

Article **NMR Assignments of Six Asymmetrical N-Nitrosamine Isomers Determined in an Active Pharmaceutical Ingredient by DFT Calculations**

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Abstract: N-nitrosamines, which are well-known pro-mutagens, are found in drugs, pickled food and tobacco. Therefore, controlling their concentrations is very important. When an HPLC, GC or NMR analysis is conducted to investigate certain asymmetrical N-nitrosamines, two sets of signals attributed to the asymmetric N-nitrosamine isomers are usually observed. However, few reports on the NMR assignment of asymmetrical N-nitrosamine isomers have been published. In this study, we investigated the NMR assignments of the *Z/E* isomers of six asymmetrical N-nitrosamines by means of density functional theory (DFT) calculations. The configuration of the major isomer of asymmetrical N-nitrosamine **3** was the Z-configuration. The configuration of the major isomers of asymmetrical N-nitrosamines **4**–**7** was the *E*-configuration. Then, we determined the *Z/E* ratios of these asymmetrical N-nitrosamines by means of variable temperature (VT) and room temperature (RT) ¹H-NMR experiments. The ratios of the *Z/E* isomer **3** quickly increased beyond 100% in the VT ¹H NMR experiments. The ratios of Z/E isomers 4–7 were increased in the range of 10–60% in the VT 1 H NMR experiments. The results of this study indicate that identifying the isomers of asymmetrical N-nitrosamine is necessary to control the quality of N-nitrosamines for active pharmaceutical ingredients (APIs).

Keywords: asymmetrical N-nitrosamines; isomers; NMR assignment; density functional theory calculation; variable temperature 1 H-NMR experiments

1. Introduction

N-Nitrosamines are well-known pro-mutagens that can react with DNA following metabolism to produce DNA adducts, such as O⁶-alkyl-guanine. These adducts can result in DNA replication miscoding errors, leading to GC > AT mutations and an increased risk of genomic instability and carcinogenesis [\[1\]](#page-9-0). In 2018, N-nitrosodimethylamine (NDMA, **1**), a genotoxic carcinogen, was detected as a synthesis impurity in some valsartan drugs, while other N-nitrosamines, such as N-nitrosodiethylamine (NDEA, **2**), were later detected in other sartan products. In September 2019, the FDA stated that a low amount of NDMA had been detected in ranitidine. The FDA also announced that it had found excessive levels of NDMA in metformin in February 2022. Some N-nitrosamines, such as N-nitrososarcosine (NSAR, **3**), N-nitrosomethylvinylamine (**4**), 3-(methylnitrosamino)propionitrile (MNPN, **5**), 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK, **6**), N-nitrosornicotine (NNN, **7**) and N-methyl-N-nitrosourea (MNU, **8**), occur not only in drugs but also in pickled foods and tobacco (Figure [1\)](#page-1-0). Therefore, controlling their concentrations in drugs, foods and tobacco is very important.

Citation: Guan, H.-Y.; Feng, Y.-F.; Sun, B.-H.; Niu, J.-Z.; Zhang, Q.-S. NMR Assignments of Six Asymmetrical N-Nitrosamine Isomers Determined in an Active Pharmaceutical Ingredient by DFT Calculations. *Molecules* **2022**, *27*, 4749. [https://doi.org/10.3390/](https://doi.org/10.3390/molecules27154749) [molecules27154749](https://doi.org/10.3390/molecules27154749)

Academic Editor: Artur M. S. Silva

Received: 4 June 2022 Accepted: 20 July 2022 Published: 25 July 2022

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Figure 1. The chemical structures of some N-nitrosamines. **Figure 1.** The chemical structures of some N-nitrosamines.

