelet-derived growth factor receptor

PIGF: Placental growth factor

rt: Room temperature

RTK: Receptor tyrosine kinase

SAR: Structure Activity Relationship

SARMs: Selective androgen receptor modulators

SBSSA: Silica-bonded S-sulfonic Acid

SERMs: Selective estrogen receptor modulators

SMI: Small molecule inhibitors

TCA: Trichloro acetic acid

TEA: Triethyl amine

THF: Tetrahydrofuran

TK: Tyrosine kinase

TLC: Thin layer Chromatography

USA: United States of America

VEGFR: Vascular endothelial growth factor receptor

WHO: World Health Organization

Y: Tyrosine amino acid

 μM : Micromole

Abstract:

1. Introduction

Cancer is one of the most common causes of death, taking nearly 7 million lives each year worldwide. Due to the low selectivity and the high side effects seen by the traditional chemotherapeutic agents, tremendous efforts are being exerted to get more selective anticancer agents. This required thorough study of signal transduction pathways that holds the promise of efficacy with minimal toxicity. Vascular endothelial growth factor receptor (VEGFR) was identified as one of the efficient targets for evolving new anticancer agents having the desired selectivity on cancerous cells. By targeting VEGFR, angiogenesis is greatly inhibited leading to the death of the tumor cells.

2. Rationale and Design

In our current study, new quinoxaline derivatives were explored for its activity against VEGFR-2. The targeted compounds were designed as type-II inhibitors based on comprehensive SAR study. Synthesis of the designed quinoxaline-based compounds was accomplished and their structures were confirmed by various spectral and micro analytical data.

3. Chemistry

This thesis comprises the synthesis of the following reported starting materials and intermediates:

- 1. Quinoxaline-2,3(1H,4H)-dione (I).
- 2. 6-Nitroquinoxaline-2,3(1H,4H)-dione (II).
- 3. 2,3-Dichloro-6-nitroquinoxaline (III).
- 4. Quinoxalin-2(1H)-one (XI).

- 5. 6-Nitroquinoxalin-2(1H)-one (XII).
- 6. 2-Chloro-6-nitroquinoxaline (XIII).
- 7. 1-(4-Nitrophenyl)-3-phenylurea (XIXa)
- 8. 1-(3-Chlorophenyl)-3-(4-nitrophenyl)urea (XIXb)
- 9. 1-(4-Aminophenyl)-3-phenylurea (XXa)
- 10. 1-(4-Aminophenyl)-3-(3-chlorophenyl)urea (XXb)

Also, the synthesis and the characterization of the following new intermediate compounds was achieved:

- 1. 3-Chloro-N-(4-methoxyphenyl)-6-nitroquinoxalin-2-amine (IV).
- 2. 3-((4-Methoxyphenyl)amino)-7-nitroquinoxalin-2(1H)-one (V).
- 3. 7-Amino-3-((4-methoxyphenyl)amino)quinoxalin-2(1H)-one (VI).
- 4. N-(4-Methoxyphenyl)-6-nitroquinoxalin-2-amine (XIVa).
- 5. N-(4-Chlorophenyl)-6-nitroquinoxalin-2-amine (XIVb).
- 6. N²-(4-Methoxyphenyl)quinoxaline-2,6-diamine (XVa).
- 7. N²-(4-Chlorophenyl)quinoxaline-2,6-diamine **(XVb).**Moreover, the targeted compounds synthesized were:
- 1. 1-(2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)-3-phenylurea (VIIa).
- 2. 1-(2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)-3-phenylthiourea **(VIIb).**
- 3. 1-(3-Chlorophenyl)-3-(2-((4-methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)urea (VIIc).
- 4. 1-(2-((3-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)-3-(p-tolyl)urea **(VIId).**
- 5. 1-Cyclohexyl-3-(2-((4-methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)urea (VIIe).
- 6. N-(2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)benzenesulfonamide (VIIIa).

