

## Overcome N-Nitrosamine Analysis Challenges with Chromatography and Mass Spectrometry Techniques

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## Agenda

-Why is nitrosamine assessment necessary?

- Origin of nitrosamines
- Evaluation of nitrosamines
- FDA evaluation
- High-resolution mass spectrometry
- Nominal mass spectrometry: QTRAP system
- SCIEX solution


## What are N-nitrosamines?

- They are molecules containing a nitroso functional group
- They are of concern because their impurities could be carcinogenic to humans
- Their presence in medicines is considered unacceptable



## Why is nitrosamine assessment necessary?



## Why is nitrosamine assessment necessary?

- Nitrosamines are chemical compounds that have been determined in animal studies to cause cancer in humans
- US Food and Drug Administration (FDA) and European Medicines Agency (EMA) guidelines require screening limits of $26.5 \mathrm{ng} /$ day or 96 ng/day, depending on the nitrosamine
- In February 2021, European Pharmacopoeia Comission published a new chapter (chapter 2.5.42) that proposes new procedures for the analysis of N -nitrosamines in active substances
- The new chapter focuses on 5 monographs: valsartan, losartan potassium, candesartan cilexetil, irbersartan and olmesartan medoxomil


Figure 1. Structure of a nitrosamine

- The proposed procedures cover N-nitrosamines: NDMA, NDEA, NDBA, NMBA, NDiPA, NEiPA and NDPA
- In 2018, the presence of nitrosamines (including NDMA) was detected in several blood pressure control drugs known as sartans
- Subsequently, nitrosamines were detected in lots of ranitidine (a drug for the treatment of gastritis and stomach ulcers), and as a result, it was withdrawn from the Mexican market by COFEPRIS, the Mexican ministry of health
- In 2020, the presence of nitrosamines was found in metformin, causing COFEPRIS to add it to the list of drugs that must be tested to rule out the presence of nitrosamines
- New monographs for pharmaceutical requirements were mandate by FEUM, the pharmaceutical standard issues by COFEPRIS


## Nitrosamines - limits

## FDA - CONTROL OF NITROSAMINE IMPURITIES IN HUMAN DRUGS

Table 1. AI Limits for NDMA, NDEA, NMBA, NMPA, NIPEA, and NDIPA in Drug Products

| Nitrosamine | AI Limit (ng/day) ${ }^{\mathbf{1 , 2}}$ |
| :---: | :---: |
| NDMA | 96 |
| NDEA | 26.5 |
| NMBA | 96 |
| NMPA | 26.5 |
| NIPEA | 26.5 |
| NDIPA | 26.5 |

${ }^{1}$ The AI limit is a daily exposure to a compound such as NDMA, NDEA, NMBA, NMPA, NIPEA, or NDIPA that approximates a $1: 100,000$ cancer risk after 70 years of exposure. Appendix B includes a description of the AI derivation for NDMA, which is an example of how FDA applied ICH M7(R1) to set a limit.
${ }^{2}$ The conversion of AI limit into ppm varies by product and is calculated based on a drug's maximum daily dose (MDD) as reflected in the drug label ( $\mathrm{ppm}=\mathrm{AI}(\mathrm{ng}) / \mathrm{MDD}(\mathrm{mg})$ ).

These limits are applicable only if a drug product contains a single nitrosamine. If more than one of the nitrosamine impurities identified in Table 1 is detected and the total quantity of nitrosamine impurities exceeds $26.5 \mathrm{ng} / \mathrm{day}$ (the AI for the most potent nitrosamines) based on the maximum daily dose (MDD), the manufacturer should contact the Agency for evaluation. For drug products with an MDD of less than $880 \mathrm{mg} /$ day, a recommended limit for total nitrosamines of 0.03 ppm is not more than 26.5 $\mathrm{ng} /$ day and is considered acceptable. For drug products with an MDD above $880 \mathrm{mg} / \mathrm{day}$, the limit for total nitrosamines should be adjusted so as not to exceed the recommended limit of $26.5 \mathrm{ng} /$ day

