BIOREDUCTIVE METABOLISM OF SMALL MOLECULE NITROAROMATICS AND *N*-OXIDES IN HYPOXIA

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By

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The undersigned, appointed by the Dean of the Graduate School, have examined the dissertation entitled

BIOREDUCTIVE METABOLISM OF SMALL MOLECULE NITROAROMATICS AND *N*-OXIDES IN HYPOXIA

Presented by Anuruddha Rajapakse

A candidate for the degree of Doctor of Philosophy and hereby certify that in their opinion it is worthy of acceptance

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TABLE OF CONTENT

ACKNOLEDGEMENTS	ii
LIST OF SCHEMES	vii
LIST OF FIGURES	X
LIST OF TABLES	xiii
TABLE OF COMPOUND STRUCTURE AND NUMBER	xiv
ABSTRACT	xxv

Chapter 1:Nitroaromatics and N-oxide compounds as radiosensitizers,

oxygen sensors and cytotoxic agents in tumor therapy

1.1. Hypoxia	1
1.2. Ionizing radiation therapy	1
1.3. Radio sensitizing oxygen mimetic agents	4
1.3.1. Nitro aromatic reduction in hypoxic cells	6
1.3.2. Elimination of active agent through nitroaromatic reduction	8
1.4. <i>N</i> -oxides	11
1.5. Summary	14
References for chapter 1	15

Chapter 2: Hypoxia-selective, enzymatic conversion of 6-nitroquinoline into a fluorescent helicene: pyrido[3,2-f]quinolino[6,5-c]cinnoline 3oxide

2.1. Hypoxia as a parameter to be determined qualitatively and quantitatively	23
2.2. Fluorescent probes to detect hypoxia	24
2.3. Reduction of 42 to Obtain 43 under anaerobic conditions	24
2.4. Identification of products arising from the anaerobic reaction	26
2.4. Synthesis and structural characterization of 44	29
2.5. Conclusion	34
2.6. Experimental	35
References for chapter 2	55

Chapter 3: Hypoxia-selective enzymatic conversion of 6-nitroquinoline

to the fluorescent product, 6-aminoquinoline

3.1. Hypoxia is an attractive target to develop fluorescent probes
3.2. Fluorescent Probes to Detect Hypoxia
3.3. LC/MS analysis of the reaction mixtures generated by hypoxic metabolism of 42 by
xanthine/xanthine oxidase63
3.4. LC/MS analysis of the reaction mixtures generated by aerobic metabolism
of 42 by xanthine/xanthine oxidase67
3.5. Xanthine oxidase oxidizes aryl carbon, bonded to heteroatom of 42 to produce 6-
nitroquinolone 51 67

Chapter 4: Mechanistic Aanalysis Related to the Oxidative DNA
References for chapter 394
3.10. Experimental76
3.9. Conclusions74
conversion to 6-aminoquinolone 54
3.8. Enzymatic conversion of 42 to 6-nitroquinolone 51 followed by hypoxia-selective
3.7. Hypoxia-selective conversion of 6-nitroquinolone 51 to 6-aminoquinolone 54 72
3.6. Hypoxia-selective conversion of hydroxylamine 50 to amine 43 69

Damage Caused by 1,2,4-Benzotraizine Dioxide

4.1. Introduction
4.2. Mechanistic evidence for the oxidizing radical formation by TPZ
4.3. Hypothesis and design of experiments100
4.4. Examine the dehydration mechanism in relation to the release of oxidizing specie
from 1,2,4-benzotraizine-di-oxide102
4.5. Chemical Synthesis of 1,2,4-benzotraizine 1,4-dioxide103
4.6. DNA-damaging properties of TPZ and TPZ analogs103
4.6.1. TPZ analogs perform concentration dependent DNA damage103
4.6.2. DNA damage is decreased by radical scavengers10
4.7. Examining chemical mechanism of bio-reductive metabolism of 55 and 60 111
4.8. Metabolic studies of 55 and 60 with organic substrate
4.9 Deuterium incorporation into 55115
4.10. Isotope washout from drug 60 116

Chapter 5: Synthesis of bioreductivly-activated nitroaromatic trigger	S
References for chapter 4	132
4.13. Experimental	119
4.12. Conclusion	118
4.11. Isotope replacement analysis and dehydration mechanism	117

5.1. Qualitative and quantitative determination of hypoxia
5.2. Goal: Constructing suitable nitroaromatic fluorescent probes for hypoxia140
5.3. Synthesis of 5-nitrothienyl moeity, 2-(5-Nitrothien-2-yl) propan-2-ol 73 141
5.4. Synthesis of 1-methyl-2-nitro-5-hydroxymethyl imidazole 79 142
5.5. Synthesis of 80 and 81 144
5.6. Synthesis of 3-acetylquinoline-1,2,4-benzotraizine 1,4-dioxide 84 144
5.7. Experimental145
References for chapter 5164
VITA

LIST OF SCHEMES

Chapter 1
Scheme 1.1 Gamma radiolysis generates radical species1
Scheme 1.2 Hydroxyl radical abstract hydrogen from DNA1
Scheme 1.3 DNA radical on C4' is fixed by oxygen2
Scheme 1.4 Formation of ribonolactone
Scheme 1.5Thiols can repair DNA radical damage
Scheme 1.6 Radiolysis induced nitro-reduction and DNA radical formation4
Scheme 1.7 Oxygen of nitro group is donated to DNA5
Scheme 1.8 Enzyme mediated-Nitro reduction undergo in hypoxia5
Scheme 1.9 Hydroxylamine produces glyoxal-dialdehyde alkylator5
Scheme 1.10 Nitroaromatics reduction in hypoxia produces the active drug7
Scheme 1.11 Nitrophenyl-mustard alkylating agents7
Scheme 1.12 Nitrophenyl-mustard alkylating agents
Scheme 1.13 Hydroxylamine release the active drug9
Scheme 1.14 Phosphoramidate forms azide upon elimination of leaving group9
Scheme 1.15 Cyclophophoramide (18) metabolism by CYP ₄₅₀ 9
Scheme 1.16 Nitroquinoline phosphoramide prodrug release10
Scheme 1.17 Nitrophenyl, nitrofuryl and nitrothienyl phosphoramide conjugates10
Scheme 1.18 Nitrothienyl and nitrophenyl dimethyl pro-drugs11
Scheme 1.19 <i>N</i> -oxide radiosentising agents12
Scheme 1.20 Enzyme mediated reduction of 33 in hypoxia12

Scheme 2.1. Enzymatic reduction profile of nitroaromatic compound	24
Scheme 2.2. Hypoxic metabolism of 42 is expected to form fluorescent 43	25
Scheme 2.3. Metabolites formed by the reduction of 42 with NADPH/CYP450R	29
Scheme 2.4. Mechanism for the formation of 44 under anaerobic conditions	34
Chapter 3	

Scheme 3.1. Enzymatic reduction steps of a typical nitroaromatic compound60
Scheme 3.2. Hypoxic metabolism of 42 forms fluorescent 43 61
Scheme 3.3. CYP450R mediates conversion of 42 into fluorescent metabolites61
Scheme 3.4 Hypoxic metabolism of 42 by xanthine and xanthine oxidase64
Scheme 3.5 Enzymatic generation of 51 by xanthine and xanthine oxidase68
Scheme 3.6 Enzymatic generation of 43 by xanthine and xanthine oxidase
Scheme 3.7 Enzymatic generation of 54 from 51 by xanthine and xanthine oxidase is
hypoxia selective72
Scheme 3.8 Enzymatic generation of 51 from 42 and production of 54 from 51 73

Scheme 4.1 Enzymatic reduction of 33 produces DNA damaging radicals and oxidative
stress
Scheme 4.2 Different mechanisms are proposed to explain enzymatic metabolism of 33
Scheme 4.3 Enzymatic reduction of 55 under low oxygen concentrations forms major
metabolite 59
Scheme 4.4 Isotopic content of major metabolite of 55/60 determines mechanism102
Chapter 5
Scheme 5.1. Bio-reducible moieties can be used as oxygen sensors
Scheme 5.2. Nitro phenyl benzyl phosphoramadite prodrugs140
Scheme 5.3. 1,6-elimination of active drug species140
Scheme 5.4. Synthesis of 70 141
Scheme 5.5. Synthesis of 2-(5-nitrothien-2-yl) propan-2-ol 73
Scheme 5.6. Synthesis of 76 from sarcocine ethyl ester 74 143
Scheme 5.7. Synthesis of 1-methyl-2-nitro-5hydroxymethyl imidazole 79 143
Scheme 5.8. Fluorescent probes 83 and 84144
Scheme 5.9. Synthesis of 84 using triphosgene 82 and 43 144

LIST OF FIGURES

Chapter 2

Figure 2.1. Enzymatic conversion of 42 into a fluorescent product under hypoxic
conditions
Figure 2.2. LC/MS analysis of the reaction mixture generated by anaerobic metabolism of
42 (0.8 mM) by cytochrome p450 reductase (1.1 U/mL) and NADPH (6.4 mM)28
Figure 2.3. In 44, the 4 and 4'-hydrogens (see numbering system in Scheme 2.2) are close
in space
Figure 2.4. Fluorescence spectrum of authentic 44 (50 μ M, λ ex 307 nm) in sodium
phosphate buffer

Figure 3.1. Enzymatic conversions of 42 to a fluorescent product selectively under
hypoxic conditions
Figure 3.2. LC/MS analysis of the reaction mixture generated by anaerobic metabolism of
42 (0.8 mM)65
Figure 3.3. LC/MS analysis of authentic
compounds
Figure 3.4. LC/MS analysis of the reaction mixture generated by aerobic metabolism of
42 (0.8 mM)
Figure 3.5. ORTEP diagram of 51

Figure 3.6. Enzymatic conversion of 50 into a fluorescent 43 under hypoxic
conditions70
Figure 3.7. LC/MS analysis of the reaction mixture generated by anaerobic metabolism of
50 (0.8 mM)71
Figure 3.8 Enzymatic conversions of 51 to 54 under hypoxic conditions72
Figure 3.9 Enzymatic conversion of 42 to 51 and reduction to 54 in hypoxia74
Figure 3.10 Fluorescence spectra of control reactions

Figure 4.1. Cleavage of supercoiled plasmid DNA by $33 (50-250 \ \mu\text{M})$ in the presence of
NADPH:cytochrome P450 reductase as an activating system104
Figure 4.2. Cleavage of supercoiled plasmid DNA by 55 (50-250 μ M) in the presence of
NADPH:cytochrome P450 reductase as an activating system105
Figure 4.3. Cleavage of supercoiled plasmid DNA by 60 (50-250 μ M) in the presence of
NADPH:cytochrome P450 reductase as an activating system105
Figure 4.4. Comparison of DNA cleavage by reductively activated 33 , 55 and 60 under
anaerobic conditions
Figure 4.5. Cleavage of supercoiled plasmid DNA by $33 (25 \ \mu M)$ in the presence of
NADPH:cytochrome P450 reductase as an activating system is reduced by radical
scavengers

Figure 4.6. Cleavage of supercoiled plasmid DNA by $55 (50 \ \mu M)$ in the presence of
NADPH:cytochrome P450 reductase as an activating system is reduced by radical
scavengers109
Figure 4.7. Cleavage of supercoiled plasmid DNA by $60 (50 \ \mu M)$ in the presence of
NADPH:cytochrome P450 reductase as an activating system is reduced by radical
scavengers110
Figure 4.8. Comparison of DNA cleavage by reductively activated 33 , 55 or 60
under anaerobic conditions and DNA cleavage is reduced by radical scavengers
Figure 4.9. LC/MS analysis of anaerobic metabolism of 55 and 60 (0.5 mM) by
cytochrome p450 reductase (0.4 U/mL)/NADPH (0.5 mM)113
Figure 4.10. LC/MS analysis of authentic 60 , 63 , 55 and 59 114
Figure 4.11. HRMS of the major metabolite 1- <i>N</i> -oxide 59 arising from metabolism of 60
under reductively activated conditions in hypoxia116
Figure 4.12. HRMS of the major metabolite 1- <i>N</i> -oxide 63 arising from metabolism of 60
under reductively activated conditions in hypoxia

LIST OF TABLES

Chapter 2	
Table 2.1. NMR Data (CDCl ₃) for compound 44	31
Chapter 4	
Table 4.1. Cleavage of plasmid DNA in control reactions	07

Compound structure	Number
	1
	2
	3
	4
	5
NO ₂ OH N N N Br	6
NO ₂ HN N	7
NO ₂ HN N	8
	9

Compound structure	Number
	10
O_2N H OPO_3^{-2} OPO_3	11
H_2 O_2N N O_2N N OPO_3^{-2} OPO_3^{-2} OPO_3^{-2}	12
$ \begin{array}{c} $	13
$\begin{array}{c c} & O \\ & \\ & \\ & \\ & \\ & \\ & \\ & \\ & \\ &$	14
HOHN N HNH Br	15

Compound structure	Number
	16
HO-P-N Br HN H Br	17
$ \begin{array}{c} $	18
	19
$ \begin{array}{c} $	20
	21
$H_{2}N$ P HO $N(CH_{2}CH_{2}CI)_{2}$	22
EtO O O CI O-P-N NH ₂ CI	23
$ \begin{array}{c} EtO & O & CI \\ H & O - P - N & \\ N & H_2 & CI \\ H_2N & & \\$	24
EtO O H N H ₂ N	25

Compound structure	Number
	26
$O_2 N O_2 O_2 N O_2 O_2 N O_2 O_2 N O_2 O_2 O_2 O_2 O_2 O_2 O_2 O_2 O_2 O_2$	27
$O_2 N \underbrace{S}_{O_2} N \underbrace{S}_{O_2}$	28
	29
O_2N S O O O O	30
$O_2 N \xrightarrow{N=} S \xrightarrow{N=} N$	31
O N O DNA	32

Compound structure	Number
$ \begin{array}{c} $	33
	34
	35
N N N NH ₂	36
$ \begin{array}{c} $	37
$ \begin{array}{c} $	38
	39

Compound structure	Number
	40
	41
	42
H ₂ N N	43
	44
	45
	46

Compound structure	Number
	47
	48
NO	49
NHOH	50
O NO2	51
	52
	53

Compound structure	Number
H ₂ N N H O	54
$ \begin{array}{c} $	55
	56
O ⁻ N ⁺ N N H OH	57
	58
	59
$ \begin{array}{c} $	60

Compound structure	Number
	61
O ⁻ N ⁺ N · N OH	62
	63
	64
	65
N N H	66
	67

Compound structure	Number
O ₂ N-	68
нобосо	69
	70
o s	71
HO	72
	73
	74
ONa	75
	76

Compound structure	Number
	77
	78
	79
$O_2 N $ N O O O O	80
O_2N	81
	82
	83
$ \begin{array}{c} $	84

ABSTRACT

Hypoxia in tumors causes adverse effects to therapy and negatively impacts on patient prognosis. Identification and quantification of hypoxia is considered to have a strong impact on treatments in tumor therapy. Fluorescent-based detection to mark hypoxia may be vital to be used along with available methods such as radiochemical and immunohistochemical staining.

In this work, the non-fluorescent 6-nitroquinoline (**42**) was used to investigate the production of a fluorescent 6-aminoquinoline (**43**) and other metabolites under bioreducing hypoxic conditions. In the presence of the enzymatic reducing system NADPH:cytochrome P450 reductase/NADPH, 6-nitroquinoline (**42**) produced the fluorescent helicene (**44**), along with the non-florescent azo (**45**). An authentic sample of (**44**) was chemically synthesized and characterized and used to confirm the production of this molecule in the enzymatic process. Interestingly, the expected fluorophore (**43**) is not produced by NADPH:cytochrome P450 reductase/NADPH.

In another study, the enzymatic reducing system xanthine/xanthine oxidase was used to reduce (42) under hypoxia to obtain (43). In these experiments (43) was produced and the yield is increased with xanthine concentration. Metabolic identification revealed that intermediates of typical nitro reduction pathway are present along with 6-nitroquinolone (51).which is formed by xanthine oxidase mediated oxidation of (42). The absence of (44) as a metabolite with xanthine/xanthine oxidase system highlights the complexity of bio-reduction of nitroaromatics under hypoxia.

In our laboratory, bio-activation of di-*N*-oxides such as tirapazamine (TPZ, **42**) has been studied. TPZ undergoes one-electron bio-reduction to produce oxidizing radical, which causes DNA damage under hypoxia. In our laboratory, the mechanism by which TPZ mediated DNA damage has been investigated using TPZ and its analogs.

Our evidence suggests that upon undergoing bio-reduction, TPZ produces hydroxyl radical as the DNA damaging radical species. Others have suggested another mechanism, which proposes the formation benzotriazine radical (**38**) upon dehydration process over the bioreduction step. In the current work, TPZ analog 1,2,4-benzotraizine-1,4-dioxide (**55**) and deuterated (**60**) were used to test the dehydration mechanism. Isotopic content analysis of metabolites, derived from bio-reducing metabolism of (**55**) and its deuterated analog (**60**), using HRMS show evidence against the dehydration mechanism.

Chapter 1

Nitroaromatics and *N*-oxide compounds as radiosensitizers, oxygen sensors and cytotoxic agents in tumor therapy

1.1 Hypoxia.

Low oxygen levels (hypoxia) is considered as an important physiological factor in tumor biology.¹ The oxygen concentration, found in a normal tissue falls within a range of 20 μ M to 90 μ M.² It is well established that solid tumors contain cell populations having low oxygen concentrations.³ Hypoxia is the end physiological result, caused by the presence of irregular vasculature in tumors.⁴ The inconsistent blood flow in tumors may produce acute or chronic hypoxia.¹ Hypoxic conditions can diminish effects of ionizing radiation mediated tumor therapy.⁵ Ionizing radiation is a key method in tumor therapy and hypoxia has drawn attention as a challenge which should be addressed to achieve clinical success.⁶

1.2 Ionizing radiation therapy

In the presence of ionizing radiation water molecules break down to form highly reactive, oxidizing hydroxyl radicals (Scheme 1.1).⁷

 $H_2O \xrightarrow{\text{radiolysis}} e_{aq}^- + OH^- + H^- + H_2 + H_2O_2$

Scheme 1.1. Gamma radiolysis generates radical species

The hydroxyl radical is able to abstract hydrogen from organic substrates such as DNA, which can cause cell death (Scheme 1.2).⁸

Scheme 1.2. Hydroxyl radical abstract hydrogen from DNA

The oxidative abstraction of hydrogen atoms from DNA produces DNA radicals.⁹ DNA radicals can be created on the DNA bases or on sugar phosphate backbone. DNA radicals, formed on thymidine or guanine DNA bases would develop into strand breaks.¹⁰ The hydrogen atom abstraction, which occurs on the sugar phosphate backbone produces carbon centered radicals on C1', C2', C3', C4'and C5'corbons and oxygen is required to make the radical damage permanent and induce strand breaks.⁹ The radical fixation, which is mediated by oxygen on DNA backbone carbon radicals, produces characteristic DNA lesions.¹¹ The damage, on C4' and C5'carbons, produces 3'-phosphoglycolate and strand breaks (Scheme 1.3).¹²



Scheme 1.3. DNA radical on C4' is fixed by oxygen

Formation of a ribonolactone occurs when oxygen fixes a C1' DNA radical.¹³ Under basic conditions **1**, ribonolactone undergo elimination to yield strand breaks. (Scheme 1.4).⁸



Scheme 1.4. Formation of ribonolactone

Once the DNA damage, either on backbone or DNA base, is made permanent by producing stand breaks, a cascade of cellular events triggers cell death.¹⁴

Under hypoxic conditions, the low oxygen levels diminish DNA radical fixation.³ Hence DNA radical-mediated cell death might not occur in solid tumors.¹⁵ It is noted that the DNA radicals created by ionizing radiation would be trapped by cellular thiols such as glutathione.^{7, 16} The chemical repair of DNA damage by thiols under low oxygen levels may cause the tumor cell resistance to radiation therapy.¹³ The cellular glutathione levels are present in millimolar levels under physiological conditions (Scheme 1.5).⁷



Scheme 1.5. Thiols can repair DNA radical damage

Accordingly, the fate of DNA radicals in tumors depends on the oxygen concentration of the cell.⁸ The lack of oxygen causes tumor cell to resist radiation therapy.³ Thus there was a need for alternative agents that can fix DNA radicals under low oxygen concentrations to potentiate radiation therapy.

