

## 1. Principle:

This method involves the use of HS-GC-MS (single quad) for the determination of N-Nitrosodimethylamine (NDMA).

## 2. Scope:

This method is applicable to Active Pharmaceutical Ingredients (API) and Powdered Tablets. These samples are preliminarily screened in Scan mode, **Procedure A**. If NDMA is found to be present, samples undergo a NDMA Quantification method, outlined in **Procedure B**. If no NDMA is found samples follow **Procedure C**.

## 3. Apparatus:

- 3.1 **HS-GC-MS:** Shimadzu GC-2010Plus Gas Chromatograph (Item No. 1043B), Headspace HS-20 auto-sampler (Item No. 1043A), GC-MS QP2020 Mass Spectrometer (Item No. 1043C), or equivalent.
- 3.2 **Autopipettes, Gilson or equivalent:** (1,000  $\mu\text{L}$ , 200  $\mu\text{L}$ , 100  $\mu\text{L}$ , 20  $\mu\text{L}$ , 10  $\mu\text{L}$ ).
- 3.3 **Capillary GC Column:** Restek Rtx-624 (30m x 0.25 mm I.D, 1.4 $\mu\text{m}$ ).

## 4. Reagents:

- 4.1 **Solvent:** Dimethyl sulfoxide (DMSO), (Merck SupraSolv, Dimethyl Sulfoxide for headspace gas chromatography), Catalogue no. 101900.
- 4.2 Helium gas (CP grade), BOC supplied or equivalent.
- 4.3 **Reference Standard:** NDMA (N-nitrosodimethyl amine), Restek Catalog no. 31427, Concentration 1000 $\mu\text{g}/\text{mL}$  in Methanol (Reference Standard).
- 4.4 **Quality Control Standard:** NDMA (N-nitrosodimethyl amine), Supelco Catalog no. 48670, Concentration 200 $\mu\text{g}/\text{mL}$  in Methanol (QC).

**Prepared solutions are protected from light prior to analysis.**

## 5. Calibration Standards:

- 5.1 **Stock standard Solution (NDMA) 200  $\mu\text{g}/\text{mL}$**   
Dilute 200 $\mu\text{L}$  of NDMA Reference Standard (4.3) to 1mL in DMSO, in a volumetric flask.
- 5.2 **1 $\mu\text{g}/\text{mL}$  NDMA Standard:**  
Dilute 10 $\mu\text{L}$  of stock standard (200 $\mu\text{g}/\text{mL}$ ) (5.1) to 2mL with DMSO, in a volumetric flask.

## 6. Quality Control Standard:

### 6.1 2µg/mL NDMA QC Solution:

Dispense 10µL of **Quality Control Standard, 200µg/mL (4.4)** into a headspace vial, add 1.0 mL of DMSO, cap and crimp.

## 7. Methods of Analyses:

### 7.1 Procedure A - Preliminary scan\*

#### 7.1.1 2µg/mL NDMA Check Standard:

Dispense 10µL of stock standard (200µg/mL) (**5.1**) into a headspace vial, add 1.0 mL DMSO, cap and crimp.

(A higher concentration standard may be used to achieve a greater response).

#### 7.1.2 Sample Preparation

Place 0.20-0.25g of powdered tablet or API in a headspace vial, add 1.0 mL of DMSO, cap and crimp.

#### 7.1.3 Analyses

Perform a full mass scan on the standard (7.1.1) and sample (7.1.2) using the GC and Headspace conditions specified in **Procedure A** (Annex I).

Establish the retention time, and confirm that the mass spectrum obtained from the eluted peak in the standard solution is that of NDMA.

Continue with Quantification of NDMA, **Procedure B (7.2)**, if NDMA is detected in the sample, or with **Procedure C (LOD/LOQ determination, 7.3)** if NDMA is not detected.

\*This preliminary scan method can detect NDMA at a level of 10 µg/g. As LOD/LOQ determination (Procedure C) has a lower detection limit of 0.04 µg/g, if an appreciable amount of NDMA is observed when carrying out LOD/LOQ determination (Procedure C) (7.3) the sample in question will be reanalysed using Quantification of NDMA (Procedure B).

## 7.2 Procedure B - Quantification of NDMA

### 7.2.1 Sample Preparation (Tablets)

Accurately weigh the same amount of sample (0.20-0.25g) into each of 4 Headspace vials.

7.2.1.1 Add 1.0mL of DMSO to Vial 1, cap and crimp.

7.2.1.2 Add 2µg (10µl of Stock standard solution (5.1)) of NDMA to Vial 2 and make up to 1.0mL with DMSO, cap and crimp.

7.2.1.3 Add 4µg (20µl of Stock standard solution (5.1)) of NDMA to Vial 3 and make up to 1.0mL with DMSO, cap and crimp.

7.2.1.4 Add 6µg (30µl of Stock standard solution (5.1)) of NDMA to Vial 4 and make up to 1.0mL with DMSO, cap and crimp.

7.2.1.5 Run all solutions using the GC and Headspace conditions described in **Procedure B** (Annex 1). Plot the standard addition curve and obtain the sample NDMA concentration (µg/mL) from the intercept. See calculated example in Annex 2.