| Common Name and Chemical Name | Acronym | CAS \# | Structure | Chemical Formula | Acceptable Intake Limits (ng/day) |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Nitrosodimethylamine; <br> $N$-Methyl- -nitrosomethanamine | NDMA | 62-75-9 |  | $\mathrm{C}_{2} \mathrm{H}_{6} \mathrm{~N}_{2} \mathrm{O}$ | 96 |
| Nitrosodiethylamine; $N$-Ethyl- $N$-nitrosoethanamine | NDEA | 55-18-5 |  | $\mathrm{C}_{4} \mathrm{H}_{10} \mathrm{~N}_{2} \mathrm{O}$ | 26.5 |
| N -nitrosomethylphenylamine | NMPA | 614-00-6 |  | $\mathrm{C}_{7} \mathrm{H}_{8} \mathrm{~N}_{2} \mathrm{O}$ | 26.5 (USFDA) / 34.5 (EMA)* |
| Nitrosoisopropyethylamine; $N$-Ethyl- N -nitroso-2-propanamine | NIPEA | $\begin{gathered} 16339-1 \\ 04-1 \end{gathered}$ |  | $\mathrm{C}_{5} \mathrm{H}_{12} \mathrm{~N}_{2} \mathrm{O}$ | 26.5 |


| Common Name and Chemical Name | Acronym | CAS \# | Structure | Chemical Formula | Acceptable Intake Limits (ng/day) |
| :---: | :---: | :---: | :---: | :---: | :---: |
| Nitrosodiisopropylamine; $N$-Isopropyl- N -nitrosoisopropylamine | NDIPA | 601-77-4 |  | $\mathrm{C}_{6} \mathrm{H}_{14} \mathrm{~N}_{2} \mathrm{O}$ | 26.5 |
| N-Nitroso-N-methyl-4-aminobutyric Acid; <br> 4-[Methyl(nitroso)amino] butanoic acid | NMBA | $\begin{gathered} 61445- \\ 55-4 \end{gathered}$ |  | $\mathrm{C}_{5} \mathrm{H}_{10} \mathrm{~N}_{2} \mathrm{O}_{3}$ | 96 |
| Nitrosodibutylamine; N-Butyl-N-nitroso-1-butanamine | NDBA | 924-16-3 |  | $\mathrm{C}_{8} \mathrm{H}_{18} \mathrm{~N}_{2} \mathrm{O}$ | 26.5 |
| 1-methyl-4-nitrosopiperazine | MeNP | $\begin{gathered} 16339- \\ 07-4 \end{gathered}$ |  | $\mathrm{C}_{5} \mathrm{H}_{11} \mathrm{~N}_{3} \mathrm{O}$ | 26.5 |

## Root cause of Nitrosamine contaminated

- Sodium nitrite (NaNO2)
- Contaminated Solvent or reagents
- Recycled solvents
- Contaminated intermediate
- Manufacturing process
- Storage process


## Evaluation of nitrosamines

## System Components



## Components of MS



## LC-MS VS LC-MS/MS

Ionization Source:
ESI, APCI

LC-MS


Ionization Source:
ESI, APCI
Collision cell
(Fragmentation)
LC-MS/MS


## Triple Quadrupole Mass Spectrometer; QQQ



## Triple Quadrupole Linear Ion Traps Mass Spectrometer; QTRAP



## Quadrupole Time of Flight (QTOF)



## Advantages of high-resolution mass spectrometry

- QTOF can distinguish between compounds of similar mass
- $\quad X 500 R=30,000$ resolution, 300 Da compound, $\Delta \mathrm{m}=0.01 \mathrm{Da}$
- QTOF can accurately measure molecular weight to several decimal places
- 300 Da compound, 5 ppm mass error $=0.0015 \mathrm{Da}$

High-resolution mass spectrometry
can distinguish these pesticides!

Kresoxim-methyl
$\mathrm{C}_{18} \mathrm{H}_{19} \mathrm{NO}_{4}$
Mass = 313.1214 Da


Isazophos
$\mathrm{C}_{9} \mathrm{H}_{17} \mathrm{CIN}_{3} \mathrm{O}_{3} \mathrm{PS}$
Mass $=313.0417 \mathrm{Da}$


## FRAGMENTATION <br> 

Fragmentation
Energy


SCIEX

## Example : Reserpine MSMS



## Evaluation: FDA

Triple quadruple evaluation


SCIEX Triple Quad 6500+ and QTRAP 6500+
systems


SCIEX 7500 system

High-resolution evaluation


X500 QTOF system
SCIEX

High resolution systems

## Search for unknowns

## BATCH-BATCH INSPECTION USING LC-HRMS

- Characteristics of the X500 QTOF system
- Reliable, easy to calibrate
- SWATH acquisition
- SCIEX OS software

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SCIEX OS
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X500R QTOF system