1.3 Radiosensitizing oxygen mimetic agents

In an effort to reduce tumor cell resistance to radiation therapy, investigations have been carried out to find agents that can mimic the behavior of oxygen in radiotherapy.¹⁷ As a part of the search nitro aromatic and *N*-oxide drugs have been tested as radiosensitizing agents to accompany radiotherapy in treatments.^{17b}

Potential agents such as TEMPO and misonidazole, **2** were tested in cytotoxicity assays with radiation.¹⁸ Nitroaromatics became the leading candidates in the search for radiation sensitizing agent.^{17a} The sensitizing capacity of nitroaromatics can be radical fixation which can occur through oxygen mimetic ability of nitro group. Or the ability of nitro group to undergo reduction to form amine can be contribute for the radiation sensitivity.^{17a} The higher electron affinity of nitroaromatic compounds can facilitate oxidation of DNA from which the charge distribution has been altered by radiolysis.¹⁹ This can produce DNA radical cations and oxygen sensitive nitroradicals which oxidize back to parent nitro group in the presence of oxygen (Scheme 1.6).¹⁰



Scheme 1.6. Radiolysis induced nitro-reduction and DNA radical formation

There is evidence for donation of an oxygen atom from a nitro group to a DNA radical.²⁰ Goldberg and researchers used an ¹⁸O-labeled nitro group containing

misonidazole **2** and DNA radical precursors in his ¹⁸O-incorporation experiments. When misonidazole interacts with C5' DNA radical, nitroxide intermediate forms, followed by fragmentation caused strand breaks (Scheme 1.7).²¹



Scheme 1.7. Oxygen of nitro group is donated to DNA

Further studies on misonidazole-mediated radionsensitization revealed that **2** causes toxicity without ionizing radiation.²² The higher electron affinity of nitroaromatic compounds makes them substrate for cellular reductases.²³ It was suggested that cellular reducing systems such as NADPH cytochrome P450 reductase may reduce nitro group to hydroxylamine and to amine groups via six consecutive e⁻ reduction steps under hypoxic conditions (Scheme 1.8).²⁴

$$Ar - NO_2 \xrightarrow{e^-} Ar - NO_2 \xrightarrow{e^-} Ar - NO \xrightarrow{e^-} Ar - NOH \xrightarrow{$$

Scheme 1.8. Enzyme mediated Nitro reduction undergo in hypoxia

The hydroxylamine intermediate may cause cytotoxicity by forming reactive intermediates.²⁵ The reduction of 2-nitro-5-alkyl-nitroimidazole **3** would produce the hydroxylamine and then converts to the glyoxal-dialdehyde **4** form which may alkylate nucleophilic sites on DNA (Scheme 1.9).²⁶

$$NO_{2}$$

$$NO_{2}$$

$$NH$$

$$NH$$

$$NH$$

$$NH$$

$$NH$$

$$NH$$

$$NH$$

$$H^{+}$$

$$NH$$

$$H^{+}$$

$$NH$$

$$H^{+}$$

$$H^{+}$$

$$H^{+}$$

$$H^{+}$$

$$H_{2}$$

$$H_{2}N$$

$$NHR$$

$$H_{2}$$

$$H_{2}N$$

$$H_{2}$$

$$H_{2$$

Scheme 1.9. Hydroxylamine produces glyoxal-dialdehyde alkylator 4

The clinical test, carried out using 2 produced neurotoxicity among patients. The observed toxicity may have arisen due to the formation of hydroxylamine intermediate.

1.3.1 Nitroaromatic reduction in hypoxic cells

Studies on reduction of nitroaromatic-radiosensitizing drugs established nitro reduction mechanism which may occur in cells.^{17a, 27} The stepwise electron addition would produce the hydroxylamine intermediate. Further reduction produces the amino product.²⁸ The nitro group reduction is mediated by cellular enzymes such as NADPH cytochrome P450 reductase, xanthine oxidase, nitroreductases and DT diaphorase.^{17a, 24} These enzymes can be overexpressed or already abundant in tumor environment.^{27, 29} The hypoxic conditions in tumors would permit sequential e- reduction to occur and produce reduced metabolites such as hydroxylamine and amine.³⁰ The enzyme-mediated functional group transition from nitro to hydroxylamine has been considered as an electronic switch.²⁷ The electron poor nitro group is converted to an electron rich hydroxylamine, and further reduction produces the amine moiety.³¹ For some drug candidates electron rich hydroxylamine represents the active form of the drug to be effective in tumor cells.³² The first nitro imidazole aziridine containing agent RSU1069, 5, explored hypoxia selective, redox activated generation of an alkylating agent.³³ Similar nitro-imidazole-containing mustards such as RB6145 6 and 5 were tested in tumor cells.³⁴ In addition to mustard-type alkylating agents, DNA intercalating moieties such as acridine **7** and quinoline **8** groups were used as bio reductively activated agents. Upon bio-reduction, the intercalating ability of amine compounds of **7** and **8** is enhanced to cause interferences during DNA replication (Scheme 1.10).³⁵



Scheme 1.10. Nitro aromatics reduction in hypoxia produces the active drug

Mustard groups have been attached to nitrophenyl moiety, as a continuation of efforts to develop nitroaryl-aziridine conjugates.³⁶ Nitrobenzene aziridines CB 1954, **9**, SN 23862, **10**, and PR 104, **11** explore nitro reduction as the mean of mustard activation in tumor cells (Scheme 1.11).³⁷





The aziridine alkylating moiety would attain greater activity upon the reduction of nitro group to amine group under hypoxia. Specific enzymes such as *E. coli* nitroreductases has been used as the reducing enzyme under gene directed enzyme prodrug therapy GDEPT to test nitrobenzyl mustard 9^{32} In addition, DT diaphorase has been used with nitrophenyl-aziridines and nitrogen mustards to test the enhanced selectivity toward hypoxia and improved cytotoxicity.³⁸ In the mechanism, of which nitroaryl-mustards attain activity, nitro compound **11** undergoes reduction to produce amine **12**.


Scheme 1.12. Nitrophenyl-mustard alkylating agents

1.3.2 Elimination of active agent through nitroaromatic reduction

The electronic properties of a molecule can undergo a major shift when a pendent nitro group is reduced to the respective hydroxylamine and to the amine group in hypoxia mediated by cellular reductases. The increase of electron density on hydroxylamine nitrogen has been employed release an active agent. The active drug is attached to a suitable nitro aromatic group in its prodrug form.⁴⁰ The activity of the agent is diminished or masked due to the ligation with the nitro aromatic group. The structural difference of conjugate **14**, nitroimidazole-phosphoramidate to the active agent **17**, a phosphoramidate, may cause the reduced effect of drug.⁴¹ Once the nitro group on **14** is reduced in hypoxia, to the hydroxylamine group bearing **15**, the enhanced electron density on nitrogen of hydroxylamine will eject the active agent **17**, which is a good leaving group.⁴² This electron movement will trigger covalent bond scission, which releases the active drug **17** from the pro-drug complex (Scheme 1.13) while forming imine methide **16**.⁴³



Scheme 1.13. Hydroxylamine releases the active drug

The phosphoramidate **17** can form aziridine, which acts as an electrophile that can alkylate cellular nucleophiles (Scheme 1.14).



Scheme 1.14. Phosphoramidate forms azide upon elimination of leaving group

There are number of nitroaromatic-prodrugs designed to carry phosphoramide toxins, structurally and functionally similar to phosphoramidate, such as **18** to cells. The parent cyclophosphoramide drug **18** has been widely used anti-cancer agent with excellent toxicity toward various tumor types.⁴⁴ Although the positive results were encouraging, the parent cyclophosphamide showed lethal side effect, occurred due to release of acrolein **21** along the CYP₄₅₀-mediated metabolic pathway via forming intermediates **19** and **20** (Scheme 1.15).⁴⁵



Scheme 1.15. Cyclophophoramide 18 metabolism by CYP_{450}

Delivering phosphoramide, 22, selectively to tumor is considered important in order to avoid such toxicity reported with 18.⁴⁶ The nitroquinoline-phosphoramide mustard 23 was developed as a pro-drug to test the ejection of phosphoramide toxin 22. Upon the reduction of the nitro group on quinoline, the electron rich quinoline nitrogen on 24 triggers beta elimination of 22 leaving 25 as a metabolite. Tenfold increase of cytotoxicity was observed in hypoxia and evidence for alkylation occurred by

phosphoramide confirmed the expected release of phosphoramide **22** upon nitro reduction (Scheme 1.16).⁴⁰



Scheme 1.16. Nitroquinoline-phosphoramide prodrug release

Other nitro-aromatics nitrobenzyl, nitrofuryl and nitrothienyl have been used as bio-reducible triggers for conjugation with phosphoramides. These prodrugs, constructed from tagging phosphoramide with nitroaromatics have shown encouraging results; low cytotoxicity but enhanced tumor selectivity. Compound **24** generated DNA interstrand cross links in hypoxic HT-29 cells, with a selectivity ratio of 90.⁴⁷ Nitrophenyl **26**, nitrofuryl **27** and nitrothienyl **28** derivatives show low toxicity in aerobic assays (Scheme 1.17).⁴⁸



Scheme 1.17. Nitrophenyl, Nitrofuryl and nitrothienyl phosphoramide conjugates

In addition to the phosphoramide mustards, various anti-cancer agents are conjugated to nitroaromatics. Combrestatin, **29** and its nitrothienyl couple **30**, and nitrophenyl-mercaptopurine prodrug **31** have shown effective release of agent upon bioreduction (Scheme 1.18).⁴⁹



Scheme 1.18. Nitrothienyl and nitrophenyl dimethyl prodrugs

The importance of nitroaromatic reduction in tumor therapy and prodrug designing is well established in medicinal chemistry and bioorganic chemistry. In the coming chapters, interesting metabolic and fluorescence studies on 6-nitroquinoline reduction will be discussed. Moreover, the oxygen sensitivity of 6-nitroquinoline reduction, under two enzymatic reducing systems will be presented. Several novel findings related to the 6-nitroquinoline reduction will add complexity to enzyme mediated nitroaromatic reduction in hypoxia.

1.4. *N*-oxides

Investigations carried out to develop radio sensitizing agents tested nitroxyl radical TEMPO. It has been discovered that TEMPO connects with the DNA radical, which is formed by radiolysis under hypoxia to produce DNA adduct **32**.¹⁸ In search for backups to *N*-oxide radiosensitizing agents, Brown and coworkers tested tirapazamine (TPZ), *N*-oxide **33** as an oxygen mimetic agent in radiolysis of cells. They found that **33** was toxic as a single agent and the cytotoxicity was 200 fold higher for hypoxic cells.⁵⁰ The anti-cancer properties shown by **33** in the absence of γ radiation was stirred interest and the mechanism for the anti-tumor activity of **33** has been subjected further for research (Scheme 1.19).⁵¹





TPZ is believed to be activated by enzyme systems such as cytochrome P450 and cytochrome P450 reductase, xanthine and xanthine oxidase, aldehyde oxidase and nitric oxide synthase in cells.⁵² The activation produces a TPZ radical which back oxidizes to the parent TPZ by oxygen under aerobic conditions to produce superoxide radical.^{23, 50, 53} The superoxide radical disproportionate to yield hydrogen peroxide by super oxide dismutase (SOD) and hydrogen peroxide is converted to water and hydroxide ion by catalase (CAT).²³ Unless the superoxide radical is handled consecutively by SOD and CAT, radical-mediated oxidative damage may occur to biomolecules.²³ Under hypoxia, the TPZ radical **34** persists and produces an oxidizing radical which cause DNA damage.^{51, 54} The in vivo enzymatic reduction process produces metabolites **35**, the major metabolite and **36** (Scheme 1.20).⁵⁵



Scheme 1.20. Enzyme mediated reduction of 33 in hypoxia

The DNA damage resulted by TPZ in hypoxia is believed to cause cytotoxicity in tumors.⁵⁶ The mechanism of TPZ-mediated DNA damage is not properly understood.⁵⁷ There are three mechanisms proposed to describe the nature of the DNA damaging species.⁵⁸

The neutral benzotriazine dioxide radical **34**, formed from **37** upon enzymatic reduction of **33** has been proposed by Brown's group as the oxidizing species which causes the DNA damage.⁵⁹ In this proposal, a proton on DNA is abstracted by **34** to form **38**. A dehydration event proceeds via **38** to release water and **35** (Scheme 1.21).⁶⁰



Scheme 1.21. Enzyme mediated reduction of 33 in hypoxia abstract proton from DNA, followed by dehydration releases 35 as the major metabolite

Alternatively, a homolytic bond scission of N-OH bond in neutral benzotriazine dioxide radical **34** can form a hydroxyl radical and the major metabolite **35** (Scheme 1.22 upper arm).⁶¹The hydroxyl radical, released from **34** is capable of performing oxidative damage on DNA.⁶² Oxidative DNA damage occurs in tumor cells can initiate a cascade of events which result in cytotoxicity.⁶³ Denny and co-workers suggest a mechanism based on dehydration that might occur on the neutral benzotriazine di-oxide radical **34** forms a benzotriazinyl 1-oxide radical (structures **39**, **40** and **41**) which is responsible for the DNA damage (Scheme 1.22 lower arm).⁶⁴



Scheme 1.22. The enzyme mediated reduction of 33 in hypoxia may produce hydroxyl radical or benzotriazine radicals 39, 40 or 41 as the oxidizing species

Research carried out by our group support the mechanism involving hydroxyl radical mediated DNA damage.⁶⁵

1.5. Summary

Nitroaromatic compounds have become a prominent drug class in medicinal chemistry research.⁶⁶ The nitroaromatic reduction that occurs in low oxygen concentrations is mediated by reductive enzymes and has become an attractive concept in bioreductive prodrug therapy.⁵⁸ Nitroaromatic reduction reactions are complex due to the presence of various intermediates and byproducts.⁶⁷ The work presented in this thesis describes the use of small molecule 6-nitroquinoline as a fluorescent probe that can detect hypoxia.⁶⁸ A rich metabolic study is accompanying the fluorescent results in coming chapters. In addition the lead *N*-oxide tirapazamine, which has been in phase trials I, II and III for clinical therapy over a decade and its analogs were used to study the DNA-

damaging mechanism of *N*-oxides.⁶⁹ The chemical basis for the DNA damage, caused by **33** depends on the reduction mechanism of these di-oxide.⁶⁵ The chemical nature of the DNA-damaging species has become an interesting topic in research. In the current thesis, a mechanistic study is presented analyze the reduction mechanism and the chemical nature of the oxidizing species.

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Chapter 2

Hypoxia-selective, enzymatic conversion of 6-nitroquinoline into a fluorescent helicene: pyrido[3,2-f]quinolino[6,5-c]cinnoline 3-oxide

2.1 Hypoxia as a parameter to be determined qualitatively and quantitatively.

Hypoxia or low oxygen concentrations exist in disease conditions such as ischemia, stroke, inflammation and solid tumors, and in normal human physiology.¹ Transient regions of hypoxia, reportedly present in stem tissues may have an effect on controlling cell division and differentiation during hematopoiesis and embryogenesis.²

Oxygen concentration in a normal healthy cell is within a range of 20 to 90 μ M (14–65 mm Hg).³ Any concentration below 20 μ M is considered hypoxia.⁴ Efforts were made to quantify hypoxia using an oxy probe, radiochemical imaging and immunohistochemical staining methods.⁵ Practical and technical difficulties limit accuracy and applicability of these techniques.⁶ Hence, there is a demand for a noninvasive tool which can qualitatively and quantitatively characterize tumor hypoxia in biological conditions. Fluorescent probes can be designed to light up inside the hypoxic tumor under physiological conditions, and the fluorescence outcome can be used as a parameter that can be measured and relate to the oxygen concentration of tumors.⁷

2.2 Fluorescent probes to detect hypoxia

Several approaches have been used to deliver a fluorescent agent into the tumor setting to mark hypoxic tissues. One method is to use nitro-aromatic non-fluorescent compound which converts to a fluorescent amino metabolite under hypoxic conditions.⁷⁻⁸ Enzyme mediated cellular reduction of nitroaromatics, under low oxygen levels, has been reported and developed as a concept in biochemical research. The reduction process consists of consecutive addition of six electrons, in a stepwise manner to produce the final reduced product, the respective arylamine.⁹ The hypoxia selectivity arises within the first reduction step where the nitro radical anion back-oxidizes to the parent nitro compound in the presence of oxygen.^{9d, e, 10} The first electron addition step is oxygen sensitive and the remaining one electron addition steps may be oxygen sensitive. Niroso compound would next be converted to hydroxylamine intermediate by adding two electrons and in the final two electrons addition produces the amino product. (Scheme 2.1).¹¹

$$\operatorname{ArNO}_{2} \xrightarrow[-1e^{-}]{} \operatorname{ArNO}_{2} \xrightarrow{-1e^{-}} \operatorname{ArNO}_{2} \xrightarrow{-1e^{-}} \operatorname{ArNO} \xrightarrow{+1e^{-}} \operatorname{ArNOH} \xrightarrow{+1e^{-}} \operatorname{ArNHOH} \xrightarrow{+1e^{-}} \operatorname{ArNHOH} \xrightarrow{+1e^{-}} \operatorname{ArNH}_{2} \xrightarrow{-1e^{-}} \operatorname{ArNH$$

Scheme 2.1. Enzymatic reduction profile of nitroaromatic compound

2.3 Reduction of 42 to obtain 43 under anaerobic conditions

Non-fluorescent nitroaromatic compound 6-nitroquinoline **42** was used as a small molecule nitroaromatic probe to detect hypoxia. The compound **42** may be reduced under low oxygen levels and under bio-reductive conditions to produce fluorescent metabolite, 6-aminoquinoline (**43**, Scheme 2.2)



Scheme 2.2. Hypoxic metabolism of 42 is expected to form fluorescent 43

The amino compound 43 is a known fluorescent molecule and the reduction of 42 to 43 step yields a good Strokes shift of 205 nm.¹² The probe 42 is non-fluorescent in aqueous sodium phosphate buffer at pH 7.4 (Figure 1A, column 1).¹¹ The enzyme NADPH:cytochrome P450 reductase, a known reductase that reduces nitrocompounds in cells is used as the reducing enzyme with assistance of the substrate NADPH to reduce 42 under hypoxia.^{9c, 13} The hypoxic reduction reaction forms fluorescence with an impressive 63-fold increase at 445 nm, indicating conversion of the non-fluorescent 42 to a fluorescent metabolite (Figure 1A, column 5). The enzymatic reduction of 42 under aerobic conditions produced no fluorescence (Figure 1A, column 4). Similarly, when non fluorescent electron acceptor benzotriazine 1,2,4-di-oxide was used in aerobic and anaerobic enzymatic reduction reactions, very low fluorescence was observed (Figure 1A, columns 2 and 3). Careful inspection of the shape of the fluorescent curve in Figure 1, column 5 showed that the fluorescence emission curve does not resemble the fluorescence curve of authentic 43. The fluorescence emission curve of 43 is broader at 445 nm and 530 nm regions (Figure 1B blue line) and, instead consists of a pair of emission maxima at 440 and 460 nm. The unexpected fluorescence, yielded in the hypoxic metabolism of 42, was explored to identify and characterize the fluorescent metabolite.