### 7.2.2 Sample Preparation (API)

7.2.2.1 Accurately weigh the same amount of sample (0.05-0.2g) into each of 4 vials.

7.2.2.2 Add 1.0mL of DMSO to Vial 1, cap and crimp.

7.2.2.3 Add 2µg (10µl of Stock standard solution (5.1)) of NDMA to Vial 2 and make up to 1.0mL with DMSO, cap and crimp.

7.2.2.4 Add 4µg (20µl of Stock standard solution (5.1)) of NDMA to Vial 3 and make up to 1.0mL with DMSO, cap and crimp.

7.2.2.5 Add 6µg (30µl of Stock standard solution (5.1)) of NDMA to Vial 4 and make up to 1.0mL with DMSO, cap and crimp.

7.2.2.6 Run all solutions using the GC and Headspace conditions described in **Procedure B** (Annex 1). Plot the standard addition curve and obtain the sample NDMA concentration (µg/mL) from the intercept. See calculated example in Annex 2.

7.2.3 Include a 2.0µg/mL NDMA Check Standard (7.1.1), and a 2.0µg/mL NDMA QC Solution (6.1) with each analytical run.

The peak areas of the 2.0µg/mL standard and QC solution must correspond within ±10%.

7.2.4 The correlation coefficient (r) of the calibration curve must be ≥0.990.

### **7.3 Procedure C - LOD/LOQ determination**

#### **7.3.1 Sample Preparation (API/ Finished products)**

Accurately weigh in duplicate 0.5 g of each sample (powdered) into a headspace vial.

**7.3.1.1** Add 1.0mL of DMSO to Vial 1, cap and crimp.

**7.3.1.2** Add 20 $\mu$ l (0.02 $\mu$ g NDMA) of 1 $\mu$ g/mL NDMA Standard (**5.2**), and 1.0mL of DMSO to Vial 2, cap and crimp.

**7.3.1.3** Run all solutions using the conditions described in **Procedure C** (Annex 1).

Ensure that a peak with a S/N of at least 3 is obtained for the 0.02 $\mu$ g/mL NDMA standard. Examine all chromatograms and if no NDMA peak is observed, or a peak area less than that of the standard (0.02 $\mu$ g/mL) is observed in the samples, results are reported as <0.04 $\mu$ g/g.

If the sample peak area is significantly greater than that of the standard, proceed with **Procedure B** (7.2).

**Annex 1** – GC-MS conditions – Procedures A, B and C

**Annex 2** – Standard Addition Plot

**Procedure A**

[Comment]

==== Analytical Line 1 =====

[HS-20]

Oven Temp. :120.0 °C  
 Sample Line Temp. :150.0 °C  
 Transfer Line Temp. :150.0 °C  
 Shaking Level :2  
 Multi Injection Count :1  
 Pressurizing Gas Pressure :80.0 kPa  
 Equilibrating Time :10.00 min  
 Pressurizing Time :3.00 min  
 Pressure Equilib. Time :0.10 min  
 Load Time :0.50 min  
 Load Equilib. Time :0.10 min  
 Injection Time :0.08 min  
 Needle Flush Time :5.00 min  
 GC Cycle Time :35.00 min  
 Check System Ready :ON  
 Extended System Ready Check Limit :45 min  
 Check GC Ready :ON  
 Extended GC Ready Check Limit :10 min  
 Analysis Mode :Constant  
 Needle Check :Yes  
 Action on Leak Check Error :Stop  
 Action with No Vial on Tray :Stop

[GC-2010]

Column Oven Temp. :70.0 °C  
 Injection Mode :Split  
 Flow Control Mode :Linear Velocity  
 Pressure :61.8 kPa  
 Total Flow :23.4 mL/min  
 Column Flow :0.97 mL/min  
 Linear Velocity :36.1 cm/sec  
 Purge Flow :3.0 mL/min  
 Split Ratio :20.0  
 High Pressure Injection :OFF  
 Carrier Gas Saver :OFF  
 Splitter Hold :OFF  
 Oven Temp. Program  

Rate	Temperature(°C)	Hold Time(min)
-	70.0	12.00
3.00	100.0	2.00
60.00	240.0	2.00