 \mathcal{L} we performed HPLC or GC analyses of certain asymmetrical N-nitrosamines, \mathcal{L} When we performed HPLC or GC analyses of certain asymmetrical N-nitrosamines, we often observed two peaks for one nitrosamine. This finding was attributed to the fact $r₁$ N_n, respectively, resulting a single variation in the anisotropic effects. that asymmetrical N-nitrosamine may have configurational isomers due to the hindered rotation of a single bond (N-N), resulting in strong variations in the anisotropic effects. response to the *E/Z* isomers relative to the $\frac{E}{Z}$ isomers relative to the LC–Cs $\frac{E}{Z}$. The two conformers have features similar to those of the E/Z isomers relative to a double bond (Figure [2\)](#page-1-1). A similar phenomenon has been reported, in which the stereospecific response of the *E/Z* isomers of NSAR (3) was determined by LC–ESI–MS/MS [\[2\]](#page-9-1). NSAR (3) assignment of asymmetrical $\frac{1}{\sqrt{2}}$ is the above phenomenon, inspired by the abov and MNPN (**5**) have also been shown to produce two isomer peaks in the UPLC–MS/MS assay [\[3\]](#page-9-2). In this paper, we report a series of asymmetrical N-nitroamines (**3**–7) displaying IMP gianals. However, four studies have reported the NMP a two groups of NMR signals. However, few studies have reported the NMR assignment of asymmetrical N-nitroamines isomers. Inspired by the above phenomenon, variabletemperature (VT) ¹H-NMR experiments were carried out to determine the percentage changes of the two configurational isomers, which revealed the configurational isomerism phenomenon. As density functional theory (DFT) calculations are widely used to determine NMR assignments for the characterization of complex structures [\[4,](#page-9-3)[5\]](#page-9-4), we performed DFT calculations to assign the NMR signals of these conformers. To our knowledge*,* this is the first report of the NMR assignment of configurational isomers of N-nitrosamines.

When $R_1 \neq R_2$, cis/trans isomers usually be obtained

Figure 2. The possible mechanism of the generation of Z/E isomers of asymmetrical N-nitrosamines.

2. Results and Discussion

As shown in Figures S1–S12, the ¹H-NMR spectrum of N-nitrososarcosine **3** showed one group of major signals (δ H 3.79 and 4.28) and a set of minor signals (δ H 3.01 and 5.01). In addition, the major carbon signals of **3** were observed at δ_C 40.0, 47.3 and 167.6, and the minor signals were observed at $δ$ ^H 33.0, 54.6 and 170.3. Similarly, the ¹³C-NMR spectrum of N-nitrososarcosine **4** showed two sets of different carbon signals. However, some of the ¹H-NMR signals had differences, such as signals of -NCH₃ (δ _H 3.15 vs. δ _H 3.89) and H-1 (δ _H 7.89 vs. δ _H 7.58). Two conformers of 5 showed two groups of distinct 1D NMR signals, of which the maximum difference in the 1 H-NMR and 13 C-NMR spectra between the two isomers was 0.77 ppm for -NCH₃ (3.03 vs. 3.80 ppm) and 8.6 ppm for C-3 (49.1 vs. 40.5 ppm), respectively. Differences in the ¹H-NMR spectra between the two isomers of **6** were present in the alkyl chain, including H-2, H-3 and H-4. Furthermore, the differences in their ¹³C-NMR spectra were associated with -NCH₃ and the chain from C-2 to C-4. Two groups of NMR signals in the spectrum of **7** can be easily distinguished. Above all, the major and minor signals were also assigned based on the peak integration (Tables [1](#page-2-0) and [2\)](#page-2-1). Furthermore, the configurational exchange and conformer ratios of **3**–**7** were investigated via a VT ¹H-NMR experiment.