Figure 2.1. Enzymatic conversion of 42 into a fluorescent product under hypoxic conditions. A. Fluorescence emission at 445 nm (λ ex 307 nm) for: (1) a control sample of compound 42 alone (0.8 mM), (2) a control reaction composed of NADPH:cytochrome P450 reductase (1.1 U/mL), NADPH (2.4 mM), and a non-fluorescent electron acceptor 1,2,4-benzotriazine 1,4-dioxide (6.4 mM) under aerobic conditions, (3) a control reaction composed of NADPH:cytochrome P450 reductase, NADPH, and a non-fluorescent electron acceptor 1,2,4-benzotriazine 1,4-dioxide (6.4 mM) under anaerobic conditions, (4) compound 42 (0.8 mM) + NADPH:cytochrome P450 reductase and NADPH under aerobic conditions, (5) compound 42 (0.8 mM) + cytochrome P450 reductase and NADPH anaerobic. Reactions were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C, then diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4) and the fluorescence measured (λ_{ex} 307 nm, λ_{em} 445 nm). It is important to note that NADPH exhibits fluorescence with an emission maximum at 445 nm. However, control experiments showed that any NADPH left unconsumed at the end of the anaerobic reactions described here is ultimately converted to the non-fluorescent NADP+ product by enzyme-driven redox cycling of the electron accepting organic substrate upon opening the reaction vessel to air and dilution with aerobic buffer prior to fluorescence measurements. B. Fluorescence spectrum of the reaction mixture generated in the anaerobic metabolism of 42 by NADPH:cytochrome P450 reductase as described for reaction 5 above (orange line, with emission maxima at 440 and 450 nm) and fluorescence spectrum of 6-aminoquinoline (43, 50 μ M, λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4).¹¹

2.4 Identification of products arising from the anaerobic reaction

The anaerobic reaction mixture of metabolism of **42**, mediated by NADPH:cytochrome P450 reductase was analyzed using LC/MS. Two major products were identified in addition to the remaining starting material **42** (Figure 2.2 A). Confirming the analysis of the fluorescence spectrum of the anaerobic reaction mixture, **43**, the product expected by the original six electron reduction process was not observed in the LC/MS analysis. Under the same LC/MS conditions **43** appears at approximately 4.5 min (Figure S1). One of the products, eluting at 19.4 min in the UV trace has m/z

value of 301 (Figure 2.2 B). The [M+H]⁺ ion of 6,6'-azoxyquinoline would have a massto-charge ratio of 301 (**45**, Scheme 2.2). Formation of **45** under relevant conditions is expected to be produced, based on precedents which suggest condensation of intermediates 6-nitrosoquinoline and 6-hydroxylaminoquinoline that are formed along the reduction path.¹⁴ An authentic sample of **45**, synthesized from reducing **42** by hydrazine hydrate in the presence of Raney nickel gave similar LC/MS spectra with a peak at 19.4 min (Figures 2.2 E and F).¹⁵ Compound **45** is non-fluorescent under the applied conditions in the solution. Hence the fluorescence should arise from the product appearing at 15 min in the LC trace. There is evidence that complex dimmers such as **44** could be fluorescent.¹⁶ The mass-to-charge ratio of the new product was 299 (Figure 2.2 C). A simple, quinoline dimer such as azoxy or azo does not have a m/z of 299, rather a more complex quinoline-based bi aryl compound such as pyrido[3,2-*f*]quinolino[6,5*c*]cinnoline 3-oxide (**44**, Scheme 2.3) or dipyrido[3,2-a:3',2'-h]phenazine 7-oxide (**46**, Scheme 2.3) does have the observed m/z value.



Figure 2.2. LC/MS analysis of the reaction mixture generated by anaerobic metabolism of **42** (0.8 mM) by cytochrome p450 reductase (1.1 U/mL) and NADPH (6.4 mM). The enzymatic reduction of **42** was carried out as described in the experimental section and the legend of Figure 2.1. The reaction was dried and products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC of the anaerobic reaction mixture monitoring absorbance at 254 nm. Panel B: LC/MS spectrum of the product eluting at 19.1 min. Panel C: LC/MS spectrum of the product eluting at 15.1 min. Panel D: LC/MS spectrum for of the product eluting at 17.1 min. Panel E: HPLC retention time of authentic **45** monitoring absorbance at 254 nm. Panel G: HPLC retention time of authentic **44** monitoring absorbance at 254 nm. Panel H: LC/MS spectrum of authentic **44**.



Scheme 2.3. Metabolites formed by the reduction of 42 with NADPH/CYP450R

According to precedents, helicenes are structurally similar to **44**, and are fluorescent.¹⁶ Hence, the enzymatic reduction of **42**, under above condition might be producing **44**.The two structures **44** and **46** have same molecular formula. Huisgen proposed that compound **44** is formed in a reaction when **42** is reduced by sodium methoxide.¹⁷ Farrar claimed that Huisgen was obtaining compound **46**, not **44**.¹⁸ Moreover, Farrar carried out reduction of **42**, with alkaline glucose as suggested by Galbraith *et al* to produce **45**. Farrar claimed that alkaline glucose mediated reduction of **42** actually produces **44** not **45**.¹⁸

2.4 Synthesis and structural characterization of 44

Galbraith's alkaline glucose reduction of **42** has been successfully used as the chemical method to synthesize **44**.¹⁹ The thin layer chromatographic (TLC) properties of the product of enzymatic reduction of **42** are compared with that of the product, obtained by the chemical synthesis. The blue fluorescent product showed similar migration with different solvent systems on TLC, suggesting two different reactions produce the same chemical product. Hence, we separated the suspected product from the chemical synthesis by preparative TLC and carried out full spectroscopic characterization (see materials and methods). The molecular formula obtained from a high-resolution mass

spectrometric analysis of product, formed by alkaline glucose reduction of 42, matches with structures 44 or 46. Presence of 18 different ¹³C resonances suggested that the dimmer is not symmetric, but rather contains a complex asymmetric structure. The ¹H NMR analysis showed ten hydrogen resonances; aryl-aryl bridge between two quinoline molecules might be present in the structure. The 5 proton of 46 was expected to be downfielded to \geq 9.3 ppm due to its proximity to the N-oxide oxygen (We used a quinolone based numbering system in the section).²⁰ In the product, a resonance at 9.3 ppm is absent. The fluorescence of enzymatic metabolite and NMR properties are supportive of 44 as the possible structure for the metabolite. Moreover, COSY and TOCSY spectra analysis allowed assigning resonances for 4 and 4' protons for structure 44. NOE experiment results showed a correlation between 4 and 4' protons that arises due to close proximity between two protons. The NOE correlation between 4 and 4'can be only present in 44. In 46, the protons 4 and 4' are unable to produce NOE resonance. Ultimately, the actual structure obtained from alkaline glucose reduction of 42 shows the distance between protons 4 and 4' is 2.5 Å (Figure 4).

The NMR data obtained from the enzymatically synthesized **44** was compared with the NMRs of chemically synthesized **44**. The ¹H NMR resonances and peak shifts obtained from the enzymatic reaction matched with that obtained from the glucose reduction. NOE spectrum of the enzymatic product shows a correlation between 4 and 4' protons, similar to the NOE result obtained from the glucose reduction. This observation confirms that product **44** is the metabolite produced in the anaerobic enzymatic reaction. The complete NMR analysis including TOCSY, COSY, HMQC, and HMBC data were consistent with the azoxy-helicene **44** (Table 1).

position	$\delta_{\rm C}$	$\delta_{\rm H}({\rm J~in~Hz})$	COSY	TOCSY	HMBC ^a	NOE
2'	153.4	9.15 1H, d (4.5)	3'	3', 4'	4', 8a'	3'
2	151.5	9.05 1H, m	3	3, 4	4, 8a	3
3'	120.5	7.46 1H, dd (9.0, 4.5)	2', 4'	2', 4'	4a'	2', 4'
3	120.7	7.41 1H, dd (9.0, 4.5)	2, 4	2, 4	4a	2, 4
4'	136.0	8.87 1H, d (9.0)	3'	3', 2'	2', 8a'	4
4	134.8	8.67 1H, d (9.0)	3	3, 2	2, 8a	4'
5'	128.0					
5	114.2					
4'a	123.4					
4a	123.5					
7'	121.8	9.05 1H, m	8'	8'	8a', 5'	8'
7	127.4	8.23 1H, d (9.0)	8	8	8a, 5	8
8'	133.4	8.43 1H, d (9.0)	7'	7'	6', 4a'	7'
8	134.3	8.41 1H, d (9.0)	7	7	6, 4a	7
6'	137.1					
6	144.1					
8'a	149.7					
8a	148.5					

 Table 1. NMR Data (CDCl₃) for compound 44^aHMBC correlations are from the proton to the stated carbon(s).

The ultimate confirmation of the structure **44** was carried out by X-ray crystallographic analysis (Figure 2.3).²¹



Figure 2.3. In 44, the 4 and 4'-hydrogens (see numbering system in Scheme 2.2) are close in space¹¹

In summary, the spectroscopic and crystallographic characterization of **44** arising from the alkaline glucose reduction is consistent with Farrar's claim; **44** produced in the alkaline glucose reduction of **42**. More importantly **44**, produced by alkaline glucose method used as an authentic compound for comparison with the enzymatically produced **44**. LC/MS properties of **44**, produced under chemical and enzymatic methods showed matching retention times and m/z results (Figure 2.2). The ¹H NMR analysis of the enzyme product resembles the authentic compound **44**, made by the glucose reduction reaction. In addition, NOE experiment clearly shows the close distance between 4 and 4' protons of enzymatically-generated **44**. The fluorescence spectrum of **44**, obtained from the glucose reduction (Figure 2.4) resembles the fluorescence spectrum obtained from the

enzymatic reaction (Figure 2B). Close analysis of the spectra shows the similarity of emission maxima at 440 and 460 nm of both curves (Figure 2.1 and 2.4).



Figure 2.4. Fluorescence spectrum of authentic 45 (50 μ M, λ ex 307 nm) in sodium phosphate buffer (12 mM, pH 7.4).

The azoxy functional group is known to be reduced to the corresponding azo group by NADPH:cytochrome P450 reductase.²² In this particular reaction compound **45** is not reduced to an azo product.



Scheme 2.4. Mechanism for the formation of 44 under anaerobic conditions

2.5 Conclusion

In conclusion, intermediate hydroxylamino or amino product were not observed in NADPH:cytochrome P450 reductase mediated reduction of **42** under hypoxic conditions. The azoxy compound **45** and the bi aryl bonded dimer **44** were formed under reductive conditions. The mechanism for the formation of **44** in the enzymatic reaction is complex. A possible pathway can be initiated when a nitroaryl radical **47** and a nitrosoaryl radical **48** are condensed to form a bi aryl bond to connect two quinolone groups and then tautomerization occurs toward an intramolecular condensation between hydroxylamine and nitroso moieties to produce **44** (Scheme 5).

Nitro aryl compounds are good candidates to selectively label hypoxic cells using fluorescence under bio-reductive conditions.^{8a, 23} Many probes have been synthesized but the products resulting from the bioreduction have not been characterized.^{7a, 23a, 24} Our work underlines the importance of characterization of complex metabolites that can arise in these reduction reactions of nitro-aromatic probes.

2.6 Experimental

Materials and methods. Materials were purchased from following sources: NADPH, cytochrome p450 reductase, sodium phosphate, DMF, glucose, Raney nickel slurry in water, silica gel (0.04-0.063 mm pore size) for column chromatography, and silica gel plates for thin layer chromatography from Sigma chemical company (St. Louis, MO); 6-nitroquinoline, 6-aminoquinoline, and hydrazine hydrate from Alfa-Aesar (Ward Hill, MA); ethyl acetate, hexane, dichloromethane, methanol, ethanol, HPLC acetonitrile and HPLC water from Fischer; Deuterated NMR solvents were from Cambridge Isotope Laboratories (Andover, MA). The compound 1,2,4-benzotriazine-1,4-di-N-oxide was synthesized according literature methods.¹ High resolution mass spectrometry (HRMS) analyses were performed at the mass spectroscopy facility of the University of Illinois Champaign-Urbana and low resolution mass spectroscopic analyses were carried out at

the University of Missouri-Columbia. ¹H and ¹³C NMR experiments and were done on a Bruker Avance DRX300 with 5 mm broadband probe and Bruker Avance DRX500 with CPTCI probe using deuterated NMR solvents methanol (CD_3OD) and chloroform(CDCl₃) at the University of Missouri-Columbia. The reference peaks were set to 3.31 ppm and 49.00 ppm for deuterated methanol and 7.26 ppm and 77.00 ppm for deuterated chloroform from tetramethylsilane for the ¹H and ¹³C spectra respectively. The fluorescence spectra were obtained on a Varian Cary Eclipse Fluorescence Spectrophotometer equipped with xenon flash lamp with instrumental slit width settings at 10 nm employing a 10 mm path length quartz cuvette.

Procedure for hypoxic metabolism.

In a typical enzymatic reaction, **42** ($4 \mu L$ from 50 mM in DMF, final concentration 0.8 mM) or non-fluorescent electron acceptor (24 μL from 50 mM in 15 % DMF water, final concentration 6.4 mM), was mixed with NADPH (20-160 μL of 10 mM, final concentration 0.8 mM-6.4 mM), cytochrome p450 reductase (2 μL from 140 U/mL, final concentration 1.1 U/mL), sodium phosphate buffer (6 μL from 50 mM, final concentration 12 mM, pH 7.4) and HPLC water to obtain the final solution (0.25mL, less than 2% DMF) at room temperature (24⁰C). For anaerobic reactions, all reagents except NADPH and cytochrome p450 reductase were de-gassed in glass tubes by three freeze pump thaw cycles. The glass tubes were broke open inside an argon purged glove bag and bubbled with argon for five minutes. Solid NADPH was dissolved in HPLC water to make stock solution inside the glove bag and cytochrome p450 reductase was used as is from the original sample from the supplier. Upon mixing, the containers were wrapped with aluminum foil to prevent exposure to light.

Procedure for Fluorescence experiment

Upon completion of incubation reaction solution was diluted up to 1 mL with sodium phosphate buffer (50 mM, pH 7.4) in HPLC water, and then was added to the cuvette. In anaerobic experiments, upon completion the reaction mixtures were taken out of glove bag and kept 1 h under atmospheric conditions prior to the dilutions.

Procedure for LC/MS analysis.

In vitro enzymatic metabolism of **42** was carried out as described above, and the resulting products were extracted into ethyl acetate and dried using brine followed by roto vap evaporation of ethyl acetate. The solid was re-dissolved in methanol and analyzed by LC/MS in the positive ion mode. Separation of metabolites was carried using a C18 reverse phase Phenomenex Luna column (5 µm particle size, 100 A0 pore size, 150 mm length, 2.00 mm i.d.) and a ThermoSeparations liquid chromatograph (TSP4000), the metabolites were detected by their UV-absorbance at 254 nm. The elution started with a gradient of A, 99% HPLC water (0.1% acetic acid) and B acetonitrile (0.1% acetic acid) followed by a linear increase to 90 % B over the course of 30 min. The elution was continued at 90% B for 3 min and decreased to 1% over the next 8 min. A flow rate of 0.35 mL/min was used. The LC/ESI-MS analyses were carried out in the positive ion mode on a Finnigan TSQ 7000 triple quadrupole instrument using a 250 kV needle voltage and at a capillary temperature of 250 °C.



Figure S1. LC/MS analysis of **43**. (A) UV chromatogram of **43**, (B) LC/MS analysis of the product eluting at 4.6 min in the chromatogram.



Figure S2. (A) Fluorescence spectrum of NADPH (50 μ M, λ_{ex} 307 nm, in sodium phosphate buffer, 10 mM, pH 7.4). It is noteworthy that the shape of the fluorescence emission peaks of NADPH and **44** are distinct. (B) NADPH fluorescence diminishes over the course of 1 h when the reactions are exposed to aerobic conditions. Reactions contained **42** (0.8 mM), NADPH:cytochrome P450 reductase (1.1 U/mL), and NADPH (3 mM) in sodium phosphate buffer, 10 mM, pH 7.4 (λ_{ex} 307 nm, λ_{em} 460 nm). Reactions described here were incubated quenched with aerobic buffer and incubated for approximately 1 h before fluorescence analysis. Thus, the control experiment provides evidence that fluorescence detected in the metabolism of **42** is not due to residual NADPH.



Figure S3. Fluorescence emission at 445 nm (λ ex 307 nm) for reactions: compound **42** (0.1-0.8 mM) + NADPH:cytochrome P450 reductase (1.1 U/mL), NADPH (0.1-0.8 mM) under anaerobic(blue) and aerobic (red), and a non-fluorescent electron acceptor 1-methyl-2-nitro-5-carbethoxyimidazole (0.1-0.8 mM) + NADPH:cytochrome P450 reductase (1.1 U/mL), NADPH (0.1-0.8 mM) under anaerobic (green) and aerobic (purple). Reactions were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C, then diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4) and the fluorescence measured (λ ex 307 nm, λ em 445 nm). It is important to note that NADPH exhibits fluorescence with an emission maximum at 445 nm. However, control experiments showed that any NADPH left unconsumed at the end of the anaerobic reactions described here is ultimately converted to the non-fluorescent NADP+ product by enzyme-driven redox cycling of the electron accepting organic substrate upon opening the reaction vessel to air and dilution with aerobic buffer prior to fluorescence measurements.

Synthesis of 1,2-di(quinolin-6-vl)diazene oxide (45). We employed a variation on the literature procedure of Boge *et al.*² To a solution of compound **42** (0.5 g, 2.87 mmol) in a mixture of EtOH:CH₂Cl₂ (1:1, 20 mL) at 0 °C in an ice/salt bath was added Raney nickel slurry (0.5 mL, active catalyst in water, Sigma-Aldrich cat. number 221678). To this mixture, hydrazine hydrate (1.5 mL, 30 mmol) portions were added over the course of 3 h with stirring until 42 was consumed (TLC) and the resulting mixture stirred overnight. The solid was removed by filtration and the resulting solution dried by extraction with brine and then over sodium sulfate. The compound was purified by column chromatography on silica gel eluted with ethyl acetate in the first column separation and second column chromatography separation on silica gel was done with MeOH:CH₂Cl₂ (99:1) to obtain 45, a yellow solid, in pure form (100 mg, R_f value = 0.25 in 4% MeOH in CH₂Cl₂) ¹H NMR (CDCl₃, 300 MHz): δ ppm 9.14 (d, J = 2.5 Hz, 1H), δ 9.00 (dd, J = 4.5 Hz, J = 1.5 Hz, 1H), δ 8.93 (dd, , J = 4.5 Hz, J = 1.5 Hz, 1H), δ 8.82 (d, J = 2.5 Hz, 1H), δ 8.67 (d, J = 9.0 Hz, 1H), δ 8.31 (dd, J = 9.0 Hz, J = 1.5 Hz, 1H), δ 8.21 (m, 4H), δ 7.49 (dd, J = 8.5 Hz, J = 4.5 Hz, 1H), 7.42 (dd, J = 8.5 Hz, J = 4.5 Hz, 1H), 1.23 grease. ¹³C NMR (CDCl₃, 75.5 MHz): δ 152.86, 151.97, 149.64, 148.72, 146.01, 141.93, 137.88, 137.76, 130.95, 130.32, 129.32, 128.46, 127.73, 123.76, 123.40, 122.68, 122.64, 122.09; HRMS (ESI, $[M+H]^+$) m/z calcd for C₁₈H₁₃N₄O 301.1089, found 301.1080. ²Boge, N.; Kruger, S.; Schroder, M.; Meier, C.; Synthesis 2007, 24, 3907-3914.