## Chromatogram of metformin analysis


(a) NDMA; (b) NMO; (c) NMBA; (d) NDEA; (e) NEIPA;
(f) NDIPA; (g) NDPA; (h) NMPA; (i) NDBA

## Search for unknowns

## BATCH-BATCH INSPECTION USING LC-HRMS



## Search for unknowns using SWATH acquisition

## ELECTROSPRAY IONIZATION (ESI)




## ChemSpider and auto-fragmentation tool in SCIEX OS software 1.7



## Compound identification by standard addition



QTRAP system

## Nitrosamine compounds analyzed

## QTRAP 6500+ SYSTEM

| Compound Name | CAS Number | Molecular Formula |
| :---: | :---: | :---: |
| N-Nitrosodimethylamine (NDMA) | 62-75-9 | $\mathrm{C}_{2}{\mathrm{H} 6 \mathrm{~N}_{2} \mathrm{O}}$ |
| N-Nitrosodibutylamine (NDBA) | 924-16-3 | $\mathrm{C} 8 \mathrm{H} 18 \mathrm{~N}_{2} \mathrm{O}$ |
| N-Nitrosodi-n-propylamine (NDIPA) | 621-64-7 | $\mathrm{C} 6 \mathrm{H} 14 \mathrm{~N}_{2} \mathrm{O}$ |
| N-Nitrosomethylethylamine (NMEA) | 10595-95-6 | $\mathrm{C} 3 \mathrm{H} 8 \mathrm{~N}_{2} \mathrm{O}$ |
| N-Nitrosodiethylamine (NDEA) | 55-18-5 | $\mathrm{C} 4 \mathrm{H} 10 \mathrm{~N}_{2} \mathrm{O}$ |
| 1-Nitrosopyrrolidine (NPYR) | 930-55-2 | $\mathrm{C} 4 \mathrm{H} 8 \mathrm{~N}_{2} \mathrm{O}$ |
| 1-Nitrosopiperidine (NPIP) | 100-75-4 | $\mathrm{C}_{5} \mathrm{H}_{10} \mathrm{~N}_{2} \mathrm{O}$ |
| 4-Nitrosomorpholine (NMOR) | 59-89-2 | $\mathrm{C}_{4} \mathrm{H}_{8} \mathrm{~N}_{2} \mathrm{O}_{2}$ |

## Positive XIC and HPLC separation



## Calibration and accuracy

- All calibration curves for both quantifier and qualifier transition have an $r$ value $>0.99$
- Accuracies at each level of the calibration curve for all analytes between $70 \%$ and $130 \%$
- Calibration curve range between $10 \mathrm{pg} / \mathrm{mL}$ and $5,000 \mathrm{pg} / \mathrm{mL}(50-5,000) \mathrm{pg} / \mathrm{mL}$ for NMEA and NPYR)

Calibration for NDMA 1: $y=1.56540 e 6 x+251.28403\left(r=0.99664, r^{2}=0.99329\right)$ (weighting: $1 / x$ )


## LOD and LOQ results

- A limit of quantification (LOQ) of $10.00 \mathrm{pg} / \mathrm{mL}$ of $2.50 \mathrm{pg} / \mathrm{mL}$ achieved for the majority of compounds
- 2 compounds have a slightly raised LOQ and LOD of $50.00 \mathrm{pg} / \mathrm{mL}$ and $10.00 \mathrm{pg} / \mathrm{mL}$ respectively
- \&CV achieved for all compounds (6 injections) at both LOQ and 10x LOQ is well within acceptable limits or trace analysis.

| Compound Name | LOQ $(\mathrm{pg} / \mathrm{mL})$ | LOD $(\mathrm{pg} / \mathrm{mL})$ | \%CV at LOQ | \%CV at 10x LOQ |
| :---: | :---: | :---: | :---: | :---: |
| N-Nitrosodimethylamine (NDMA) | 10.00 | 2.50 | 4.61 | 3.23 |
| N-Nitrosodibutylamine (NDBA) | 10.00 | 2.50 | 3.06 | 1.29 |
| N-Nitrosodi-n-propylamine (NDIPA) | 10.00 | 2.50 | 2.60 | 2.04 |
| N-Nitrosomethylethylamine (NMEA) | 50.00 | 10.00 | 3.24 | 1.31 |
| N-Nitrosodiethylamine (NDEA) | 10.00 | 2.50 | 5.19 | 1.69 |
| 1-Nitrosopyrrolidine (NPYR) | 50.00 | 10.00 | 2.43 | 0.63 |
| 1-Nitrosopiperidine (NPIP) | 10.00 | 2.50 | 2.20 | 0.95 |
| 4-Nitrosomorpholine (NMOR) | 10.00 | 2.50 | 4.68 | 2.03 |