H Atmos		3		4		5		6		7
No.	Major	Minor								
NCH ₃	3.79	3.01	3.153	3.89	3.03	3.8	3.1	3.1		
1			7.89	7.58						
$\overline{2}$	4.28	5.01	5.16	5.16	4.42	3.81	3.08	2.95	8.58	8.38
			4.86	4.87						
\mathfrak{Z}					3.07	2.76	2.25	1.99		
$\overline{\mathbf{4}}$							4.27	3.8	7.73	7.51
5									7.41	7.33
6									8.53	8.43
2^{\prime}							9.15	9.15	5.69	5.16
3'									2.5	1.84
4 [′]							8.2	8.2	1.99	2.02
5^{\prime}							7.4	7.4	3.67	4.48
6^{\prime}							8.79	8.79		

Table 2. ¹³C-NMR chemical shifts of asymmetrical N-nitrososarcosine **3**–**7**.

To further investigate the configurational behavior of asymmetrical N-nitrosamines **3**–**7**, DFT quantum chemical calculations were conducted [\[6\]](#page-9-5). Because the hindered rotation of the nitryl formed *E* and *Z* configurations, resembling the *Z*/*E* isomers relative

to the double bond, two configurational isomers (a/b) were converted to Z/E for further calculations (Figure [2\)](#page-1-1).

Compoun[d](#page-3-0) 3 may contain 4 isomers $3a-3d$ (Figure 3). The DFT calculations showed that the Gibbs free energies of isomers **3c** and **3d** are higher than those of **3a** and **3b** (Figure [3\)](#page-3-0), suggesting that they are more unstable than **3a** and **3b**; thus, we mainly consid-3), suggesting that they are more unstable than **3a** and **3b**; thus, we mainly considered the ered the contributions of **3a** and **3b** to the NMR data. contributions of **3a** and **3b** to the NMR data.

Figure 3. The Gibbs free energies and energy difference of the four possible conformers **3a–3d**.

For compound 4, we considered four possible stable conformers, and their energies were calculated. As shown in Figure 4, the interaction of N=O and sp^2 CH can be represented through the energy difference between E_1 and E_2 . Similarly, the interaction between $N_{\rm c}$ C_n and S_2 ² CH can be represented by representation of E_1 . In addition, the interaction between the nitrogen atoms of N=O and sp^2 CH₂ can be interpreted by the energy calculation of E_3 and E_1 . On the basis of their energy differences, the closer sp^2 values of CH or CH₂ and N=O are, the more unstable they are. Thus, for compound 7, the pyridine ring is rich in electrons, similar to the double bond in compound **4**, which repels of CH or CH2 and N=O are, the more unstable they are. Thus, for compound **7**, the pyri-the *E*-configuration of **7** is more stable than the *Z*-configuration, which is consistent with the energy calculation. Compounds 4 and 7 have sp^2 CH or CH₂, which could affect the stability of the isomers. N=O and sp^2 CH₂ can be shown through the energy difference of E_4-E_1 . In addition, the the N=O-containing electrons. Meanwhile, considering the steric hindrance of pyridine,

Figure 4. The Gibbs free energies and energy differences of four possible conformers for compound **Figure 4.** The Gibbs free energies and energy differences of four possible conformers for compound **4**.

Intriguingly, N-nitrososarcosine 8 showed only one set of NMR signals, suggesting that only one optimized conformer was present in 8, which was caused by the key hydrogen bond between the oxygen or nitrogen in the nitryl moiety and the hydrogen in urea, bond between the bxygen of hubgen in the httryf molety and the hydrogen in their, restricting its configurational exchange. The presence of hydrogen bonds was established by energy calculations at the M062X/Def2TZVP level of theory. Both the *E* configuration by energy calculations at the M062X/Def2TZVP level of theory. Both the E configuration
(8a) and the Z configuration (8b) might form a hydrogen bond. The E configuration (8a) was predicted to be 4.97 Kcal/mol lower in energy than the *Z* configuration (**8b**), indicating that the *F*_c configuration (**8**c) means to the other calculation calculation calculation can the *E* configuration (**8a**) may be the stable configuration, with an intermolecular hydrogen bond of approximately 2.225 Å (Figure 5A). The DFT quantum chemical calculations showed that the calculated ¹³C NMR data for the *E* configuration (**8a**) were less different showed that the calculated \sim CNNK data for the *L* comiguration (*oa*) were less different from the experimental data. Based on the above evidence, one set of NMR signals was

Figure 5. The possible conformers (A), their energy values (A) and the calculated ¹³C-NMR data (**B**) for N-nitrosamines of **8**. (**B**) for N-nitrosamines of **8**.