Figure S3. ¹H NMR of 45 (CDCl₃, 300 MHz)



Figure S4. ¹³C NMR of **45** (CDCl₃, 75.5 MHz)

Preparation of pyrido[3,2-f]quinolino[6,5-c]cinnoline 3-oxide (44) via alkaline glucose reduction of 42.³ A solution of 42 (1.0 g, 5.61 mmol) in NaOH (20% aqueous solution, 10 mL) and was heated to 90 °C with stirring. To this solution, D-(+) glucose (1.3 g, 7.21 mmol) was added over 30 min and stirred for 1 h. The mixture was extracted with EtOAc (20 mL) and the combined organic extracts washed with brine and dried over magnesium sulfate. The mixture separated by column chromatography on silica gel and eluented with ethyl acetate and MeOH (99:1) to obtain the helicene 44, a yellow solid(300 mg, 18% yield). ¹H NMR (CDCl₃, 500 MHz.): δ 9.15 (d, J = 4.5 Hz 1H), 9.05 (m, 2H), 8.87 (d, J = 9.0 Hz, 1H), 8.67 (d, J = 9.0 Hz, 1H), 8.44 (d J = 9.0 Hz, 1H), 8.40 (d J = 9.0 Hz, 1H), 8.23 (d, J = 9.0 Hz, 1H), 7.46 (dd, J = 9.0 Hz, J = 4.5 Hz, 1H), 7.41 (dd, J = 9.0 Hz, J = 4.5 Hz, 1H). ¹³C-NMR (CDCl₃, 125.8 MHz,): δ 153.35, 151.47, 149.71, 148.53, 144.08, 137.09, 136.02, 134.79, 134.28, 133.41, 128.00, 127.45, 123.52, 123.34, 121.75, 120.56, 120.46, 114.21; HRMS (ESI, [M+H]⁺) m/z calcd C₁₈H₁₁N₄O calculated mass 299.0933; actual mass 299.0934 Crystals for X-ray analysis were obtained by dissolving the pure compound in minimum amount of warm MeOH, followed by slow evaporation (3 d) in a 2 mL vial.

³Galbraith, H. W.; Degering, E. F.; Hitch, E. F. J. Am. Chem. Soc. **1951**, 73:1323


Figure S5. ¹H NMR of 44 (CDCl₃, 500 MHz)



Figure S6. ¹H NMR of 44 aromatic region (CDCl₃, 500 MHz)



Figure S6. ¹³C NMR of 44 (CDCl₃, 125.77 MHz)



Figure S7. ¹H–¹H TOCSY of 44 (CDCl₃, 500 MHz)



Figure S8. ¹H–¹H COSY of 44 (CDCl₃, 500 MHz)



Figure S9. ¹H–¹³C HMQC of **44** (CDCl₃, 500 and 125.77 MHz):



Figure S10. ¹H–¹³C HMBC of **44** (CDCl₃, 500 and 125.77 MHz):



Figure S11. ¹H-¹H NOESY of **44** (CDCl₃, 500 MHz):

Enzymatic generation of pyrido[3,2-*f*]quinolino[6,5-*c*]cinnoline 3-oxide (44) Compound 42 (50 mM, in 0.2 mL DMF) was mixed with sodium phosphate buffer (0.3 mL, 10 mM, pH 7.4) and water (12.0 mL) in an argon-purged glove bag and the solution purged with argon (20 min). To this mixture was added NADPH (25 mg, 0.033 mmol) and NADPH:cytochrome P450 reductase (0.03 mL of a 0.35 U/mL solution). The resulting mixture was stirred inside the argon-filled glove bag for 18 h. The reaction was then extracted with ethyl acetate (20 mL), the combined organic extract washed with brine and dried with magnesium sulfate. Column chromatography on silica gel eluted with ethyl acetate and MeOH (99:1), followed by preparative TLC eluted with ethyl acetate and MeOH (99:1) gave 4 (five reactions combined to yield 0.300 mg, 2% yield). The 1H-NMR and LC/MS properties of this material matched that of authentic 44 prepared as described above.



Figure S12. ¹H NMR of **44** (CDCl₃, 500 MHz), obtained from NADPH and NADPH:cytochrome P450 reductase mediated synthesis



Figure S13. ¹H-¹H NOESY of **44** (CDCl₃, 500 MHz), obtained from NADPH and NADPH:cytochrome P450 reductase mediated synthesis

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Chapter 3

Hypoxia-selective enzymatic conversion of 6-nitroquinoline to the fluorescent product, 6-aminoquinoline

3.1 Hypoxia is an attractive target to develop fluorescent probes

Studies carried out on tumor physiology suggested that solid tumors contain low oxygenated areas (hypoxic regions).¹ Irregular vascularization, present inside tumors causes hypoxic conditions.² Further research, conducted on hypoxia over decades had established the importance of hypoxia in tumor biology.³ Hypoxia selects for malignant phenotypes, which are unable to undergo apoptosis and result in poor prognosis.⁴ Moreover, hypoxic regions contain cancer stem cells which can differentiate and cause metastases.⁵ Hence, hypoxic regions are considered as targets of interest in tumor biology. Fluorescent based probing agents may be useful to mark low oxygenated regions.⁶ Organic compound which can produce fluorescent response, selectively within tumor, may select as a candidate fluorescent probe for detecting hypoxic tumors.

3.2 Fluorescent Probes to Detect Hypoxia

Nitroaryl groups can undergo enzyme mediated reduction in hypoxia.⁷ The final product of the reduction process is hydroxyl amine and/or amine.⁸ Under normal oxygenated conditions, single electron reduced nitro radical gets back oxidized to nitro group.⁹ Hence the first reduction step is oxygen sensitive. ^{7d, 10} This sensitivity has been exploited by nitroaromatic prodrugs to spare normal oxygenated cells.¹¹ Nitro-based

anticancer prodrugs are selectively toxic to low-oxygenated tumors and that may be due to the oxygen-sensitive reduction of nitro group.¹² These prodrugs have been further tested for their oxygen sensitivity and enzymatic activation in hypoxia.¹¹ Nitro-based agents which are used to mark hypoxic regions in radio imaging and immunihistochemical staining techniques.¹³ Along with these methods, nitro-based fluorescent probes would provide an attractive mean to visualize low oxygenated regions.^{6a, b, 14} In the designing step, a non-fluorescent nitroaromatic compound can be selected as a fluorescent probe when the respective amino compound is fluorescent. In addition, these probes should be substrates for cellular reductases, which can supply electrons to nitro-amine reduction (Scheme 3.1).





Based on this strategy, non-fluorescent 6-nitroquinoline (**42**) is tested as a nitroaryl fluorescent probe to detect hypoxia.¹⁵ In addition, a metabolic study is carried out to identify fluorescent and non-fluorescent metabolites. Under hypoxia, a reductive metabolism of **42** can be reduced to 6-aminoquinoline (**43**, Scheme 3.2), which is a known fluorophore used in biochemical assays.¹⁶ The production of non-fluorescent dimer 6,6'-azoxyquinoline **45** also can be anticipated (Scheme 3.2). Moreover, 205 nm stokes shift can be obtained by the reduction assay.¹⁶



Scheme 3.2. Hypoxic metabolism of 42 forms fluorescent 43

Similar hypoxic metabolism of **42** by NADPH:cytochrome P450 reductase (CYP450R) produced **45** and fluorescent helicene, pyrido[3,2-*f*]quinolino[6,5-*c*]cinnoline 3-oxide (**44**, chapter 1 scheme 3.3).¹⁵ The anticipated fluorescent product **43** was not produced by the reducing system CYP450R (Scheme 3.2). Alternatively, another enzymatic reducing system xanthine and xanthine oxidase may be used to test metabolism of **42** in hypoxia.



Scheme 3.3. CYP450R mediates conversion of 42 into fluorescent metabolites

Xanthine and xanthine oxidase system is known to reductively activate bio reducible compounds and conduct one electron reduction under hypoxic conditions.¹⁷ Accordingly, hypoxic conditions were applied to solutions, by conducting three cycles of freeze-pump-thawing.¹⁸ The deoxygenated reaction solutions, **42** and reducing system were mixed inside an argon purged glove bag. The compound **42** is non-fluorescent in solutions. Anaerobic incubation of **42** with xanthine and xanthine oxidase produced 12-

fold fluorescence increase at 530 nm (Figure 3.1A, purple column). When xanthine concentration is increased, emission at 530 nm is increased.



Figure 3.1 Enzymatic conversions of 42 to a fluorescent product selectively under hypoxic conditions. A. Fluorescence emission at 530 nm (λ_{ex} 340 nm). Each set of assays depicted in the bar graph consists of (from left to right): a control sample of compound 42 alone (0.8 mM) xanthine oxidase (2.4 U/mL) and xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) under aerobic conditions , a control reaction composed of xanthine oxidase (2.4 U/mL) and xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) under anaerobic conditions, a control reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and the non-fluorescent electron acceptor, 1,2,4-benzotriazine 1,4-dioxide, (6.4 mM) under aerobic conditions \blacksquare , a control reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and the non-fluorescent electron acceptor, 1,2,4-benzotriazine 1,4-dioxide, (6.4 mM) under anaerobic conditions –, a reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and 42 under aerobic conditions , a reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and 42 under anaerobic conditions. Reactions were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C, diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4), and the fluorescence measured (λ_{ex} 340 nm, λ_{em} 530 nm). **B**. Fluorescence spectra of reaction mixtures generated in the aerobic and anaerobic metabolism of 42 by xanthine oxidase (2.4 U/mL) and xanthine (6.4 mM) carried out as described in the Experimental Section and fluorescence spectrum of 6aminoquinoline (43, 0.1 mM, λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4).

When the fluorescent emission of anaerobic **42** reduction by xanthine and xanthine oxidase is inspected, the shape of the fluorescent curve is clear different from that of **44**, which is generated by the metabolism of **42** by NADPH:cytochrome P450 reductase.¹⁵ The fluorescence curve of **44** contains two distinct emission maxima, at 440 and 460 nm. The shape of the curve, obtained from xanthine oxidase mediated

metabolism of **42** resembles fluorescence spectrum of **43** (Figure 3.1B, green and red curves). The fluorescence intensity of aerobic reaction, containing **42**, at 530 nm region, is low relative to the corresponding anaerobic reaction (Figure 3.10, E). When non fluorescent electron acceptor benzotriazine 1,2,4-di-oxide is incubated with xanthine and xanthine oxidase under aerobic and anaerobic conditions, low fluorescence intensity is detected at 530 nm region (Figure 3A, columns red and green).¹⁵ Xanthine and xanthine oxidase produced fluorescence, in low intensities under aerobic and anaerobic conditions may be due to the decomposition of cofactor of xanthine oxidase (Figure 3.10, C and D).¹⁹

3.3 LC/MS analysis of the reaction mixtures generated by hypoxic metabolism of 42 by xanthine/xanthine oxidase

To identify metabolites, produced in the enzymatic reduction reaction we analyzed reaction mixtures using LC/MS. The complete LC/MS analysis includes results of reaction mixtures and authentic compounds (Figures 3.2 and 3.3). The anaerobic reaction mixture of two equivalents of xanthine shows the presence of **50** (Figure 3.2 panels A, B and E). Compound **50** is fluorescent at 450 nm region (Figure 3.10, A). The contribution of **50** to the fluorescence at 530 nm region is minimal because it is unstable due to condensation with **49** to form **45**. The mass to charge value (m/z) of M+H ion of peak at 3.1 min on HPLC matches with that of authentic **50** (Figure 3.3, A and B). In the same mixture, the m/z of M+H ion of peak at 4.5 min on the HPLC (Figure 3.2, F) is the same as that of the authentic **43** (Figure 3.3, C and D), consistent with the fluorescent results (Figure 3.1B, curves green and red). The m/z of (M+H) ion of the eluent at 5.5 min shows 285.1, which is the M+H m/z value of **53** (Figure 3.2, A and scheme 3.4). In

the same reaction mixture the product eluting at 14.6 min showed m/z of 190.9 (Figure 3.2, A and G). The authentic LC analysis of **51** is consistent with the product eluting at 14.6 min in Figure 3.2, panel A (Figure 3.3 panels E and F). When **42** is incubated in the presence of xanthine oxidase, formation of **51** is possible as a metabolite along the reduction profile.^{15, 20} The product eluting at 16.4 min shows m/z value of 158.9, which is the M+H ion of nitroso, **49**. (Figure 3.2, A, B, C and H)

The product eluting at 19.1 min on HPLC showed m/z of 301.1 as the (M+H) ion (Figure 3.2 panels A and I). We employed Raney nickel mediated chemical reduction of **42**, with hydrazine hydrate to obtain **45**.²¹ The authentic LC analysis of **45** is consistent with the product eluting at 19.1 min (Figure 3.3, I and J). There is no contribution to the fluorescence of anaerobic reactions by **45** (Figure 3.1A, purple column). The product appears at 24.7 min, with m/z of 282.9 may be an isomer of **52**, which is not formed in these reactions (Figure 3.2, A and J, Figure 3.3, K and L, scheme 3.4).



Scheme 3.4. Hypoxic metabolism of 42 by xanthine and xanthine oxidase

The reaction mixture containing 2.4 mM xanthine shows diminished amounts of **51** (Figure 3.2, B). Similarly, in 4.0 mM anaerobic xanthine assay, **51** and **50** are not present (Figure 3.2, C). When the xanthine amount is increase to 6.4 mM, under anaerobic conditions, as seen on the HPLC trace only **43**, **45** and an isomer of **52** are

formed (Figure 3.2, D). Fluorescent product **44** is not detected in the current study (Figure 3.3, G and H).



Figure 3.2. LC/MS analysis of reaction mixture, generated by anaerobic metabolism of 42. Compound 42 (0.8 mM), xanthine oxidase (2.4 U/mL) and xanthine were mixed under anaerobic conditions and the reaction was carried out as described in the experimental section. The reaction was dried and products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC trace of the anaerobic reaction mixture with xanthine (1.6 mM) monitoring absorbance at 254 nm. Panel B: HPLC of the anaerobic reaction mixture with xanthine (2.4 mM) monitoring absorbance at 254 nm. Panel C: HPLC trace of the anaerobic reaction mixture with xanthine (4.0 mM) monitoring absorbance at 254 nm. Panel D: HPLC trace of the anaerobic reaction mixture with xanthine (6.4 mM) monitoring absorbance at 254 nm. Panel E: LC/MS spectrum of product eluting at 3.08 min in panels A and B. Panel F: LC/MS spectrum of the product eluting at 4.50 min in panels A, B, C and D. Panel G: LC/MS spectrum for of the product eluting at 14.60 min in panel A. Panel H: LC/MS spectrum for of the product eluting at 16.40 min in panels A, B, and C. Panel I: LC/MS spectrum for of the product eluting at 19.10 min in panels A, B, C and D. Panel J: LC/MS spectrum for of the product eluting at 24.50 min in panels A, B, C and D.



Figure 3.3. LC/MS analysis of authentic compounds. The compounds were dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC trace of **50** monitoring at 254 nm. Panel D: LC/MS spectrum of **50**. Panel C: HPLC trace of **51** monitoring at 254 nm. Panel D: LC/MS spectrum of **51** eluting at 4.50 min. Panel E: HPLC trace of **51** monitoring at 254 nm. Panel F: LC/MS spectrum of **51** eluting at 14.60 min. Panel G: HPLC trace of **44** monitoring at 254 nm. Panel H: LC/MS spectrum of **44** eluting at 15.10 min. Panel I: HPLC trace of **45** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **54** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **50** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel J: LC/MS spectrum of **45**. Panel K: HPLC trace of **52** monitoring at 254 nm. Panel K: LC/MS spectrum of **50**.

3.4 LC/MS analysis of the reaction mixtures generated by aerobic metabolism of 42

by xanthine/xanthine oxidase

Starting compound **42** is remaining in the mixture while **51** and **45** appeared as new products under aerobic conditions (Scheme 3.4). None of the compounds are fluorescent.



Figure 3.4 LC/MS analysis of the reaction mixture generated by aerobic metabolism of **42.** Compound **42** (0.8 mM) xanthine oxidase (2.4 U/mL) and xanthine (6.4 mM) were mixed and the reaction was carried out as described in the experimental section. The reaction was dried and products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC of the aerobic reaction mixture monitoring absorbance at 254 nm. Panel B: LC/MS spectrum of the product eluting at 14.60 min. Panel C: LC/MS spectrum of the product eluting at 19.10 min.

3.5 Xanthine oxidase oxidizes aryl carbon, bonded to heteroatom of 42 to produce 6-

nitroquinolone 51

The compound **51** (Figure 3.3, E), was synthesized using xanthine oxidase and **42** as the starting material. There is evidence for oxidation of aromatic carbon, adjacent to nitrogen by enzyme xanthine oxidase.²² It was clear from the metabolic results of aerobic reaction of **42** by xanthine oxidase that xanthine oxidase does oxidation chemistry on **42**, as a substrate when reduction of **42** is diminished in the presence of oxygen (Figure 3.4,

A). Moreover, at lower concentration of xanthine, under hypoxia **51** was produced as a main metabolite.

We speculated that xanthine oxidase should be able to convert **42** to **51** under aerobic conditions and xanthine is not required for the oxidation process. When **42** stirred with xanthine oxidase in aqueous media, **51** was obtained in milligram amounts (Scheme 3.5).



Scheme 3.5. Enzymatic generation of 51 by 42 using xanthine oxidase

Chemical characterization of **51** was conducted by NMR, HRMS and crystallography analysis (Figure 3.5 and experimental). Analysis of the ¹H-NMR spectrum of **51** clearly shows the absence of the resonance for the proton adjacent to the nitrogen of the heterocyclic quinoline ring and a new resonance is seen on ¹³C spectrum at 165 ppm diagnostic for the carbonyl carbon of the quinolone system.



Figure 3.5. ORTEP diagram of 51

When enzymatically synthesized **51** was analyzed on LC/MS (Figure 3.3, E and F), retention time and m/z matched with that which eluted with anaerobic and aerobic reactions (Figures 3.2, A and G, 3.3, E and F and 3.4, A and B).

3.6 Hypoxia-selective conversion of hydroxylamine 50 to amino 43

It is well established that enzymatic reduction of nitroaroamtics proceeds via intermediates nitroso and hydroxylamine to produce amine product.^{7a-c, 10, 23} The final reduction step from intermediate hydroxylamine to amine is not well studied in the current literature.²⁴ The final reduction step of the reduction profile of **42** is studied using **50** and the reduction of **50** is tested by xanthine and xanthine oxidase system under aerobic and anaerobic conditions. Characterization of enzyme mediated reduction of aromatic hydroxylamine to amine has not been reported (Scheme 3.6).



Scheme 3.6 Enzymatic generation of 43 by xanthine and xanthine oxidase

Hydroxylamine **50** has been chemically synthesized using hydrazine hydrate in the presence of Raney nickel and characterized using NMR, HRMS and crystallographic methods. The LC/MS characterization of **50** shows spontaneous formation of **49** and **45** (Figure 3.3, panels A and B). The hypoxic incubation of **50** with xanthine oxidase and xanthine shows fluorescence growth at 530 nm and the fluorescence increases with xanthine concentration (Figure 3.6 A).