## Chromatography for nitrosamine analysis in sartan family

## NITROSAMINES IN LOSARTAN

- MRM signals for 6 nitrosamines

|  | LLOQ: 0.4 ng/mL or 0.01 ppm <br> Losartan | Threshold: $1.2 \mathrm{ng} / \mathrm{mL}$ or <br> 0.03 ppm <br> Losartan |  |  |
| :--- | :---: | :---: | :---: | :---: |
| Analyte | \%CV | Avg Accuracy | \%CV | Avg <br> Accuracy |
| NDMA | 9.21 | 89.36 | 4.15 | 81.81 |
| NMBA | 8.36 | 79.77 | 4.47 | 78.01 |
| NDEA | 2.83 | 98.72 | 4.10 | 90.85 |
| NEIPA | 3.00 | 94.46 | 4.31 | 82.93 |
| NDIPA | 2.19 | 88.64 | 4.54 | 77.22 |
| NDBA | 4.83 | 111.01 | 2.54 | 98.38 |




## Representative calibration curves

## NITROSAMINES IN LOSARTAN

- Calibration curves ranging from $0.2 \mathrm{ng} / \mathrm{mL}$ to $153.6 \mathrm{ng} / \mathrm{mL}$ for all nitrosamines evaluated correspond to $0.005-3.8 \mu \mathrm{~g} / \mathrm{g}$ with respect to losartan
- In all cases, linearity is demonstrated with an $r$ value $>0.99$



## Chromatography for nitrosamine analysis in sartan family

## NITROSAMINES IN VALSARTAN

 correlation values $r>0.99$

- Recovery in the matrix was also evaluated at the LOD at the LOQ and at the daily exposure limit specified by the FDA ( 0.03 ppm in the API)



## Chromatogram for ranitidine analysis

## NDMA IN RANITIDINE

- MRM signals for NDMA - 2 transitions are monitored

| Sample | Concentration in <br> $50 \mathrm{mg} / \mathrm{mL}$ <br> Ranitidine | Avg. <br> Accuracy <br> $\%$ | Precision <br> $\% R S D$ | Recovery <br> $\%$ |
| :--- | :---: | :---: | :---: | :---: |
| LOD <br> $(0.01 \mathrm{ppm})$ | $0.5 \mathrm{ng} / \mathrm{mL}$ | $101 \%$ | 1.5 | $80-120$ |
| LLOQ <br> (0.03ppm) | $1.5 \mathrm{ng} / \mathrm{mL}$ | 102.8 | 2.5 | $80-120$ |
| Spec Level <br> (0.09ppm) | $4.5 \mathrm{ng} / \mathrm{mL}$ | 104.1 | 1.4 | $80-120$ |




## Enhanced product ion scan

 SEARCH IN LIBRARIES USING THE QTRAP SYSTEM
## QTRAP system technology

## WHAT IS A QTRAP SYSTEM?

- In a QTRAP system, a linear ion trap (LIT) is added to the Q3 of a typical triple quadruple instrument
- This allows for a multitude of additional workflows beyond basic MRM applications for better specificity and quantitative performance

| Scan Type | Triple Quad | QTRAP |
| :---: | :---: | :---: |
| Precursor | $\bullet$ | $\bullet$ |
| MRM | $\bullet$ | $\bullet$ |
| Neutral Loss | $\bullet$ | $\bullet$ |
| Product lon | $\bullet$ | $\bullet$ |
| Enhanced MS (EMS) |  | $\bullet$ |
| Enhanced Multiply Charged (EMC) |  | $\bullet$ |
| Enhanced Resolution |  | $\bullet$ |
| Enhanced Product Ion |  | $\bullet$ |
| $\mathrm{MS}^{3}(\mathrm{MS} / \mathrm{MS} / \mathrm{MS})$ and MRM 3 |  | $\bullet$ |



## What is an enhanced product ion scan?

## FAST AND SENSITIVE MS/MS SCAN

- Precursor ions are filtered in Q1

- The ions are then fragmented in the LINAC collision cell
- Trapping is performed in Q3 (fixed or dynamic fill time)
- Trapped ions are scanned to give a full MS/MS spectra
- This scan can be performed alongside typical MRM
 analysis to provide a further level of confirmation to your analysis
- If a library of target compounds is present, this can be used to provide a library match and hit score, which provides further confidence in the specificity of the analysis without having to perform multiple injections