A summary of these calculated NMR data and their comparisons with experimental A summary of these ca[lc](#page-6-0)ulated ω assign the TVWR signals for the Ω and Γ comparations of N-nitrososarcosine **3**–**7**. Table 6 shows the Gibbs free energy values (G, Kcal/mol) of Z/E isomers for compounds 3–7 at the M062X/Def2TZVP level of theory with Grimme's D3
correction. The major calculated molecular models of 3–7 are shown in Figure 6 values are presented in Tables [3](#page-5-0) and [4,](#page-5-1) and the correlation coefficients are presented in Table [5;](#page-5-2) these data were used to assign the NMR signals for the *Z* and *E* configurations of correction. The major calculated molecular models of **3**–**7** are shown in Figure [6.](#page-6-1)

H Atmos		3		4		5	6			7
No.	3a	3 _b	4a	4 _b	5a	5b	6a	6b	7a	7 _b
NCH ₃	3.21	4.19	3.58	5.04	4.47	3.28	5.13	2.65		
	3.21	3.71	3.58	2.35	3.63	3.08	4.77	2.65		
	2.83	3.96	4.57	2.35	3.87	3.07	5.02	3.18		
$\mathbf{1}$			8.04	8.19						
$\overline{2}$	5.12	4.28	5.00	5.05	3.31	4.54	4.23	2.74	8.75	8.58
	5.12	4.02	5.17	5.19	4.11	4.31	3.98	3.08		
$\ensuremath{\mathfrak{Z}}$					2.25	2.68	3.38	2.54		
					2.79	2.60	3.85	2.08		
$\boldsymbol{4}$							5.01	3.87	7.56	7.57
							5.14	4.36		
$\mathbf 5$									7.59	7.52
$\boldsymbol{6}$									8.73	8.66
2^{\prime}							10.39	9.24	5.97	5.16
3'									2.53	2.39
									1.98	1.78
4^{\prime}							9.69	8.23	1.90	2.14
									1.92	1.99
5'							8.92	7.69	3.62	4.56
									3.89	4.67
6^{\prime}							10.06	8.91		

Table 3. ¹H NMR chemical shifts for asymmetrical N-nitrososarcosine **3**–**7** determined by DFT calculations.

Table 4. ¹³C NMR chemical shifts for asymmetrical N-nitrososarcosine **3**–**7** determined by DFT calculations.

C Atmos		3		4		5		6		7
No.	3a	3 _b	4a	4 _b	5a	5b	6a	6b	7a	7b
NCH ₃	35.8	40.9	37.3	25.0	41.5	36.0	39.7	35.4		
	168.7	165.4	121.5	136.1	117.8	117.3	198.0	199.6		
2	56.3	49.6	97.0	95.6	16.5	21.3	35.1	36.8	146.5	146.1
3					44.2	52.0	24.9	27.0	137.8	135.8
4							44.3	56.0	131.6	131.1
5									121.3	121.3
6									147.1	146.7
2^{\prime}							149.4	148.9	65.3	62.6
3'							128.5	130.0	36.5	36.0
4^{\prime}							135.2	135.2	22.3	25.0
5'							121.4	121.2	49.1	53.0
6^{\prime}							152.4	152.4		

Table 5. Correlation coefficients of the calculated and experimental ¹³C-NMR chemical shifts for N-nitrososarcosine **3**–**7**.