< Ready Check Heat Unit >

Column Oven : Yes  
 HS Flow : Yes  
 MS : Yes  
 < Ready Check Detector(FTD/BID) >  
 < Ready Check: Baseline Drift >  
 < Ready Check: Injection Flow >  
 HS Flow Carrier : Yes  
 HS Flow Purge : Yes  
 < Ready Check APC Flow >  
 APC1 : Yes  
 < Ready Check Detector APC Flow >  
 External Wait :No  
 Equilibrium Time :3.0 min  
 < Additional Flow >  
 APC1 Pressure :80.0 kPa

[GC Program]

[GCMS-QP2020]

IonSourceTemp :250.00 °C  
 Interface Temp. :250.00 °C  
 Solvent Cut Time :4.00 min  
 Detector Gain Mode :Absolute  
 Detector Gain :0.93 kV  
 Threshold :0

[MS Table]

--Group 1 - Event 1--

Start Time :6.00min  
 End Time :22.00min  
 ACQ Mode :Scan  
 Event Time :0.30sec  
 Scan Speed :3333  
 Start m/z :30.00  
 End m/z :800.00

## Procedure B

[Comment]

==== Analytical Line 1 =====

[HS-20]  
 Oven Temp. :120.0 °C  
 Sample Line Temp. :150.0 °C  
 Transfer Line Temp. :150.0 °C  
 Shaking Level :2  
 Multi Injection Count :1  
 Pressurizing Gas Pressure :80.0 kPa  
 Equilibrating Time. :10.00 min  
 Pressurizing Time. :3.00 min  
 Pressure Equilib. Time :0.10 min  
 Load Time :0.50 min  
 Load Equilib. Time :0.10 min  
 Injection Time :0.08 min  
 Needle Flush Time :5.00 min  
 GC Cycle Time :25.00 min  
 Check System Ready :ON  
 Extended System Ready Check Limit :45 min  
 Check GC Ready :ON  
 Extended GC Ready Check Limit :10 min  
 Analysis Mode :Constant  
 Needle Check :Yes  
 Action on Leak Check Error :Stop  
 Action with No Vial on Tray :Stop

[GC-2010]  
 Column Oven Temp. :70.0 °C  
 Injection Mode :Split  
 Flow Control Mode :Linear Velocity  
 Pressure :61.8 kPa  
 Total Flow :23.4 mL/min  
 Column Flow :0.97 mL/min  
 Linear Velocity :36.1 cm/sec  
 Purge Flow :3.0 mL/min  
 Split Ratio :20.0  
 High Pressure Injection :OFF  
 Carrier Gas Saver :OFF  
 Splitter Hold :OFF  
 Oven Temp. Program  

Rate	Temperature(°C)	Hold Time(min)
-	70.0	12.00
40.00	240.0	2.00

< Ready Check Heat Unit >  
 Column Oven : Yes  
 HS Flow : Yes  
 MS : Yes  
 < Ready Check Detector(FTD/BID) >  
 < Ready Check Baseline Drift >  
 < Ready Check Injection Flow >  
 HS Flow Carrier : Yes  
 HS Flow Purge : Yes  
 < Ready Check APC Flow >  
 APC1 : Yes  
 < Ready Check Detector APC Flow >  
 External Wait :No  
 Equilibrium Time :3.0 min  
 < Additional Flow >  
 APC1 Pressure :80.0 kPa

[GC Program]

[GCMS-QP2020]  
 Micro Scan Width :0.00 amu  
 IonSourceTemp :250.00 °C  
 Interface Temp. :250.00 °C  
 Solvent Cut Time :4.00 min  
 Detector Gain Mode :Absolute  
 Detector Gain :0.93 kV

[MS Table]

--Group 1 - Event 1--  
 Start Time :8.00min  
 End Time :12.00min  
 ACQ Mode :SIM  
 Event Time :0.30sec  
 Ch1-m/z :74.00  
 Ch2-m/z :42.00  
 Ch3-m/z :43.00

Sample Inlet Unit :GC



Feidhmeannacht na Seirbhíse Sláinte  
Health Service Executive

Determination of NDMA (HS-GC-MS)  
Method 3/30-Annex 1 GC-MS Conditions  
Issue No. 1

Public Analyst's Laboratory,  
Galway, Ireland.  
Email: PALG.OMCL@hse.ie

Procedure C

==== Analytical Line 1 =====

[HS-20]  
Oven Temp. :145.0 °C  
Sample Line Temp. :150.0 °C  
Transfer Line Temp. :150.0 °C  
Shaking Level :2  
Multi Injection Count :1  
Pressurizing Gas Pressure :80.0 kPa  
Equilibrating Time. :15.00 min  
Pressurizing Time. :3.00 min  
Pressure Equilib. Time :0.10 min  
Load Time :0.50 min  
Load Equilib. Time :0.10 min  
Injection Time :0.08 min  
Needle Flush Time :5.00 min  
GC Cycle Time :15.00 min  
Check System Ready :ON  
Extended System Ready Check Limit :45 min  
Check GC Ready :ON  
Extended GC Ready Check Limit :10 min  
Analysis Mode :Constant  
Needle Check :Yes  
Action on Leak Check Error :Stop  
Action with No Vial on Tray :Stop