Figure 3.6. Enzymatic conversion of 50 to fluorescent 43 under hypoxic conditions. A. Fluorescence emission at 530 nm (λ_{ex} 340 nm). Each set of assays depicted in the bar graph consists of (from left to right): a control sample of compound 50 alone (0.8 mM) \blacksquare , a control reaction composed of xanthine oxidase (2.4 U/mL) and xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) under aerobic -, a control reaction composed of xanthine oxidase (2.4 U/mL) and xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) under anaerobic conditions –, a control reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and the non-fluorescent electron acceptor, 1,2,4-benzotriazine 1,4dioxide, (6.4 mM) under aerobic conditions ■, a control reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and the non-fluorescent electron acceptor, 1,2,4benzotriazine 1,4-dioxide, (6.4 mM) under anaerobic conditions =, a reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and 50 under aerobic conditions a reaction composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and 50 under anaerobic conditions . Reactions were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C, diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4), and the fluorescence was measured (λ_{ex} 340 nm, λ_{em} 530 nm). **B.** Fluorescence spectra of aerobic and anaerobic reaction mixtures containing 50 (0.8 mM), xanthine oxidase (2.4 U/mL), and xanthine (3.2 mM).

In the aerobic reaction, fluorescence growth is not detected (Figure 3.10 panel F). The shape of the fluorescence curve of the anaerobic reaction is similar to **43** in solution (Figure 3.6 B). The LC/MS analysis of anaerobic reaction shows the presence of **43** and **45**. The evidence shows the oxygen sensitivity of reduction of **50** by xanthine and xanthine oxidase, to form **43** (Figure 3.7).



Figure 3.7. LC/MS analysis of the reaction mixture generated by anaerobic metabolism of **50.** Compound **50** (0.8 mM), xanthine oxidase (2.4 U/mL) and xanthine (6.4 mM) were mixed and the reaction was carried out as described in the experimental section. The reaction was dried and products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC trace of the anaerobic reaction mixture monitoring absorbance at 254 nm. Panel B: LC/MS spectrum of the product eluting at 4.70 min. Panel C: LC/MS spectrum of the product eluting at 19.20 min.





Scheme 3.7. Enzymatic generation of 54 from 51 by xanthine and xanthine oxidase is hypoxia selective

We speculated that the 6-aminoquinolone **54** may be fluorescent. The compound **54** was chemically synthesized by reducing **51** on palladium/charcoal hydrogenation to obtain the fluorescent spectrum (Figure 3.10 panel B). Then, hypoxia selective reduction of **51** by xanthine and xanthine oxidase system is tested. The anaerobic reaction produced expected fluorescence of **54** (Scheme 3.7). A Sixteen fold increase of fluorescence is obtained against the aerobic reaction (Figure 3.8).



Figure 3.8. Enzymatic conversions of **51** to **54** under hypoxic conditions. A. Fluorescence emission at 485 nm (λ ex 390 nm) for **51** (0.8 mM) + xanthine oxidase (2.4 U/mL) and xanthine (3.2 mM) under aerobic conditions, **51** (0.8 mM) + xanthine oxidase (2.4 U/mL) and xanthine (3.2 mM) under anaerobic conditions, Reactions were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C, then diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4) and the fluorescence measured (λ_{ex} 390 nm, λ_{em} 485 nm). B. Fluorescence spectra (in sodium phosphate buffer, 10 mM, pH 7.4) of the reaction mixture generated in the aerobic metabolism of **51** by xanthine oxidase (2.4 U/mL) and xanthine (3.2 mM) (pink, λ_{em} 485 nm) and fluorescence spectrum (in sodium phosphate buffer, 10 mM, pH 7.4) of the reaction mixture generated in the aerobic metabolism of **51** by xanthine oxidase (2.4 U/mL) and xanthine (3.2 mM) (pink, λ_{em} 485 nm) and fluorescence spectrum (in sodium phosphate buffer, 10 mM, pH 7.4) of the reaction mixture generated in the aerobic metabolism of **51** by xanthine oxidase (2.4 U/mL) and xanthine (3.2 mM) (blue) λ_{em} 485 nm.

3.8 Enzymatic conversion of 42 to 6-nitroquinolone 51 followed by hypoxia-selective conversion to 6-aminoquinolone 54

LC/MS analysis of anaerobic and aerobic metabolism of **42** reveals that under low concentrations of xanthine, **42** was oxidized to form **51** and that oxidation can dominate over reduction of nitro under low oxygen levels. Upon forming **51**, xanthine oxidase can perform nitro reduction on **51**, under hypoxia to produce **54** in the same reaction mixture (Scheme 3.8).



Scheme 3.8 Enzymatic generation of 51 from 42 and production of 54 from 51

In the assay we used 0.5 molar equivalent of xanthine, 0.4 mM, with **42** and xanthine oxidase and carried out the normal enzymatic reactions under anaerobic and aerobic conditions. In the fluorescence assays a ten-fold increase of fluorescence was obtained against the aerobic reaction mixture (Figure 3.9).



Figure 3.9 Enzymatic conversion of **42** to **51** and reduction to **54** in hypoxia. A. Fluorescence emission at 485 nm (λ ex 390 nm) for 1 (0.8 mM) + xanthine oxidase (2.4 U/mL) and xanthine (0.4 mM) under aerobic conditions.Compound 1 (0.8 mM) + xanthine oxidase (2.4 U/mL) and xanthine (0.4 mM) were incubated for 18 h in sodium phosphate buffer at (12 mM, pH 7.4) at 24 °C under hypoxia, then diluted with aerobic sodium phosphate buffer (12 mM, pH 7.4) and the fluorescence measured (λ ex 390 nm, λ em 485 nm). B. Fluorescence spectra (in sodium phosphate buffer, 10 mM, pH 7.4) of the reaction mixtures generated in the anaerobic(red) and aerobic(blue) metabolism of 42 by xanthine oxidase (2.4 U/mL) and xanthine (0.4 mM) (λ em at 485 nm)

3.9 Conclusions

In the current work, we provide evidence for the hypoxia-selective conversion of 6-nitroquinoline **42** to 6-aminoquinoline **43**, by xanthine/xanthine oxidase enzyme system. The reduction steps are consecutive one electron additions, as seen in scheme 3.1. In addition, condensation occurs between **50** and **49** to produce **45**. The chemical synthesis and complete characterization of **50** facilitates the analysis of the oxygen sensitivity of final reduction step. Fluorescent and LC/MS analysis of reduction of **50** in hypoxia, by xanthine and xanthine oxidase show the presence of fluorescent **43**. This finding is important and striking because the existing evidence in the literature discusses only the oxygen sensitivity of the first reduction step of nitro compounds.^{7d, 10, 25} The evidence we provide supports the existence of multiple oxygen sensitive reduction steps over the enzymatic reduction of nitro aromatic compound. In an early work, related to the

reduction of **42** by CYP450R¹⁵, together with current xanthine and xanthine oxidasemediated reduction of **42** in hypoxia shows different product profile and metabolism that may occur on a single nitro compound. The comparison reveals that the inability of CYP450R to reduce intermediate **50**, under the conditions we applied, leaving them to condense to form byproducts.

We observed the oxidation of 42 to 51, conducted by xanthine oxidase (51, Scheme 3.4). The ability of xanthine oxidase to oxidize aromatic carbon atoms next to nitrogen is well documented.^{22b, 22d} The oxidizing capability of xanthine oxidase is responsible for the transformation of 42 to 51. The aerobic assays show the oxidation product 51 as a major product. Upon reduction 51 produces fluorescent 54, which emits at 490 nm (data not shown) under assay conditions. In assays, when xanthine concentration is increased the yield of 51 decreases. Hence, it can be concluded that under anaerobic conditions xanthine/xanthine oxidase system efficiently reduces 42. The oxidizing ability of xanthine oxidase slows when conditions for reduction is favored.

Reduction of **51**, in a separate experiment by xanthine/xanthine oxidase system, under hypoxia produces fluorescence at 485 nm. The emission parameters of **54** match with the fluorescence obtained from the anaerobic metabolism of **51** (data not shown). The fluorescent enhancement obtained with **51** grants future experiments on **51** as a potential fluorescent probe to detect hypoxia.

Finally, the work we presented shows the ability of **42** to be used as a fluorescent probe that can be activated by one electron reductases, under hypoxia. Chemical characterization of metabolites, produced from enzymatic reduction of nitroaromatic compounds is essential to understand the complexity of nitroaromatic reduction.

3.10 Experimental

Materials and methods. Chemicals were purchased from following sources: Sodium phosphate, glucose, NADPH, cytochrome p450 reductase, DMF, Raney nickel slurry in water, silica gel plates for thin layer chromatography and silica gel (0.04-0.063 mm pore size) for column chromatography were obtained from Sigma Aldrich (St. Louis, MO); 6aminoquinoline, 6-nitroquinoline, and hydrazine hydrate from Alfa-Aesar (Ward Hill, MA). deuterated NMR solvents were from Cambridge Isotope Laboratories (Andover, MA); ethyl acetate, dichloromethane, methanol, hexane, ethanol, HPLC water and HPLC acetonitrile from Fischer; The compound 1,2,4-benzotriazine-1,4-di-N-oxide was made following literature methods.¹ High resolution mass spectrometry (HRMS) analyses were performed at the mass spectroscopy facility of the University of Illinois Champaign-Urbana and low resolution mass spectroscopic analyses were carried out at the University of Missouri-Columbia. ¹H and ¹³C NMR experiments and were done on a Bruker Avance DRX300 with 5 mm broadband probe and Bruker Avance DRX500 with CPTCI probe using deuterated NMR solvents methanol (CD₃OD) and chloroform(CDCl₃) at the University of Missouri-Columbia. The reference peaks were set to 3.31 ppm and 49.00 ppm for deuterated methanol and 7.26 ppm and 77.00 ppm for deuterated chloroform from tetramethylsilane for the ¹H and ¹³C spectra respectively. The fluorescence spectra were obtained on a Varian Cary Eclipse Fluorescence Spectrophotometer equipped with xenon flash lamp with instrumental slit width settings at 10 nm employing a 10 mm path length quartz cuvette.



Figure 3.10. Fluorescence spectra of control reactions. A: Fluorescence spectrum of **50** (0.03 mM, λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4). B: Fluorescence spectrum of **54** (0.003 mM, λ_{ex} 390 nm, in sodium phosphate buffer, 10 mM, pH 7.4). C: Fluorescence spectra (λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4). C: Fluorescence spectra (λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, and a non-fluorescent electron acceptor 1,2,4-benzotriazine 1,4-dioxide (6.4 mM) under aerobic conditions (referred to brown bar in figure 3.1,). D: Fluorescence spectra of control reactions composed of xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and a non-fluorescent electron acceptor 1,2,4-benzotriazine 1,4-dioxide (6.4 mM) and a non-fluorescent electron acceptor 1,2,4-benzotriazine 1,4-dioxide (6.4 mM) and a non-fluorescent electron acceptor 1,2,4-benzotriazine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and a non-fluorescent electron acceptor 1,2,4-benzotriazine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and a non-fluorescent electron acceptor 1,2,4-benzotriazine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and **42** under aerobic conditions (blue bar in figure 3.1 A,), F: Fluorescence spectra (λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4) of reactions composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and **42** under aerobic conditions (blue bar in figure 3.1 A,), F: Fluorescence spectra (λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4) of reactions composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and **42** under aerobic conditions (blue bar in figure 3.1 A,), F: Fluorescence spectra (λ_{ex} 340 nm, in sodium phosphate buffer, 10 mM, pH 7.4) of reactions composed of xanthine oxidase (2.4 U/mL), xanthine (2.4 mM, 3.2 mM, 4.0 mM and 6.4 mM) and **50** under aerobic conditions.

Synthesis of 6-hydroxylaminoquinoline 50:¹



6-nitroquinoline (0.5 g, 2.87 mmol) **42** was stirred in 20 mL of EtOH/CH₂Cl₂ (1:1) at 0⁰C and 0.5 mL of was Raney nickel slurry (active catalyst in water-sigma 221678) was added. Then, 10 molar eq. of hydrazine hydrate was added drop wise and stirred for 1 hour while purging nitrogen gas. The solid was filtered and the organic mixture was dried using brine and sodium sulfate. The compound **50** was separated by column chromatography using EtOAc and MeOH/ CH₂Cl₂ solvents. To obtain crystals, the pure product was dissolved in warm EtOAc and was cooled rapidly to isolate yellow crystals. ¹H – NMR (CD₃OD, 300 MHz,): δ 8.53 (d, J = 5.0 Hz, 1H), 8.07 (d, J = 8.0 Hz, 1H), 7.82 (m, 1H), 7.33 (m, 3H). ¹³C NMR (CD₃OD, 300 MHz): δ 151.40, 147.64, 144.76, 136.72, 131.05, 129.15, 122.54, 121.01, 107.68. HRMS (ESI, M+H⁺) *m/z* calcd for C₉H₉N₂O 160.0715, found 160.0707

Synthesis of 1,2-di(quinolin-6-yl)diazene oxide 45



We employed a variation on the literature procedure of Boge *et al.*² To a solution of compound 42 (0.5 g, 2.87 mmol) in a mixture of EtOH:CH₂Cl₂ (1:1, 20 mL) at 0 °C in an ice/salt bath was added Raney nickel slurry (0.5 mL, active catalyst in water, Sigma-Aldrich cat. number 221678). To this mixture, hydrazine hydrate (1.5 mL, 30 mmol) portions were added over the course of 3 h with stirring until 42 was consumed (TLC) and the resulting mixture stirred overnight. The solid was removed by filtration and the resulting solution dried by extraction with brine and then over sodium sulfate. The compound was purified by column chromatography on silica gel eluted with ethyl acetate in the first column separation and the second column chromatography separation on silica gel was done with MeOH:CH₂Cl₂ (99:1) to obtain the product, a yellow solid, in pure form (100 mg, R_f value = 0.25 in 4% MeOH in CH₂Cl₂) ¹H NMR (CDCl₃, 300 MHz): δ ppm 9.14 (d, J = 2.5 Hz, 1H), δ 9.00 (dd, J = 4.5 Hz, J = 1.5 Hz, 1H), δ 8.93 (dd, J = 4.5 Hz, J = 1.5 Hz, 1H), δ 8.82 (d, J = 2.5 Hz, 1H), δ 8.67 (d, J = 9.0 Hz, 1H), δ 8.31 (dd, J = 9.0 Hz, J = 1.5 Hz, 1H), δ 8.21 (m, 4H), δ 7.49 (dd, J = 8.5 Hz, J = 4.5 Hz, 1H), 7.42 (dd, J = 8.5 Hz, J = 4.5 Hz, 1H), 1.23 grease. ¹³C NMR (CDCl₃, 75.5 MHz): δ 152.86, 151.97, 149.64, 148.72, 146.01, 141.93, 137.88, 137.76, 130.95, 130.32, 129.32, 128.46, 127.73, 123.76, 123.40, 122.68, 122.64, 122.09; HRMS (ESI, $[M+H]^+$) m/z calcd for C₁₈H₁₃N₄O 301.1089, found 301.1080. ²Boge, N.; Kruger, S.; Schroder, M.; Meier, C.; Synthesis 2007, 24, 3907-3914.
Synthesis of 52



The compound **44** (0.01 g, 0.0335 mmol) in 70 % EtOH:water (2.5 mL) was added with sodium dithionite(0.012 g, 0.07 mmol) and was refluxed for 30 min. The reaction mixture was filtered and dried with brine and magnesium sulfate. The crude material was separated by silica gel column chromatography using EtOAc to obtain the product **52**. ¹H – NMR (CDCl₃, 500 MHz): δ 9.11 (d, J = 4.5 Hz, 2H), 9.01 (d, J = 8.0 Hz, 2H), 8.85 (d, J = 9.0 Hz, 2H), 8.46 (d, J = 9.0 Hz, 2H), 7.43 (dd, J = 8.0 Hz, J = 4.5 Hz, 2H). ¹³C-NMR (CDCl₃, 125.77 MHz): δ 152.66, 149.77, 146.06, 136.07, 132.75, 130.81, 123.18, 120.14, 119.28. HRMS (ESI, M+H⁺) *m/z* calcd C₁₈H₁₁N₄ calculated mass 283.0984; actual mass 283.0982

Synthesis of 6-nitroquinolone 51



6-nitroquinoline (250 mg, 1.315 mmol) **42** was dissolved in warm DMF (1 mL) and squirted into warm water (300 mL) while stirring vigorously. Then warm sodium phosphate (500 mM, 100 mL, pH 7.4) was added while stirring. Then xanthine oxidase (100 μ L, 0.005 U/mL) was added in 12-hour intervals for 3 days. The organic material was extracted to EtOAc and dried using brine and sodium sulfate. The product was

separated by column chromatography using hexane and ethyl acetate to obtain 4 mg of product **51**. The crystals were obtained by dissolving the pure compound in minimum amount of warm ethyl acetate and slow evaporation for 3 days.

¹H – NMR (CD₃OD, 500 MHz): δ 8.64 (d, J = 2.5 Hz, 1H), 8.36 (dd, J = 9.0 Hz, J = 2.5 Hz, 1H), 8.09 (d, J = 9.0 Hz, 1H), 7.46 (d, J = 9.0 Hz, 1H), 6.73 (d, J = 9.0 Hz, 1H); ¹³C-NMR (CD₃OD, 125.77 MHz) δ 165.01, 144.11, 144.05, 142.25, 126.28, 125.37, 124.33, 120.63, 117.44 ; HRMS (ESI, M+H⁺) m/z calcd C₉H₇N₂O₃ calculated mass 191.0457; actual mass 191.0456

Synthesis of 6-aminoquinolone 54



6-nitroquinolone (10 mg, 0.05 mmol) **51** was dissolved in MeOH (10 mL) and was added with Pd on activated carbon (0.5 mg). The hydrogen gas was bubbled for 10 mins. The reaction mixture was filtered and organic material was dried using brine and sodium sulfate. The product was separated by silica gel column chromatography using 1% methanol:ethyl acetate as the mobile solvent system to obtain 2 mg of product **54**. ¹H – NMR (CD₃OD, 500 MHz,): δ 7.80 (dd, J = 9.0 Hz, J = 3.3 Hz 1H), 7.16 (d, J = 9.0 Hz, 1H), 7.02 (d, J = 9.0 Hz, 1H), 6.92 (t, J = 3.3, J = 3.1 Hz, 1H), 6.54 (dd, J = 9.0 Hz, 3.1 Hz, 1H), 1.28 grease. ¹³C-NMR (CD₃OD, 125.77 MHz): δ 164.59, 144.90, 142.29, 132.46, 122.52, 122.05, 121.45, 117.50, 112.34. HRMS (ESI, M+H⁺) *m/z* calcd C₉H₉N₂O calculated mass 161.0715; actual mass 161.0714

Procedure for hypoxic metabolism.

In a typical enzymatic reaction, **42** ($4 \mu L$ from 50 mM in DMF, final concentration 0.8 mM), **50**, **51** or non-fluorescent electron acceptor (24 μL from 50 mM in 15 % DMF water, final concentration 6.4 mM), was added to xanthine in water(20-160 μL of 10 mM, final concentration 0.8 mM-6.4 mM. Then, xanthine oxidase (20 μL from 20 U/mL, final concentration 2.4 U/mL), sodium phosphate buffer (6 μL from 50 mM, final concentration 12 mM, pH 7.4) and HPLC water were added to xanthine-**42** solution to obtain the final solution (0.25mL, less than 2% DMF) at room temperature (24^oC). In anaerobic reactions, all reagents except xanthine oxidase were de-gassed in glass tubes by three freeze pump thaw cycles. The glass tubes were broke open inside an argon-purged glove bag and bubbled with argon for five minutes. All reagents were mixed inside the glove bag. Upon mixing, the containers were wrapped with aluminum foil to prevent exposure to light.