Compounds			Difference Value
3	$-284,248.62427$	$-284,248.64091$	0.017
4	$-189,849.40075$	$-189,850.64014$	1.239
5	$-248,452.662324$	$-248,452.232420$	0.430
b	$-441,336.708517$	$-441,336.80758$	0.099
	$-369.479.165009$	$-369.479.778283$	0.613

Table 6. The Gibbs free energy values (G, Kcal/mol) of *Z*/*E* isomers for compounds **3**–**7** at the M062X/Def2TZVP level of theory with Grimme's D3 correction.

Figure 6. Optimized conformers derived from DFT calculations for asymmetrical N-nitrosamines **3**–**7**.

3–**7**. To quantify the ratios of isomers and the changes in the ratio at different temperatures, changed in the VT-NMR experiments. To determine whether these changes were affected by temperature or time, control NMR experiments were performed at room temperature **COMPOUNDED THE COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED** *COMPOUNDED* **COMPOUNDED** *COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED COMPOUNDED COMPOUN* This ratio was maintained at 120~130% even though the NMR probe temperature changed

∴ 28.861.02.85.5 Juli 1.27 NMP from 90 °C to 30 °C. In the control RT-NMR experiment of **3**, the *Z/E* ratio increased slowly from 2 to 12% within seven hours. A similar phenomenon was also observed in the VT/RT-NMR experiments of 6 (Figure [7D](#page-7-0)). The *Z/E* ratios of 4 and 5 exhibited small changes of **7** −369,479.165009 −369,479.778283 0.613 approximately 12 and 24%, respectively (Figure [7B](#page-7-0), C). In addition, **7** was shown to exhibit showed a similar *Z/E* ratio of approximately 50%. Based on these VT/RT-NMR experiments, the rapid changes in the Z/E ratios of isomers **3–7** were temperature-dependent. To our surprise, when the NMR probe temperature returned to 30 °C from higher temperatures, the *Z/E* ratios did not show a significant decrease. This means there might be a balance $\frac{1}{\sqrt{2}}$ between the two isomers in solvents. we carried out VT NMR spectroscopic studies (Figure [7\)](#page-7-0). All ratios of the **3**–**7** isomers were different changes in the *Z/E* ratios in the VT/RT-NMR experiment, but they ultimately

Figure 7. The Z/E ratios of asymmetrical N-nitrosamines $3-7(A-E)$, respectively) at different temperatures.

3. Experimental Section

3.1. Materials and Reagents

N-Nitrososarcosine (NSAR, **3**), n-nitrosomethylvinylamine (**4**), 3-(methylnitrosamino) propionitrile (MNPN, 5), 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK, 6), N'nitrosornicotine (NNN, **7**) and N-methyl-N-nitrosourea (MNU, **8**) were purchased from the Chemical Drug Control Institute of the China National Institutes for Food and Drug Control (NIFDC, Beijing, China). DMSO-*d6* with 0.03% tetramethylsilane (TMS) was purchased from Cambridge Isotope Laboratories.

3.2. NMR Experiments

NMR samples were prepared in DMSO-*d6* with 0.03% tetramethylsilane (TMS). The chemical shifts are quoted in ppm relative to TMS. 1 H-NMR and 13 C-NMR spectra were recorded on a 400 MHz Bruker NMR spectrometer (Bruker BioSpin GmbH, Ettlingen, Germany). VT ¹H-NMR spectra were recorded at 30 °C, 40 °C, 50 °C, 60 °C, 70 °C, 80 °C and 90 \degree C. Before each sample was subjected to the VT ¹H-NMR experiment, it was heated in an NMR probe at the experimental temperature (from 30 \degree C to 90 \degree C, then back to 30 \degree C) for at least 10 min. TopSpin 2.1 software (Bruker BioSpin, Billerica, MA, USA)was used for the acquisition and processing of the NMR data.