[GC-2010]  
Column Oven Temp. :80.0 °C  
Injection Mode :Split  
Flow Control Mode :Linear Velocity  
Pressure :64.9 kPa  
Total Flow :13.6 mL/min  
Column Flow :0.96 mL/min  
Linear Velocity :36.1 cm/sec  
Purge Flow :3.0 mL/min  
Split Ratio :10.0  
High Pressure Injection :OFF  
Carrier Gas Saver :OFF  
Splitter Hold :OFF  
Oven Temp. Program  
Rate Temperature(°C) Hold Time(min)  
- 80.0 8.50  
50.00 240.0 1.00

< Ready Check Heat Unit >  
Column Oven : Yes  
HS Flow : Yes  
MS : Yes  
< Ready Check Detector(FTD/BID) >  
< Ready Check Baseline Drift >  
< Ready Check Injection Flow >  
HS Flow Carrier : Yes  
HS Flow Purge : Yes  
< Ready Check APC Flow >  
APC1 : Yes  
< Ready Check Detector APC Flow >  
External Wait :No  
Equilibrium Time :3.0 min  
< Additional Flow >  
APC1 Pressure :80.0 kPa

[GC Program]

[GCMS-QP2020]  
Micro Scan Width :0.00 amu  
IonSourceTemp :250.00 °C  
Interface Temp. :250.00 °C  
Solvent Cut Time :4.00 min  
Detector Gain Mode :Absolute  
Detector Gain :0.93 kV

[MS Table]

--Group 1 - Event 1--  
Start Time :6.00min  
End Time :9.00min  
ACQ Mode :SIM  
Event Time :0.30sec  
Ch1-m/z :74.00  
Ch2-m/z :42.00  
Ch3-m/z :43.00

Sample Inlet Unit :GC

**Standard Addition Plot of Peak Area Vs  $\mu\text{g/mL}$  of added NDMA**

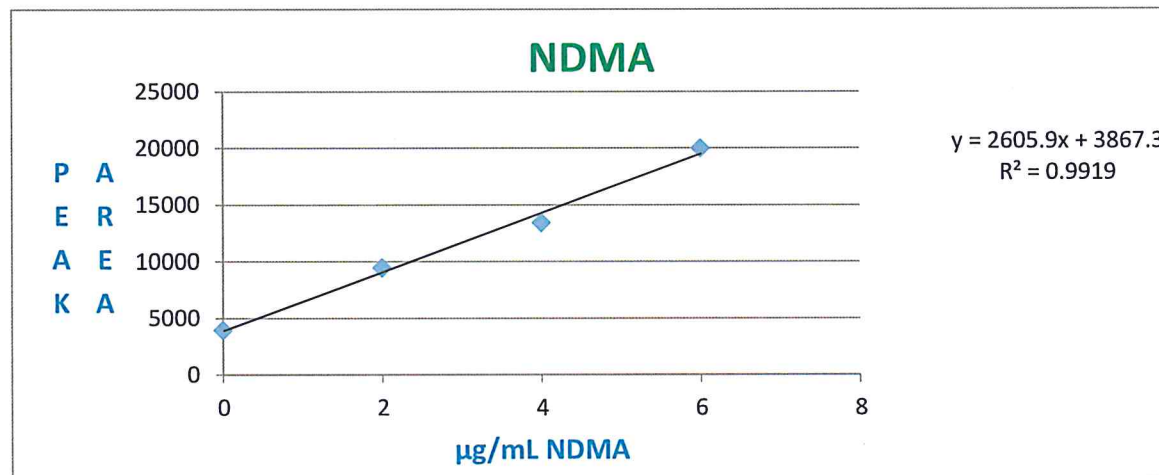
Date:

Sample

Batch:

Data Folder: GCMSsolutions\NDMA

Added NDMA ( $\mu\text{g/L}$ )	Area	sample (g)
0	3918	0.19908
2.0	9441	0.20165
4.0	13415	0.20004
6.0	19966	0.19946
	mean =	0.20006



Average tablets mass (g) = 0.083

API content of tablet (g) = 0.040

**X Intercept = -1.4475  $\mu\text{g/mL}$**

Actual value of the intercept.

→ 7.24

$\mu\text{g NDMA/g}$

Absolute value of the intercept divided by average mass (g) of sample used per vial.

→ 0.60

$\mu\text{g NDMA/tablet}$

$\mu\text{g NDMA/g}$  multiplied by average tablet mass.

→ 15.0

$\mu\text{g NDMA/g Valsartan}$

$\mu\text{g NDMA/tablet}$  divided by API content (g) of tablet.