## Enhanced product ion scan QTRAP system



NPIP


## Library entry example: NDBA

## NDBA 1

> | > { Identifier } |  |
| ---: | :--- |
| > CAS Index | $924-16-3$ |
| > Formula | C8H18N2O |
| > Molecular Weight | 158.24163 |
| > Monoisotopic Mass | 158.14191 |
| > | Libraries > |

Synonyms


Compound information

- Additional Information

Comments

- Library Search Thresholds



## Library search functionality: NDBA



- By using a nitrosamine library, we can perform confirmation to ensure the specificity of our analyte.
- In this case, NDBA has been identified with a purity of 94.6\% based on library spectra
- Therefore, this provides confidence in the assignment of the analyzed peak and can exclude any artifact peaks that may occur


## Achieved LOD, LOQ and linearity

| Methanol Diluent | Impurity | NDMA | NDEA | NEIPA | NDIPA | NDPA | NMPA | NDBA | NMBA | NMO ${ }^{\text {S }}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| USFDA Method Limits ${ }^{\# \#}$ | LOD (ppm) | 0.005 | 0.002 | 0.003 | 0.001 | 0.001 | 0.002 | 0.001 | 0.002 | NAV |
|  | LOQ (ppm) | 0.01 | 0.02 | 0.02 | 0.02 | 0.005 | 0.005 | 0.005 | 0.005 | NAV |
|  | Linearity (ppm) | 0.01-0.1 | 0.02-0.1 | 0.02-0.1 | 0.02-0.1 | 0.005-0.1 | 0.005-0.1 | 0.005-0.1 | 0.005-0.1 | NAV |

API Load ~100 mg

| Methanol Diluent | Impurity | NDMA | NDEA | NEIPA | NDIPA | NDPA | NMPA | NDBA | NMBA | NMO ${ }^{\text {S }}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Limits Achieved on | LOD (ppm) | 0.005 | 0.002 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 | 0.001 |
| QTRAP ${ }^{\text {® }}$ 5500+ | LOQ (ppm) | 0.01 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 | 0.005 |
| System | Linearity (ppm) | 0.01-2 | 0.005-2 | 0.005-2 | 0.005-2 | 0.005-2 | 0.005-2 | 0.005-2 | 0.005-2 | 0.005-2 |


| Methanol Diluent | Impurity | NDMA | NDEA | NEIPA | NDIPA | NDPA | NMPA | NDBA | NMBA | NMO ${ }^{\text {S }}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Limits Achieved on X500B System | LOD (ppm) | 0.005 | 0.001 | 0.001 | 0.001 | 0.001 | 0.005 | 0.001 | 0.001 | 0.005 |
|  | LOQ (ppm) | 0.01 | 0.01 | 0.01 | 0.01 | 0.005 | 0.01 | 0.005 | 0.005 | 0.01 |
|  | Linearity (ppm) | 0.01-1 | 0.01-1 | 0.01-1 | 0.01-1 | 0.005-1 | 0.01-1 | 0.005-0.5 | 0.005-1 | 0.01-1 |


| API Load~25 mg | Water/Acidified Water | Impurity | NDMA | NDEA | NEIPA | NDIPA | NDPA | NMPA | NDBA | NMBA | NMO ${ }^{\text {² }}$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Limits Achieved on X500B System | LOD (ppm) | 0.005 | 0.002 | 0.002 | 0.002 | 0.002 | 0.005 | 0.002 | 0.002 | 0.005 |
|  |  | LOQ (ppm) | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 | 0.01 |
|  |  | Linearity (ppm) | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 | 0.01-2 |

## Conclusions

QTRAP AND HRMS LC-MS/MS SYSTEMS

- Any of our systems has the necessary sensitivity to determine the values requested by regulatory authorities
- Extensive sample preparation is not required
- Selective, sensitive and reproducible methods for the detection and quantification of various APIs are presented and can be transferred to your laboratory immediately
- HRMS systems will help enable timely detection of nitrosamines and their precursors
- QTRAP systems allow additional contaminations to be explored by searching libraries, and aid matrix effect elimination MRM ${ }^{3}$


## Tech notes



## SCIEX

The Power of Precision

## Thank you!

## Questions?



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