3.3. Computational Details

A conformational search was performed using Crest software (Loughborough University, Loughborough, The United Kingdom), and the conformers within an energy window of 5 kcal·mol−¹ were optimized with DFT calculations at the M062X/Def2TZVP level of theory with Grimme's D3 correction [\[7\]](#page-9-6) using the Gaussian 09 program (Gaussian, Inc.: Wallingford, CT, USA) [\[8\]](#page-9-7). A frequency analysis was performed at the same level of theory to ensure that no imaginary frequencies existed and to determine the Gibbs free energies for the subsequent population analysis. Room-temperature (298.15 K) equilibrium populations were calculated according to the Boltzmann distribution law. Those conformers, accounting for over 99% of the population, were subjected to subsequent calculations.

The GIAO method [\[9–](#page-9-8)[13\]](#page-9-9) at the mPW1PW91/B3LYP/6–31+G(d, p) level of theory (in DMSO) in corresponding solvents with the IEFPCM solvent model [\[14\]](#page-9-10) was used for the NMR calculation. The chemical shifts were calculated from shielding constants by referencing TMS at 0 ppm (δ _{calcd} = σ _{TMS} – σ _{calcd}), where σ _{TMS} is the shielding constant of TMS calculated at the same level of theory. For each possible candidate, the parameters of the linear regression $\delta_{\text{cal}} = a \times \delta_{\text{exp}} + b$ and the correlation coefficient, R^2 , were determined.

The hydrogen bond energy (E_H) was calculated using the equation $E_H = E_{8a} - E_8$, where E_{8a} is the energy of the conformer without hydrogen bonding by twisting the N-N to break the hydrogen bond, and E_8 is the energy of the optimized conformer [\[15\]](#page-9-11).

Supplementary Materials: The following supporting information can be downloaded at: [https://](https://www.mdpi.com/article/10.3390/molecules27154749/s1) [www.mdpi.com/article/10.3390/molecules27154749/s1.](https://www.mdpi.com/article/10.3390/molecules27154749/s1) Figure S1: ¹H NMR spectrum of compound **3**. Figure S2: ¹³C NMR spectrum of compound **3**. Figure S3: ¹H NMR spectrum of compound **4**. Figure S4: ¹³C NMR spectrum of compound **4**. Figure S5: ¹H NMR spectrum of compound **5**. Figure S6: ¹³C NMR spectrum of compound **5**. Figure S7: ¹H NMR spectrum of compound **6**. Figure S8: ¹³C NMR spectrum of compound **6**. Figure S9: ¹H NMR spectrum of compound **7**. Figure S10: ¹³C NMR spectrum of compound **7**. Figure S11: ¹H NMR spectrum of compound **8**. Figure S12: ¹³C NMR spectrum of compound **8**.

Author Contributions: Conceptualization, Q.-S.Z. and J.-Z.N.; validation, Y.-F.F.; investigation, H.- Y.G. and B.-H.S.; writing—original draft preparation, H.-Y.G., Y.-F.F. and B.-H.S.; writing—review and editing, Q.-S.Z. and J.-Z.N.; supervision, Q.-S.Z. and J.-Z.N.; project administration, Q.-S.Z. and J.-Z.N.; funding acquisition, J.-Z.N. All authors have read and agreed to the published version of the manuscript.

Funding: National Major Scientific and Technological Special Project for "Significant New Drugs Development" (No. 2017zx09101001).

Institutional Review Board Statement: Not applicable.

Informed Consent Statement: Not applicable.

Data Availability Statement: The data presented in this study are contained within the article and supplementary materials.

Acknowledgments: This work was supported by grants from the National Major Scientific and Technological Special Project for "Significant New Drugs Development" (No.2017zx09101001). We thank Sheng-An Tang (Tianjin Medical University) for the conformer identification of the asymmetrical N-nitrosamines, Nan Qin (Tianjin Medical University) for supporting the design and providing helpful discussions regarding the VT-NMR experiments and Xing-Rong Peng (Kunming Institute of Botany, Chinese Academy of Sciences) for the DFT calculations.

Conflicts of Interest: The authors declare that they have no conflict of interest.

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