Procedure for Fluorescence experiment

Upon completion of incubation reaction solution was diluted up to 1 mL with sodium phosphate buffer (50 mM, pH 7.4) in HPLC water and then was added to the cuvette. In anaerobic experiments, upon completion the reaction mixtures were taken out of glove bag and kept 1 h under atmospheric conditions prior to the dilutions.

Procedure for LC/MS analysis. In vitro enzymatic metabolism of **42** or **50** was carried out as described above and the resulting products were extracted into ethyl acetate and dried using brine followed by roto vap evaporation of ethyl acetate. The solid was redissolved in methanol and analyzed by LC/MS in the positive ion mode. Separation of metabolites was carried using a C18 reverse phase Phenomenex Luna column (5 μ m

particle size, 100 A0 pore size, 150 mm length, 2.00 mm i.d.) and a ThermoSeparations liquid chromatograph (TSP4000) and the metabolites were detected by their UV-absorbance at 254 nm. The elution started with a gradient of A, 99% HPLC water (0.1% acetic acid) and B acetonitrile (0.1% acetic acid) followed by a linear increase to 90 % B over the course of 30 min. The elution was continued at 90% B for 3 min and decreased to 1% over the next 8 min. A flow rate of 0.35 mL/min was used. The LC/ESI-MS analyses were carried out in the positive ion mode on a Finnigan TSQ 7000 triple quadrupole instrument using a 250 kV needle voltage and at a capillary temperature of 250 °C.



¹H – NMR of **50** (300 MHz, MeOD)



¹³C NMR of **50** (MeOD, 125.77 MHz)



¹H NMR of **45** (CDCl₃, 300 MHz)



¹³C NMR of **45** (CDCl₃, 75.5 MHz)



¹H NMR of **52** (CDCl₃, 500 MHz)



¹³C NMR of **52** (CDCl₃, 125.77 MHz)



¹H – NMR of **51** (500 MHz, MeOD)



¹³C NMR of **51** (MeOD, 125.77 MHz)



¹H NMR of **54** (CDCl₃, 500 MHz)



¹³C NMR of **54** (CDCl₃, 125.77 MHz)

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Chapter 4

Mechanistic analysis related to the oxidative DNA Damage caused by 1,2,4-benzotraizine-di-oxides, TPZ and analogs of TPZ

4.1 Introduction

Tirapazamine, **33**, (**TPZ**), 3-amino-1,2,4-benzotriazine 1,4-dioxide is currently in phase I, II and III clinical trials for tumor therapy.¹ TPZ emerged as the lead compound among di N-oxide bioreductive drugs.² TPZ causes cytotoxicity to cell, as found in low oxygenated regions (hypoxic) in solid tumors.³ It is believed that the anti-cancer activity caused by TPZ originates from its ability to cleave DNA under hypoxia.⁴ The DNA damage, caused to tumor cells by TPZ arises from the drug radical anion, which is produced by the reduction of TPZ by cellular reductases under low oxygen levels.⁵ The enzymatic reduction of TPZ is an oxygen sensitive reaction.^{3a, 6} The oxygen sensitivity is due to the oxidation of TPZ radical anion 37, which is formed by the main forward reduction step, back to the parent TPZ.⁷ Molecular oxygen forms superoxide radical in the back oxidation step.⁸ The oxidative stress arises due to the superoxide radical formation, in normal oxygenated conditions, but this process is reduced by cellular defense system against reactive oxygen species, which is a collection of enzymes such as glutathione peroxidase, peroxiredoxins, catalase, and superoxide dismutase.⁹ In hypoxia TPZ radical anion 37 gets protonated to a drug radical 34.¹⁰ DNA is the prime target of the oxidizing species generated following the reduction of TPZ.¹¹ The neutral drug radical **34** generates a DNA damaging radical species before ultimately producing the major metabolite **35** (Scheme 4.1).¹²



Scheme 4.1. Enzymatic reduction of 33 produces DNA damaging radicals and oxidative stress

The oxidative damage to DNA, caused by TPZ is characterized as proton abstraction from deoxyribose sugar backbone and DNA bases.^{5b} The oxidative damage to DNA leads to DNA strand breaks.¹³ The chemical nature of the DNA damaging species that is emitted during the oxygen sensitive enzymatic reduction of TPZ is not completely characterized.^{10, 14}

4.2 Mechanistic evidence for the oxidizing radical formation by TPZ

Research carried out by our group suggests that the activated TPZ produces a radical anion **37** and under low oxygen levels **37** undergoes protonation to produce **34**, followed by a homolytic bond scission on **34** releases hydroxyl radical and produces 1-*N*-oxide metabolite **35**.^{4a, 14c, 15} Similar homolytic fragmentation is proposed on Barton's *N*-hydroxypyridinethione esters in literature.¹⁶ Another report on *N*-(alkoxy) pyridinium salts discusses homolytic fragmentation induced by photo-induction.¹⁷ Moreover, radical scavenging experiments and DNA cleavage pattern studies suggest that homolytic fragmentation of di-*N*-oxides such as **34** to produce hydroxyl radical is chemically

plausible.^{4a, 14c} Another hypothesis proposed by Denny and co-workers, suggests that **34** undergoes dehydration to form benzotriazinyl radical **38** and they provide evidence for **38** as the species that is responsible for the DNA damage caused by TPZ.^{10, 14a, b} Intermediate **34** is, generated radiolytically and has been tested for DNA damage.¹⁸ Similar organic radical formation is reported when hydroxyl radicals are generated by pulse radiolysis in the presence of toluene to produce benzyl radicals.¹⁹



Scheme 4.2. Different mechanisms are proposed to explain enzymatic metabolism of 33

We feel that mechanistic investigation of bio-reductive activation of TPZ under low oxygen concentrations may provide a better understanding on the chemical structure of the DNA damaging species and could be important in designing novel TPZ analogs.

4.3 Hypothesis and design of experiments

The benzotriazine 1,4-dioxide analog (desH) **55** may be used to analyze the dehydration mechanism of benzotriazine di-oxides. Metabolic studies of **55** when **55** was enzymatically reduced, in hypoxia may produce **59** as the major metabolite.²⁰ The enzymatic metabolism of **55** might be similar to that of 1,2,4-benzotriazine 1,4-dioxide drug class; the major metabolite formed is 1,2,4-benzotriazine 1-mono-oxide.^{14c} The reduction profile of **55** mirrors the metabolism of 1,2,4-benzotriazine 1,4-dioxide

(Scheme 4.3).²⁰ In the enzyme mediated, one electron reduction of **55**, radical anion **56**, is produced and under normal oxygen concentration, **56** can be oxidized back to **55**.²⁰ Under hypoxia **56** gets protonated to form the drug radical **57**, which produces the DNA damaging species and the major metabolite **59**.^{20b} The dehydration mechanism produces radical **58** by eliminating a water molecule. The radical **58** may abstract a proton from an organic substrate to undergo re-aromatization to form **59** (lower arm). Alternatively, hydroxyl radical mechanism performs homolytic fragmentation on **57** to produce hydroxyl radical and the major metabolite **59**.



Scheme 4.3. Enzymatic reduction of 55 under low oxygen concentrations forms major metabolite 59

In the design, we speculated that deuterated analog of 1,2,4-benzotriazine- 1,4dioxide **60** (desD) may offer a new approach to analyze the dehydration mechanism. When 1,2,4-benzotriazine- 1,4-dioxide **60** is reductively activated to radical anion **61**, protonation occurs to form neutral radical **62**. The homolytic fragmentation of **63** produces hydroxyl radical and the major metabolite **63**. When the dehydration mechanism occurs on **60**, the neutral drug radical **62** converts to radical **58** and **58** may abstract a deuterium from an organic substrate to produce **63**. Similarly, when **55** is reductively activated under hypoxia, in the presence of a deuterated organic substrate, the dehydration mechanism might produce radical **58** and, upon deuterium abstraction major metabolite **63**. Accordingly, the loss or incorporation of deuterium/hydrogen can be detected when the isotopic content of the major metabolite 1-oxide is analyzed using mass spectrometry (Scheme 4.4).



Scheme 4.4. Isotopic content of major metabolite of 55/60 determines mechanism

4.4 Examine the dehydration mechanism in relation to the release of oxidizing species from 1,2,4-benzotriazine-di-oxide

Various TPZ analogs such as 3-methyl-1,2,4-benzotriazine 1,4-dioxide (Me-TPZ) and 1,2,4-benzotriazine 1,4-dioxide, **55**, have been used in cytotoxicity assays.²¹ The anti-cancer activity of these analogs is similar and comparable to that of TPZ. Structurally and functionally similar benzotriazine di-oxide analogs can be used as tools to study the chemical nature of DNA damaging species and mechanism for the formation of DNA damaging species.^{14b, c, 22} A study carried out by Raman Junnotula in our group used 3-methyl-1,2,4-benzotriazine 1,4-dioxide (MeTPZ) to investigate the formation of benzotriazinyl radical and explored the dehydration mechanism.^{20b} The current chapter describes a similar related mechanistic study. In the beginning, compounds **55** and **60** are

synthesized. The metabolism and DNA damaging properties of **55** and **60** were compared against TPZ for their ability to cause DNA damage under reductive enzyme activated hypoxic conditions.

4.5 Chemical Synthesis of 1,2,4-benzotriazine-1,4-dioxide

The compound 1,2,4-benzotriazine 1,4-dioxide **55** was obtained by known methods using TPZ as the starting material in the preparation. Briefly, in an argon-purged glove bag two glass vials were added with TPZ in anhydrous DMF and *tert*-butyl nitrite in anhydrous DMF (argon was purged upon preparing stock solutions). Then, the *tert*-butyl nitrite solution was heated to 65° C, and to this TPZ in DMF was added slowly over 10 min. Then the mixture was cooled to room temperature. The solution was removed from the glove bag, and DMF was removed using high vacuum. Brownish yellow crude material was used to perform column chromatography, followed by preparative thin layer chromatography separated product **55**. The deuterated analog **60** was prepared using deuterated DMF as the solvent. Synthesis of **55** was followed exactly to prepare and separate **60**. The compound 3-amino 1,2,4-benzotriazine 1-*N* oxides **59** and **63**. Same procedure, which was followed to synthesize **55** was adopted in the preparation of **59**.and **63**, using deuterated DMF as the solvent.

4.6 DNA-damaging properties of 1,2,4-benzotriazine-1,4-dioxide analogs and TPZ

4.6.1 TPZ analogs perform concentration dependent DNA damage

Cytotoxicity caused by TPZ and 1,2,4-benzotriazine-1,4-dioxide **55** are similar.^{21a} In TPZ, the cytotoxicity derives from its ability to initiate oxidative damage to cellular DNA. In the current work, the damage to DNA caused by TPZ was analyzed using plasmid DNA damage based assays. In the plasmid DNA-based assay, the supercoiled form I DNA molecule converts to form II when a hydrogen atom is abstracted from the sugar phosphate backbone. The DNA which is nicked will be converted to form II and intact DNA, the form I, is detected and quantified on agarose gel-based method.²³ Similar DNA-damaging study with **55** and **60** provides a comparative DNA damage study among TPZ drug class. In the anaerobic assays TPZ, **55** or **60** were activated using NADPH:cytochrome P450 reductase and upon activation the oxidative DNA damage would assume on plasmid DNA. Gel pictures obtained upon completion of assays, conducted using **TPZ**, **55** and **60** showed an increase in the amount of form II DNA with the concentration of respective di- *N*-oxide (Figures 4.1, 4.2 and 4.3).



Figure 4.1: Cleavage of supercoiled plasmid DNA by **33** (50-250 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/ mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 6 h, followed by agarose gel electrophoretic analysis. lane 1, **33** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 0.75 ± 0.04); lane 2, **33** (100 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.25 ± 0.14); lane 3, **33** (150 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.74 ± 0.21); lane 4, **33** (200 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 2.58 ± 0.14); lane 5, **33** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.74 ± 0.21); lane 4, **500** μ M) + reductase (33 mU/mL) (S = 3.53 ± 0.32). The value S represents the mean number of strand breaks per plasmid molecule and is calculated using the equation S = -ln f_I, where f_I is the fraction of plasmid present as form I.



Figure 4.2: Cleavage of supercoiled plasmid DNA by **55** (50-250 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/ mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 6 h, followed by agarose gel electrophoretic analysis. lane 1, **55** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 0.77 ± 0.02); lane 2, **55** (100 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.10 ± 0.08); lane 3, **55** (150 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.27 ± 0.07); lane 4, **55** (200 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.71 ± 0.17); lane 5, **55** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.71 ± 0.17); lane 5, **55** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.71 ± 0.17); lane 5, **55** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.71 ± 0.17); lane 5, **55** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = -ln f_I, where f_I is the fraction of plasmid present as form I.²⁴



Figure 4.3: Cleavage of supercoiled plasmid DNA by **60** (50-250 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/ mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 6 h, followed by agarose gel electrophoretic analysis. lane 1, **60** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 0.66 ± 0.04); lane 2, **60** (100 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 0.87 ± 0.07); lane 3, **60** (150 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.12 ± 0.12); lane 4, **60** (200 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.36 ± 0.03); lane 5, **60** (250 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) (S = 1.81 ± 0.22). The value S represents the mean number of strand breaks per plasmid molecule and is calculated using the equation S = -ln f_I, where f_I is the fraction of plasmid present as form I.

The amount of nicking can be represented as S values (S = $-\ln f_I$, where f_I is the fraction of plasmid present as form I) of **TPZ**, **55** and **60**. The S values of **TPZ**, **55** and **60** show a positive correlation between DNA strand cleavage and respective drug

concentration. As the concentration of drug is increased, under identical enzyme mediated reductive activation, the DNA damage is increased (Figures 4.1, 4.2, 4.3 and 4.4). This behavior is a reported trend among *N*-di-oxides when they are metabolized in the presence of plasmid DNA under reductively activated hypoxic conditions.²⁵ In addition, control experiments were carried out without the activating enzyme, substrate or drugs to show that the observed DNA damage occurs solely due to the reductively activation of di-*N*-oxides. Reductive activation, under aerobic conditions, of TPZ, **55** or **60** is unable to produce considerable DNA damage compared to anaerobic reactions (Table 1).





Figure 4.4. Comparison of DNA cleavage by reductively activated **33**, **55** and **60** under anaerobic conditions (black line-strand cleavage by **33**, red line-**55** and green line-**60**. Supercoiled plasmid DNA (33 μ g/mL, pGL-2 Basic) was incubated with drug (50-250 μ M), NADPH (500 μ M), cytochrome P450 reductase (33 mU/mL), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (0.5-2.5% v/v), and desferal (1 mM) under anaerobic conditions at room temperature for 6 h, followed by agarose gel electrophoretic analysis. The values, S, derived from agarose gel data and represent the mean number of strand breaks per plasmid molecule and were calculated using the equation S = -ln f_I, where f_I is the fraction of plasmid present as form I.²⁴ Background cleavage in the untreated plasmid was subtracted to allow direct comparison of DNA cleavage yields between different experiments.

Reaction	% form II	S value
DNA alone	17.4	0.19±0.07
NADPH:cytochrome P450		
reductase/NADPH aerobic	14.3	0.15±0.06
NADPH:cytochrome P450 reductase	17.3	0.19±0.02
55 alone	16.5	0.18±0.03
55+NADPH:cytochromeP450		
reductase/NADPH aerobic	17.0	0.18±0.03
60 alone	29.3	0.38±0.70
60+NADPH:cytochromeP450		
reductase/NADPH aerobic	25.8	0.29±0.74
55 alone	16.5	0.18±0.03
55+NADPH:cytochromeP450		
reductase/NADPH aerobic	17.0	0.18±0.03
33 alone	11.6	0.19±0.01
33+NADPH:cytochromeP450		
reductase/NADPH aerobic	20.7	0.23±0.08

 Table 4.1. Cleavage of plasmid DNA in control reactions

To test the chemical nature of the DNA damaging species, plasmid DNA based damaging assays were carried out in the presence of radical scavenging agents as a reagent in reaction solutions. The DNA damage caused by **33**, under reductive enzyme activity in hypoxia, diminishes in the presence of radical scavenging agents such as methanol, ethanol, *t*-butanol, DMSO and mannitol. Analogous radical scavenging assays were carried out using **55** and **60**. The agarose gels obtained from the radical scavenging assays of **55** and **60** are qualitatively and quantitatively comparable with those obtained with **33** (Figures 4.5, 4.6 and 4.7). The DNA damage caused by reductive activation of **33**, **55** and **60** under hypoxia has been decreased by the addition of radical scavengers. It is well established that the radical scavengers used in the current assay reacts with hydroxyl radicals. Hence, homolytic fragmentation mechanism, which is proposed to explain the formation of hydroxyl radical in the metabolism of **33**, is also plausible to occur when **55** and **60** undergo reductive activation in our assay conditions



Figure 4.5. Cleavage of supercoiled plasmid DNA by **33** (25 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system is reduced by radical scavengers. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 4 h, followed by agarose gel electrophoretic analysis. Lane 1, **33** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) ($S = 0.67 \pm 0.09$); lanes 2-6, **33** (50 μ M) + NADPH (500 μ M) + methanol (500 mM, lane 2) ($S = 0.32 \pm 0.01$); ethanol (500 mM, lane 3) ($S = 0.35 \pm 0.04$); *tert*-butyl alcohol (500 mM, lane 4) ($S = 0.32 \pm 0.05$); DMSO (500 mM, lane 5) ($S = 0.35 \pm 0.06$); mannitol (500 mM, lane 6) ($S = 0.32 \pm 0.05$); The value *S* represents the mean number of strand breaks per plasmid molecule and is calculated using the equation $S = -\ln f_1$, where f_1 is the fraction of plasmid present as form I.



Figure 4.6. Cleavage of supercoiled plasmid DNA by **55** (50 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system is reduced by radical scavengers. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 4 h, followed by agarose gel electrophoretic analysis. Lane 1, **55** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) ($S = 0.66 \pm 0.13$); lanes 2-6, **55** (50 μ M) + NADPH (500 μ M) + methanol (500 mM, lane 2) ($S = 0.25 \pm 0.08$); ethanol (500 mM, lane 3) ($S = 0.29 \pm 0.08$); *tert*-butyl alcohol (500 mM, lane 4) ($S = 0.27 \pm 0.04$); DMSO (500 mM, lane 5) ($S = 0.30 \pm 0.04$); mannitol (500 mM, lane 6) ($S = 0.28 \pm 0.07$);. The value *S* represents the mean number of strand breaks per plasmid molecule and is calculated using the equation $S = -\ln f_{\rm I}$, where $f_{\rm I}$ is the fraction of plasmid present as form I.



Figure 4.7. Cleavage of supercoiled plasmid DNA by **60** (50 μ M) in the presence of NADPH:cytochrome P450 reductase as an activating system is reduced by radical scavengers. All reactions contained DNA (33 μ g/mL, pGL-2 Basic), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (2.5% v/v), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), and desferal (1 mM) and were incubated under anaerobic conditions at 24 °C for 4 h, followed by agarose gel electrophoretic analysis. Lane 1, **60** (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL) ($S = 0.58 \pm 0.10$); lanes 2-6, **60** (50 μ M) + NADPH (500 μ M) + methanol (500 mM, lane 2) ($S = 0.36 \pm 0.06$); ethanol (500 mM, lane 3) ($S = 0.36 \pm 0.06$); tert-butyl alcohol (500 mM, lane 4) ($S = 0.38 \pm 0.05$); DMSO (500 mM, lane 5) ($S = 0.35 \pm 0.06$); mannitol (500 mM, lane 6) ($S = 0.37 \pm 0.09$);. The value *S* represents the mean number of strand breaks per plasmid molecule and is calculated using the equation $S = -\ln f_{I}$, where f_{I} is the fraction of plasmid present as form I.