- 7. N-(2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)-4-methylbenzenesulfonamide **(VIIIb).**
- 8. 2-((2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)carbamoyl)benzoic acid **(IX).**
- 9. N-(2-((4-Methoxyphenyl)amino)-3-oxo-3,4-dihydroquinoxalin-6-yl)acetamide(X).
- 10. 1-(2-((4-Methoxyphenyl)amino)quinoxalin-6-yl)-3-phenylthiourea (XVIa).
- 11. 1-(2-((4-Chlorophenyl)amino)quinoxalin-6-yl)-3-phenylurea (XVIb).
- 12. 1-(2-((4-Methoxyphenyl)amino)quinoxalin-6-yl)-3-(m-tolyl)urea (XVIc).
- 13. 1-Cyclohexyl-3-(2-((4-methoxyphenyl)amino)quinoxalin-6-yl)urea (XVId).
- 14. 1-(2-((4-Chlorophenyl)amino)quinoxalin-6-yl)-3-cyclohexylurea (XVIe).
- 15. N-(2-((4-Methoxyphenyl)amino)quinoxalin-6-yl)benzenesulfonamide (XVIIa).
- 16. N-(2-((4-Methoxyphenyl)amino)quinoxalin-6-yl)-4-methylbenzenesulfonamide (XVIIb).
- 17. N-(2-((4-Chlorophenyl)amino)quinoxalin-6-yl)-4-methylbenzenesulfonamide (XVIIc).
- 18. N-(2-((4-Chlorophenyl)amino)quinoxalin-6-yl)acetamide (XVIII).
- 19. 1-(4-((6-Nitroquinoxalin-2-yl)amino)phenyl)-3-phenylurea (XXIa)
- 20. 1-(3-Chlorophenyl)-3-(4-((6-nitroquinoxalin-2-yl)amino)phenyl)urea (XXIb)

4. Biological evaluation

The biological evaluation was accomplished by testing both anticancer activity and enzyme inhibition activity. The anticancer activity of the synthesized compounds (VIIc, VIIIb, X, XVId, XVIIb) was evaluated at the national cancer institute (NCI), Maryland, USA. They were challenged against 60 cancer cell lines at 10 μ M. Unfortunately, they showed no significant anti-cancer activity. The twenty final compounds were evaluated for their VEGFR-2 inhibition activity. The evaluation was performed in KINEXUS Corporation, Canada. Enzyme inhibition results revealed the promising activity of the quinoxaline nucleus that can be considered for synthesis of new effective anti-angiogenic drugs. In

particular, compound **IX**, which showed 69% inhibition, was the most powerful candidate. Most of other compounds activity was between 10% and 29%.

5. Molecular modeling study

Finally, a thorough Molecular docking using GOLD software was attempted to investigate the binding mode of the targeted compounds and interpret the biological results. The unexpected low results were interpreted using Field alignment study.

1. Introduction

1.1. Cancer

1.1.1. Overview

The first description of cancer is found in an Egyptian papyrus and dates back to approximately 1600 BC. It was regarded as an incurable disease until the nineteenth century, when surgical removal was made more efficient by anaesthesia, improved techniques and histological control. ¹

Cancer is a collective term used for a group of diseases that is characterized by the loss of control of the growth, division, and spread of a group of cells, leading to a primary tumor that invades and destroys adjacent tissues. It may also spread to other regions of the body through a process known as metastasis, which is the cause of 90% of cancer deaths. The terms cancer and tumor, however, are more commonly accepted. A major problem in treating cancer is the fact that it is not a single disease. There are more than 200 different cancers resulting from different cellular defects, and so a treatment that is effective in controlling one type of cancer may be ineffective on another.²

Over the past 30 years, significant progress has been achieved in understanding the molecular basis of cancer. The accumulation of this basic knowledge has established that cancer is a variety of distinct diseases and that defective genes cause these diseases. Further, gene defects are diverse in nature and can involve either loss or gain of gene functions.³

1.1.2. Causes of cancer

Possibly as many as 30 % of cancers are caused by smoking, while another 30% are diet relates. Carcinogenic chemicals in smoke, food and the environment may cause cancer by inducing gene mutations or interfering with normal cell differentiation. The birth of a cancer (carcinogenesis) can be initiated by a chemical – usually a mutagen- but other