Figure 4.8. Comparison of DNA cleavage by reductively activated **33** (blue), **55** (red) or **60** (green) under anaerobic conditions and DNA cleavage is inhibited by radical scavengers. Supercoiled plasmid DNA (33 μ g/mL, pGL-2 Basic) was incubated with drug (50 μ M), NADPH (500 μ M), cytochrome P450 reductase (33 mU/mL), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (0.5-2.5% v/v), and desferal (1 mM) under anaerobic conditions at room temperature for 4 h, followed by agarose gel electrophoretic analysis. Lane 1, drug (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL); lanes 2-6, drug (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL); lanes 2-6, drug (50 μ M) + NADPH (500 μ M) + reductase (33 mU/mL); lanes 2); ethanol (500 mM, lane 3); *tert*-butyl alcohol (500 mM, lane 4); DMSO (500 mM, lane 5); mannitol (500 mM, lane 6); The values, S, derived from agarose gel data and represent the mean number of strand breaks per plasmid molecule and were calculated using the equation S = -ln f_I, where f_I is the fraction of plasmid present as form I. Background cleavage in the untreated plasmid was subtracted to allow direct comparison of DNA cleavage yields between different experiments.

4.7 Examining the chemical mechanism of bioreductive metabolism of 55 and 60

Metabolite identification showed that the reductive activation of drugs under anaerobic conditions produced 1-*N*-oxide. In this way, the metabolism mirrors TPZ.²⁰ Cytotoxicity assay results of TPZ and **55** show comparable anti-cancer activity. Hence, it can be suggested that TPZ and **55** would follow the same mechanism of DNA damage which forms the oxidizing radical under reductively activated conditions in hypoxia. To test the DNA damaging mechanism, we designed comparative metabolic experiments with **55** and the isotopically labeled analog of **55**, **60**.

4.8 Metabolic studies of 55 and 60 with organic substrate

Metabolic studies were carried out to test the metabolism of **60** and **55** by enzymatic reducing system in the presence of an organic substrate. To test the metabolism of **60**, NADPH:cytochrome P450 reductase and NADPH was used as the enzyme system and CH₃OH was added as the organic substrate. The reaction was carried out under anaerobic conditions in aqueous sodium phosphate buffer at pH 7.4. Upon metabolism the reaction mixture was subjected to be analyzed by LC/MS for the metabolites of **60**. Anaerobic metabolism of **60** produced **63** as the major metabolite with **64** and **65** as minor metabolites. In a metabolic analysis carried out using **55** with CD₃OD in deuterated water under anaerobic conditions using sodium phosphate buffer at pD 6.6 produced major metabolite **59** and minor metabolites **66** and **67** (Scheme 4.5).



Scheme 4.5 Enzymatic metabolism of 60 and 55 with organic substrate in anoxia

The complete LC/MS analysis for the metabolism of **60** shows retained deuterium in metabolites **63**, **64** and **65** (Figure 4.9 panels A, C, D and E). Hence benzotriazine radical **58** is unlikely to be formed in the bio-reductive metabolism of **60** (Scheme 4.4). Moreover, in the LC/MS analysis of metabolites **59**, **66** and **67**, derived from metabolism of **55** shows no exchange of deuterium into metabolites (Figure 4.9 panels F, H, I and J). Similar to the metabolism of **60**, compound **55** may not form the benzotriazine radical **58** over the anaerobic bio-reduction process (Scheme 4.4).



Figure 4.9. LC/MS analysis of anaerobic metabolism of **55** and **60** (0.5 mM) by cytochrome p450 reductase (0.4 U/mL) and NADPH (0.5 mM). The enzymatic reduction of **55/60** was carried out as described in the experimental section. The reaction was dried and products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC of the anaerobic reaction mixture of **60** monitoring absorbance at 254 nm. Panel B: LC/MS of **60**; eluting at 9.2 min. Panel C: LC/MS of metabolites of **60**; product eluting at 12.45 min. Panel D: LC/MS of metabolites of **55** eluting at 9.25 min. Panel H: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS of metabolites of **55**; product eluting at 12.54 min. Panel I: LC/MS o

LC/MS analysis of authentic **60**, **63**, **55**, and **59**, using the same LC/MS method, used to analyze anaerobic reaction mixtures of **60** and **55** metabolism shows comparable retention times and mass values with that of LC/MS analysis of **60** and **55** shown in figure 4.11.



Figure 4.10. LC/MS analysis of authentic **60**, **63**, **55** and **59**. The products dissolved in methanol. The mixture was eluted with a gradient of 99% A (water containing 0.1% acetic acid) and 1% B (acetonitrile containing 0.1% acetic acid) followed by linear increase to 90% B over 30 min. The elution was continued at 90% B for 3 min and then B was decreased to 1% over next 8 min. A flow rate of 0.35 mL/min was used and the metabolites were detected at 254 nm. Mass spectra were obtained using electrospray ionization in the positive ion mode. Panel A: HPLC of **60** monitoring absorbance at 254 nm. Panel B: LC/MS of **60** eluting at 8.56 min. Panel C: HPLC of **63** monitoring absorbance at 254 nm. Panel B: LC/MS of **63** eluting at 15.04 min. Panel E: HPLC of **55** monitoring absorbance at 254 nm. Panel F: LC/MS of **55** eluting at 9.03 min. Panel G: HPLC of **59** monitoring absorbance at 254 nm. Panel H: LC/MS of **59** eluting at 14.20 min.

4.9 Deuterium incorporation into 55

The dehydration mechanism is further tested using 55 and 60 (Scheme 4.4). In the initial one electron reduction step the di-oxide 55 or 60 will convert to a radical anion and upon protonation, drug radicals 57 and 62 may persist under low oxygen levels. In order to follow the dehydration mechanism, removal of water molecule from 57 and 62 should form radical cation 58 and 58 can abstract hydrogen from an organic substrate (Scheme 4.4). If the dehydration mechanism is plausible, the hydrogen of organic substrate may be abstracted into the major metabolite. HRMS analysis of major metabolite is able to show isotopic content which shows any hydrogen abstraction event (Scheme 4.4). To test the dehydration mechanism, 55 was activated in the presence of CD_3OD , in D_2O -sodium phosphate buffer medium at pD 6.6. The major metabolite 1-N oxide was separated and HRMS data suggests molecular formula $C_7H_5N_3O$ for the molecular ion peak (M) with m/z of 147.1. Formation of 63, resulted by dehydration mechanism might have produced a molecular ion peak having m/z of 148.1, which is the M+1 ion in the current assay. The intensity of M+1 ion is 2% higher than that of a control experiment, carried out using 55 in the presence of CH_3OH in aqueous sodium phosphate buffer at pH 7.4. The 2% difference of M/z of M+1, between 55 in CD₃OD reaction and 55 in CH₃OH control may have caused due to the presence of naturally abundant isotopes such as 13C, 15N and 2H or may be occurrence of dehydration mechanism as a minor reaction (Figure 4.11).


Figure 4.11. HRMS of the major metabolite 1-*N*-oxide **59** arising from metabolism of **55** under reductively activated conditions in hypoxia. Briefly **55** (10 mM) was incubated with NADPH (500mM) and NADPH:cytochrome P450 reductase (0.5 U/mL) in argon purged bag with either A) sodium phosphate buffer (30 mM) at pD 6.6 in D_2O and CD_3OD (2 mM) were added and incubated over 4 hours. B) sodium phosphate buffer (30 mM) at pH 7.4 in H_2O and CH_3OH (2M) were added and incubated over 4 hours. Upon completion reactions A and B were extracted to EtOAc and dried in vacuum. Thin layer chromatography was used to separate the major 1-*N*-oxide metabolite in both A and B. Then corresponding area related to the R_f value for 1-*N*-oxide was scratched using a metal blade to collect silica. The organic material was extracted to EtOAc from silica and dried in vacuum. The dry organic extract was dissolved in CH₃CN and directed for HRMS analysis.

4.10 Isotope washout from drug 60

Metabolism of **60** was carried out under anaerobic reducing conditions in the presence of CH₃OH in sodium phosphate buffer at pH 7.4 to study the isotopic content of the major metabolite using HRMS. Under dehydration mechanism, deuterium of **60** is removed as water and the major metabolite **59** may form via benzotriazinyl radical **58** (Scheme 4.4). HRMS analysis of molecular ion (M) of the major metabolite shows $C_7H_4DN_3O$ as the molecular formula with m/z of 148.1. Due to dehydration mechanism, if **59** had formed, m/z of the molecular ion should be 147.1 m/z. When the peak intensity of M-1 ion, formed from the reaction **60** with CH₃OH is compared with the control, **60** with CD₃OD in D₂O-sodium phosphate buffer medium at pD 6.6, shows only 3%

increase in the former reaction, **60** with CH_3OH . This 3% increase might have occurred due to dehydration mechanism, which had occurred as a minor reaction path (Figure 4.12).



Figure 4.12. HRMS of the major metabolite 1-*N*-oxide **63** arising from metabolism of **60** under reductively activated conditions in hypoxia. Briefly **60** (10.mM) was incubated with NADPH (500mM) and NADPH:cytochrome P450 reductase (0.5 U/mL) in argon purged bag with either A) sodium phosphate buffer (30mM) at pH 7.4 in H₂O and CH₃OH (2 mM) were added and incubated over 4 hours. B) Sodium phosphate buffer (30 mM) at pD 6.6 in D₂O and CD₃OD (2 mM) were added and incubated over 4 hours. Upon completion reactions A and B were extracted to EtOAc and dried in vacuum. Thin layer chromatography was used to separate the 1-*N*-oxide in A and B. Then corresponding area related to the R_f value for 1-*N*-oxide was scratched using a metal blade to collect silica. The organic material was extracted to EtOAc and dried in vacuum. The dry organic extract was dissolved in CH₃CN and directed for HRMS analysis.

4.11 Isotope replacement analysis and dehydration mechanism

The results of metabolic experiments of **55**, with CD₃OD and **60** in the presence of CH₃OH suggest that the dehydration mechanism may occur as a minor path, responsible for enzyme mediated activation of 1,2,4-benzotraizine-1,4-dioxides under hypoxia. Alternatively, hemolysis of N-O bond, which is evident by radical scavenging studies, suggests that hydroxyl radical might be the oxidizing radical formed in the metabolism of **55** and **60**. The homolytic fragmentation over the bio-reductive metabolism of **55** and **60** is possible to occur as the major metabolic path under hypoxic bio-reductive conditions.

4.12 Conclusion

The work related to this chapter describes the use of 1,2,4-benzotriazine-1,4dioxide **55** as a mechanistic handle to analyze dehydration mechanism. The dehydration mechanism is proposed to explain the chemical structure of the oxidizing radical, released by these *N* oxide drugs in hypoxia under reductive activation.^{10, 12, 26} The drug 1,2,4-benzotriazine-1,4-dioxide may have formed benzotriazinyl radical as a minor oxidizing radical via dehydration mechanism.¹⁰ In our study we showed that drugs **55** and **60** produce DNA cleavage, comparable to the DNA damage caused by **33**. In addition, the radical scavenging experiments with **33**, **55** and **60** showed reduced DNA damage and diminished DNA damage suggest the involvement of hydroxyl radical as the major DNA damaging process.^{4a, 14c}

The results of the experiments, carried out to test deuterium incorporation to **55** in the presence of CD_3OD and deuterium release from **60**, in the presence of CH_3OH were not consistent with the dehydration mechanism as the major mechanism in the enzymatic metabolism of 1,2,4-benzotriazine-1,4-dioxide.

Finally, based on various experiment results related to mechanistic studies on *N*di-oxides, it can be concluded that the one electron reduction of 1,2,4-benzotriazine-1,4dioxide produces hydroxyl radical as the oxidizing species which might be the major source that carries out DNA cleavage.

4.13 Experimental

4.12.1 Materials. Materials were of the highest purity available and were obtained from following sources: cytochrome P450 reductase, NADPH, sodium phosphate, mannitol, DMSO desferal, , catalase, and superoxide dismutase (SOD) from Sigma Chemical Co. (St. Louis, MO); agarose from Seakem; HPLC grade solvents (acetonitrile, methanol, ethanol, tert-butyl alcohol, ethyl acetate, hexane, and acetic acid) from Fischer (Pittsburgh, PA); ethidium bromide from Roche Molecular Biochemicals (Indianapolis, IN). Standard protocol was used to prepare plasmid DNA pGL2BASIC.²⁷ Published methods in literature were followed to prepare TPZ **1** and other N-oxides.^{20a, 28}

4.12.2 Synthesis of 1,2,4-benzotriazine-1,4-bioxide 55

Argon was purged into dry DMF for 5 min inside an argon filled glove bag. Then TPZ (115mg, 0.644 mmol) was dissolved in (2 mL) DMF. To another degassed DMF sample (2 mL) *tert*-butyl nitrite (0.25 ml, 2.05 mmol) was added and heated to 65° C inside the glove bag. To this solution, TPZ was added and heated for 10 min at 65° C with stirring. Upon completion reaction time the reaction mixture was cooled to room temperature and DMF was removed by vacuum. Then column chromatography (1:1 EtOAc/hexane) was performed to obtain (40 mg, 34 %). Deuterated DMF was used in the preparation of 3 position deuterated 1,2,4-benzotriazine-1,4-dioxide. R_f of is 0.50 (100% EtOAc): ¹H NMR (Acetone, 500 MHz,): δ 9.04 (s, 1H), 8.42 (dd, 2H), 8.15 (m, 1H), 8.03 (m, 1H). ¹³C-NMR (Acetone, 125.8 MHz,): δ 142.73, 141.01, 136.50, 136.01, 133.54, 122.20, 120.19; HRMS (ES⁺, [M+H]) *m*/*z* calcd C₇H₆N₃O₂ calculated mass 164.0460; actual mass 164.0453.

4.12.3 Synthesis of 3 position deuterated 1,2,4-benzotriazine-1,4-dioxide 60

The procedure used to synthesize **55** was followed to prepare **60**. In synthesis, deuterated DMF was used instead of DMF.

¹H NMR (Acetone, 500 MHz,): δ 8.42 (dd, 2H), 8.15 (m, 1H), 8.03 (m, 1H). ¹³C-NMR (Acetone, 125.8 MHz,): δ 142.47 (t, J = 32.7 Hz), 141.02, 136.52, 136.02, 133.54, 122.20, 120.18; HRMS (ES⁺, [M+H]) *m/z* calcd C₇H₅DN₃O₂ calculated mass 165.0523; actual mass 165.0515.

4.12.4 Synthesis of 1,2,4-benzotriazine-1-oxide 59

Anhydrous DMF was bubbled with argon for 5 min inside a argon filled glove bag. Then **35** (365mg, 2.2 mmol) was dissolved in (3 mL) DMF. To another DMF sample (3 mL) *tert*-butyl nitrite (1.07 ml, 8.8 mmol) was added and heated to 65° C inside the glove bag. To this solution TPZ was added and heated for 10 min at 65° C with stirring. Upon completion reaction time the reaction mixture was cooled to room temperature and DMF was removed by vacuum. Then column chromatography (1:1 EtOAc/hexane) was performed to obtain (77 mg, 34 %). R_f = 0.50 (100% EtOAc)

¹H NMR (Acetone, 300 MHz): δ ppm 9.05 (s, 1H), δ 8.42 (d, J = 8.5 Hz, 1H), δ 8.11 (m, 2H), δ 7.91 (m, 1H) ¹³C NMR (Acetone, 75.5 MHz): δ 155.02, 148.32, 136.66, 131.99, 130.05, 120.63; HRMS (ES⁺, [M+H]) m/z calcd $C_7H_6N_3O$ calculated mass 148.0511; actual mass 148.0517.

4.12.5 Synthesis of 1,2,4-benzotriazine-3-deuterium-1-oxide 63

The synthetic method used to prepare **59** was exactly followed to synthesized **63** and deuterated DMF was used instead of DMF. ¹H NMR (Acetone, 300 MHz): δ ppm 8.40 (d, J = 8.5 Hz, 1H), 8.08 (m, 2H), 7.88 (m, 1H) ¹³C NMR (Acetone, 75.5 MHz): δ 154.72 (t, J = 32.7 Hz), 148.34, 136.66, 131.99, 130.06, 120.64; HRMS (ES⁺, [M+H]) m/z calcd C₇H₅DN₃O calculated mass 149.0574; actual mass 149.0579.

4.12.6 DNA damage assays

In normal anaerobic DNA cleaving assay, the drug TPZ, **55** or **61** (5-25 μ M) was incubated with supercoiled plasmid DNA (33 μ g/mL, pGL-2 Basic), NADPH (500 μ M), cytochrome P450 reductase (33 mU/mL), catalase (100 μ g/mL), superoxide dismutase (10 μ g/mL), sodium phosphate buffer (50 mM, pH 7.0), acetonitrile (0.5-2.5% v/v), and desferal (1 mM) under anaerobic conditions at 25 °C for 4 h. Three freeze-pump-thaw cycles were performed on all solutions except enzymes, NADPH, and DNA. To prepare reaction mixtures deoxygenated water was used in an argon-filled glove bag and cytochrome P450 reductase was added as the last reagent to start the reaction. Then the reaction containers were kept in the argon purged glove bag upon wrapped in aluminum foil to prevent exposure to light. The reactions were quenched by addition of 5 μ L of 50% glycerol loading buffer and were loaded onto a 0.9% agarose gel and electrophoresed for approximately 2.0 h at 85 V in 1x TAE buffer. Upon completion of electrophoretic separation, the gels were removed and soaked in an aqueous ethidium bromide (0.3 μ g/mL) solution for staining for 4 h. To visualize DNA UV-transillumination was performed on gels and DNA band quantification was performed using quantity one imaging system. The values reported are not corrected for differential staining of form I and form II DNA by ethidium bromide.

The radical scavenging DNA damage assays were performed following the above typical procedure. The radical scavenging reagents methanol, ethanol, *tert*-butyl alcohol, DMSO, or mannitol (500 mM) were added inaddition to the other reagents prior to the addition of cytochrome P450 reductase. All aerobic reactions were carried out using non de oxygenated soluitons under normal atmosphericconditions.

4.12.7 Metabolic studies related to drugs

In a typical metabolic assay, all solutions except cytochrome P450 reductase (330 mU/mL), catalase (100 μ g/mL) were degassed by three cycles of freeze-pump-thaw cycles. The *N* di-oxide (μ M) was mixed with desferal (1 mM) in sodium phosphate buffer (pH 7, 50 mM), NADPH (500 μ M), catalase (100 μ g/mL), and superoxide dismutase (10 μ g/mL) followed by the addition of cytochrome P450 reductase (330 mU/mL). Upon 4 hr incubation under argon at 25 °C, the organic was extracted to EtOAc (0.5 mL) twice and dried using roto vap. Then the dry reaction mixture was dissolved in 0.5 mL MeOH and was analyzed by LC employing a C18 reverse phase Rainin Microsorb-MV column (5

µm particle size, 100 Å pore size, 25 cm length, 4.6 mm i.d.) eluted with gradient starting at 50% A (0.5% acetic acid in water) and 50% B (acetonitrile) followed by linear increase to 80% B from 0 min to 40 min. A flow rate of 0.6 mL/min was used and the products were monitored by their UV-absorbance at 254 nm. LC/ESI-MS experiments were carried out on a Finnigan TSQ 7000 triple quadrupole instrument interfaced to a ThermoSeparations liquid chromatograph (TSP4000). Positive ion electrospray was used as the means of ionization. The heated inlet capillary temperature was 250 °C and electrospray needle voltage was 4.5 kV. Nitrogen sheath gas was supplied at 80 psi and the LC/ESI-MS analysis was done in the positive ion mode.

4.12.8 HRMS studies related to drugs

In a typical metabolic assay, all solutions except cytochrome P450 reductase (330 mU/mL), catalase (100 μ g/mL) were degassed by three cycles of freeze-pump-thaw cycles. The N di-oxide (μ M) was mixed with desferal (1 mM) in sodium phosphate buffer (pH 7, 50 mM) and NADPH (500 μ M) followed by the addition of cytochrome P450 reductase (330 mU/mL). Upon 4 hr incubation under argon at 25 °C, the organic was extracted to EtOAc (0.5 mL) twice and dried using roto vap. Then the dry reaction mixture was dissolved in 0.5 mL CH₃CN and used to spot on TLC plates. The preparative TLC was run using (1:1 EtOAc/hexane) as the solvent system. The major metabolite mono N oxide was co-spotted when preparation TLC was run. Upon completion the TLC plates were dried in air and the area correspond to 1-N-oxide co-migration was scratched using a metal blade. The dry silica was re-dissolved in EtOAc and EtOAc was removed

to a glass vial. The EtOAc was dried under roto-vap, protected from light and kept in the freezer. The dry samples were sent for HRMS analysis.



¹H NMR of **55** (Acetone, 500 MHz)



¹³C NMR of **55** (Acetone, 125.77 MHz)





¹H NMR of **60** (Acetone, 500 MHz)



¹³C NMR of **60** (Acetone, 125.77 MHz)



¹H NMR of **59** (Acetone, 300 MHz)



¹³C NMR of **59** (Acetone, 75 MHz)



8.404 8.387



¹H NMR of **63** (Acetone, 500 MHz)



¹³C NMR of **63** (Acetone, 125.77 MHz)

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Chapter 5

Synthesis of bioreductivly activated nitroaromatic triggers

5.1. Qualitative and quantitative determination of hypoxia

Chapters 1, 2 and 3 described the importance of hypoxia or low oxygen concentration to tumor physiology and tumor therapy. Detection and quantification of oxygen levels is immerging as an important tool in the treatment of tumors.¹ Various methods of characterization for tumor hypoxia have been introduced to the research community.² As discussed in previous chapters, there is a demand for suitable fluorescent probes to detect hypoxia.³ A complete description of small molecule fluorescent probe, which can detect hypoxia, was included in chapters 2 and 3. In a similar approach, a compound which can undergo hypoxia selective enzymatic bioreduction and maintain oxygen sensitive reduction may be coupled to a fluorophore, to construct fluorescent probes to detect hypoxia.⁴ Nitroaromatic compounds such as para nitrobenzyl, 2-nitroimidazole and 5-nitrothienyl groups and tirapazamine might be used as a bioreductive aromatic compound which can undergo oxygen-sensitive reduction and release the fluorescent molecule (Scheme 5.1).



Scheme 5.1. Bioreducible moieties can be used as oxygen sensors

5.2 Goal: Constructing suitable nitroaromatic fluorescent probe for hypoxia

Current research on bio-reductive pro-drugs suggests that oxygen sensitive bioreducible species such as nitro-benzyl, 2-nitroimidazole and 5-nitrothienyl groups, when appended to cytotoxic agents to mask the drug activity, show encouraging selective drug delivery toward low oxygenated tumors. In order to test the performance of nitro-phenyl group as an oxygen sensor, Borche and coworkers attached phosphoramidite toxin to produce series of prodrugs (Scheme 5.2).⁵ Following the same design strategy, fluorophores can be attached to nitroaromatic groups using suitable coupling reactions.





The in vitro cytotoxicity studies with **26** suggest that nitrophenyl may be a suitable bioreducible moiety which can be reduced enzymatically in hypoxia. The reduction process produces electron rich hydroxylamine or amine compounds which can ultimately release the active compound and imine methide upon 1-6 elimination (Scheme 5.3).



Scheme 5.3. 1,6-elimination of active drug species

Such a prodrug, with a flourophore, was made using nitrophenyl benzyl bromide **68**, over a nucleophilic displacement reaction with 7-hydroxyl-4-methyl coumarine **69**, a known fluorophore which possess a better stokes shift and quantum yield, to produce nitrophenyl-coumarin compound **70** (Scheme 5.3).⁶



Scheme 5.4. Synthesis of 70

Bioreductive in vitro assays were carried out using **70**, with NADPH:cytochrome p450 reductase;NADPH and xanthine:xanthine oxidase reducing systems. The poor release of **69** is comparable to low amount of release of thiopurine, which was attached to nitrobenzyl in the pro-drug form.⁷ While concluding that nitrophenyl group is not compatible for enzymatic reducing systems NADPH:cytochrome p450 reductase;NADPH and xanthine:xanthine oxidase, however we set out to construct other nitroaromatic bioreducible groups 5-nitrothienyl and 2-nitroimidazole.

5.3 Synthesis of 5-nitrothienyl moiety, 2-(5-Nitrothien-2-yl) propan-2-ol (73)

Nitrothiephenes are bioreducible nitroaromatic group, which can be reduced by cellular reductases under low oxygen levels.⁸ In addition, methyl groups on the benzylic carbon facilitates effective drug release from the probe.⁹ Hence, Nitrothienyl 2-(5-Nitrothien-2-yl) propan-2-ol **73** was prepared as a nitroaromatic trigger candidate. Methyl magnesium bromide was added to 2-acetylthiophene **71**, in ethyl ether to afford thiophene alcohol **72**. Compound **72** was separated by column chromatography. Nitration

on the 5 carbon of **72** was done using acetic anhydride: Nitric acid nitration mixture. To a cold solution of **72** in acetic anhydride, fuming nitric acid was added while mixing at - 70^{0} C.¹⁰ Upon neutralizing, using sodium bicarbonate, the product 2-(5-nitrothien-2-yl) propan-2-ol (**73**) was separated and purified using column chromatography (Scheme 5.5).



Scheme 5.5. Synthesis of 2-(5-nitrothien-2-yl) propan-2-ol 73

5.4 Synthesis of 1-methyl-2-nitro-5-hydroxymethyl imidazole 79

The compound 2-nitro-1-methyl imidazole group has been used as a component of bioreductive prodrugs.^{2a, 4a, 11} The amino compound 1-methyl-2-amino-imidazole may be used as the starting compound to reach the desired nitro imidazole group. In the synthesis, published by Bellani and Lancini was modified in the preparation of 1-methyl-2-amino-5-carbethoxyimidazole **76**.¹² Briefly, Ethyl formate was added to ethyl sarcocine ester (**74**) powder and the mixture was cooled below 0^oC. Then NaH was added gradually and stirred for 14 hrs. Then, trituration using hexane produced a thick liquid and was separated from hexane. The residue was mixed with ethanol and HCl, followed by heating at 100^oC with vigorous stirring for 1 hr. Then the reaction was cooled and added with cyanamide, 10% acetic acid and sodium acetate and heated at 90^oC for 90 min. Then the reaction was cooled and the pH adjusted to 1 using HCl. The solvent was removed by rotary evaporation below 45^oC until the volume had reduced to one fifth of the initial volume. Then the pH was raised to 8-9 using KHCO₃. Ethyl acetate was used to separate

organic layer and the extract was dried with MgSO₄. Compound **76** was isolated by column chromatography (Scheme 5.5).



Scheme 5.6. Synthesis of 76 from sarcocine ethyl ester 74

The nitration of **76** afforded the nitro imidazole compound 1-methyl-2-nitro-5carbethoxyimidazole **77**. In the synthesis, the compound **79** was added to acetic acid and the acetic acid/**79** mixture was added to a sodium nitrite solution, which is at 0^oC, drop wise while stirring. Overnight stirring at room temperature was followed by extraction of the organic material into methylene chloride. The methylene chloride layer was dried over MgSO₄. Compound **77** was separated using column chromatography.¹³ The ester bond of **77** was hydrolyzed using 1N NaOH to obtain **78**. The carboxylic group of **78** was reduced using NaBH₃ and isoformyl chloroformate.¹⁴ The resulting solution was extracted with THF and the dry organic material was column chromatographed to obtain **79** (Scheme 5.7).



Scheme 5.7. Synthesis of 1-methyl-2-nitro-5-hydroxymethyl imidazole 79

5.5 Synthesis of 80 and 81

Prodrugs **80** and **81** may be made employing Mitsonobu coupling reactions. The nitroaromatics **73** and **79** were reacted with the coumarin fluorophore **69** under Mitsonobu conditions. The attempts to make compounds **80** and **81** were not successful (Scheme 5.8).



Scheme 5.8. Fluorescent probes 83 and 84.

5.7 Synthesis of 3-acetylquinoline-1,2,4-benzotraizine 1,4-dioxide 84

In an separate effort to prepare a probe for hypoxia was done by coupling 3amino-1,2,4-benzotraizine 1,4-dioxide (TPZ), **33** with 6-aminoquinoline **43**, a known fluorophore. TPZ was reacted with triphosgene **82** to produce intermediate **83** and then, **43** was added in situ to obtain **84** (Scheme 5.9).¹⁵



Scheme 5.9. Synthesis of 84 using triphosgene 82, 33 and 43

5.8 Experimental

5.7.1 Synthesis of paranitrophenyl-4-methyl-coumarin ether (70)

To a slurry of NaH (148 mg, 6.16 mmol) in dry DMF (10 mL), at 0^oC was added with **69** (542.6 mg, 3.08 mmol), in dry DMF. Then **68** (1000 mg, 4.6 mmol) was added to the mixture and was stirred at 0^oC for 12 h. Upon disappearance of **69** on TLC, the mixture was extracted to EtOAc, dried with brine and column chromatographed to obtain the ether **70** (214 mg, R_f value = 0.5 in 50% hexane in EtOAc). ¹H NMR (CDCl₃, 500 MHz): δ ppm 8.27 (d, J = 8.5 Hz, 2H), 7.62 (d, J = 8.5 Hz, 2H), 7.53 (d, J = 8.5 Hz, 1H), 6.94 (d, J = 8.5 Hz, 1H), 6.87 (s, 1H), 6.16 (s, 1H), 5.24 (s, 1H), 2.40 (s, 1H).¹³C NMR (CDCl₃, 125.5 MHz): δ 160.9, 155.2, 152.3, 143.1, 127.7, 125.8, 123.9, 114.3, 112.7, 112.5, 101.9, 69.0, 18.7. LRMS (ESI, [M+H]⁺) m/z calcd for C₁₇H₁₄N₁O₅ 312.09 calculated, found 311.95.

5.7.2 Synthesis of 2-thien-2-yl-propan-2-ol (72)

Compound **71**, 2-acetylthiophene (18 mL, 143 mmol) was dissolved in 300 mL Et₂O at 0⁰C and stirred. Then nitrogen was purged. Methyl magnesium bromide (65 mL from 3M in Et₂O solution) was added via a syringe. Then the reaction mixture was stirred at room temperature for 4 hr. The reaction mixture was extracted into CH₂Cl₂ and dried with brine and MgSO₄. Column chromatography afforded **72** (4.39 g, R_fvalue = 0. 4 in 100% CH₂Cl₂). ¹H NMR (CDCl₃, 300 MHz): δ ppm 7.17 (d, J = 4.5 Hz, 1H), 6.93 (m, 2H), 1.66 (m, 6H). ¹³C NMR (CDCl₃, 75.5 MHz): δ 154.7, 126.9, 124.1, 122.3, 71.6, 32.5. HRMS (ESI, [M+H]⁺) m/z calcd for C₇H₁₀OS 142.0445 calculated, found 142.0452.

5.7.3 Synthesis of 2-Thien-2-yl-Propan-2-ol (73)

The thienyl alcohol 2-thien-2-yl-Propan-2-ol **72** (2 g, 10.6 mmol) was dissolved in 30 mL acetic acid and cooled to -70° C using MeOH dry ice slurry. While stirring, fuming HNO₃ (0.7 mL, 11.6 mmol) was gradually added with vigourous stirring and reaction was run for 2 hr. Then another hour stirring was done at -40° C. Temperature was raised to 0° C and stirred for another 1 hr. Then water/ice 200 g was added and EtOAc (100 mL) was used to extract organic material. The EtOAc layer was dried using Na₂SO₄. Column chromatography performed to separate **73** (310 mg, R_f value = 0. 2 with 20% EtOAc in hexane) ¹H NMR (CDCl₃, 300 MHz): δ ppm 7.78 (d, J = 4.5 Hz, 1H), 6.86 (d, J = 4.5 Hz, 1H), 1.66 (m, 6H). ¹³C NMR (CDCl₃, 75.5 MHz): δ 163.6, 128.8, 121.2, 71.8, 31.9. HRMS (ESI, [M+H]⁺) m/z calcd for C₇H₉O₃NS 187.0303 calculated, found 187.0299.

5.7.4 Synthesis of 1-methyl-2-amino-5-carbethoxyimidazole (76)

Ethyl formate (62.5 mL) was added to sarcosine methylester hydrochloride **74** (10 g, 71 mmol) in a 500 mL r.b. and chilled at 0^{0} C. Sodium hydride (60% oil suspension, 6.58 g, 0.1645 mmol) was added slowly over 2 h and stirred for 14 h to produce **75**.^{12a} Then, trituration was done twice using 50 ml of hexane to obtain light brown slurry. The brown slurry was added to a new 500 mL r.b. and added with 50 mL EtOH and 8 mL of conc. HCl. The mixture was stirred at 90^{0} C for 1 hr. Then the mixture was cooled to room temperature and filtered. To the filterate, 10 mL of 10% aquoes HOAc, sodium acetate (10.73g, 0.13 mmol) and CH₃CN (5.5 g, 0.13 mmol) were added and stirred at for 90 min. The pH was raised to 8-9 using KHCO₃ and the organic material was extracted to

EtOAc. Ethyl acetate layer was dried using brine and concentrated. The dry organic mixture was column chromatographed to obtain **76** (1 g, R_f value = 0. 31 with 2% MeOH in EtOAc in hexane) ¹H NMR (DMSO, 500 MHz): δ ppm 7.26 (s, 1H), 6.15 (s, 2H), 4.14 (q, J= 7.0 Hz, 2H), 3.50 (s, 3H), 1.210 (t, J= 7.0 Hz, 3H). ¹³C NMR (DMSO, 125.5 MHz): δ 159.0, 154.3, 136.1, 116.86, 58.9, 30.2, 14.4. HRMS (ESI, [M+H]⁺) m/z calcd for C₇H₁₂O₂N₃ 170.0930 calculated, found 170.0929.

5.7.5 Synthesis of 1-methyl-2-nitro-5-carbethoxyimidazole (77)

Water (20 ml) was added with NaNO₂ (3g) and the solution was cooled below - 5^{0} C. Then, 1.5 g of **76** in acetic acid was added drop wise to sodium nitrite solution while maintaining the temperature below 0^{0} C. Upon completion of the reaction, ethyl acetate was used to extract organic products. The EtOAc layer was dried using MgSO₄. Compound **77** was separated by silica gel chromatography (0.6 g, R_f value = 0. 5 in 100% CH₂Cl₂). ¹H NMR (CDCl₃, 500 MHz): δ ppm 7.73 (s, 1H), 4.38 (m, 5H), 1.40 (s, 3H). ¹³C NMR (CDCl₃, 125.5 MHz): δ 159.0, 136.5, 134.64, 126.6, 61.8, 35.3, 14.1. HRMS (ESI, [M+H]⁺) m/z calcd for C₇H₁₀O₄N₃ 200.0671 calculated, found 200.0669.

5.7.6 Synthesis of 1-methyl-2-nitro-5-carboxylimidazole (78)

In 10 mL of 1N NaOH compound **77** (0.6 g, 3.015 mmol) was dissolved and the mixture was stirred overnight. The pH was adjusted to 1 using conc. HCl. Then the product **78** was extracted to EtOAc and ethyl acetate layer was dried using MgSO₄ (0.6 g, R_f value = 0.2 in 100% EtOAc). ¹H NMR (DMSO, 500 MHz): δ ppm 7.71 (s, 1H), 7.56

(s, acidic H), 4.17 (s, 3H). ¹³C NMR (DMSO, 125.5 MHz): δ 160.71, 147.8, 134.1, 127.3, 35.4. LRMS (ESI, [M+H]⁺) m/z calcd for C₅H₆O₄N₃ 172.03 calculated, found 172.11.

5.7.7 Synthesis of 1-methyl-2-nitro-5-hydroxymethylimidazole (79)

A mixture of **78** (70 mg, 0.41 mmol) and triethylamine (0.318 mL, 0.649 mmol) in anhydrous THF (1 mL) was cooled in dry acetonitrile bath (-20^oC). Isobutyl chloroformate (100 μ L, 7.7 mmol) was added dropwise, over 10 min. Then the reaction was stirred over 1 h. Then sodium borohydried (81mg) was added to the reaction mixture. Then water was added drop wise over a period of 1h and the temperature was kept below 0^oC. The products were extracted to ethyl acetate and dried with brine. Column chromatography separated pure 14 (30 mg, R_f value = 0.28 in 100% EtOAc) ¹H NMR (MeOD, 500 MHz): δ ppm 7.08 (s, 1H), 4.84 (s, 1H), 4.65 (s, 2H), 4.02 (s, 3H). ¹³C NMR (MeOD, 125.5 MHz): δ 147.4, 139.5, 127.6, 54.7, 34.9, HRMS (ESI, [M+H]⁺) m/z calcd for C₅H₈O₃N₃ 158.0566 calculated, found 158. 0575.

5.7.7 Synthesis of 3-acetylquinoline-1,2,4-benzotraizine 1,4-dioxide 84

The compound **33** (0.15 g, 0.85 mmol) was dissolved in dry toluene (2.5 mL) and the mixture was stirred and heated to 90^oC. Then triphosgene **82** (0.086 g, 0.29 mmol) was added to the TPZ mixture and the reaction was stirred for 5-10 min. Another batch of **82** (0.086 g, 0.29 mmol) was added and then the reaction was cooled to obtain crude **83**.¹⁵ To the crude **83**, **43** (0.15 g, 0.763 mmol) in 2.5 mL DMF was added and stirred at room temperature for 10 min. The yellow solid product **84** was separated (0.02 g, R_f value = 0.1 in 2% MeOH in EtOAc). ¹H NMR (DMSO, 500 MHz): δ ppm 10.45 (s, 1H), 10.30 (s, 1H), 8.79 (s, 1H), 8.30 (m, 4H), 8.05 (m, 2H), 7.78 (m,2H), 7.51 (d, J = 7.0 Hz, 1H).¹³C NMR (DMSO, 500 MHz): δ 148.7, 148.3, 145.9, 138.0, 136.6, 135.8, 132.5, 129.7, 128.5, 122.9, 121.9, 121.1, 118.0, 114.0, HRMS (ESI [M+H]⁺) m/z calcd for C₁₇H₁₃N₆O₃ 349.1049 calculated, found 349.1057.



¹H NMR of **70** (CDCl₃, 500 MHz)



¹³C NMR of **70** (CDCl₃, 125.5 MHz)



¹H NMR of **72** (CDCl₃, 300 MHz)


¹³C NMR of **72** (CDCl₃, 75.5 MHz)



¹H NMR of **73** (CDCl₃, 300 MHz)



¹³C NMR of **73** (CDCl₃, 75.5 MHz)



¹H NMR of **76** (DMSO, 500 MHz)



¹³C NMR of **76** (DMSO, 125.5 MHz)



¹H NMR of **77** (CDCl₃, 500 MHz)



¹H NMR of **78** (DMSO, 500 MHz)



¹H NMR of **79** (MeOD, 500 MHz)



¹³C NMR of **79** (MeOD, 500 MHz)



¹H NMR of **84** (MeOD, 500 MHz)



¹³C NMR of **84** (MeOD, 125.7 MHz)

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