

Pitfalls associated with the use of a simple sample preparation in the analysis of saliva with LC-ESI-MS/MS

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1. Introduction
2. Objectives
3. Overview of the experiments
4. Problem and explanation
5. Tips
6. Conclusions


Introduction: LC-MS in STA

Routine analysis of toxicological samples:

Screening:

 immunological techniques
(e.g. EMIT)

Confirmation:

 chromatographic techniques
(e.g. HPLC-DAD or FI; GC-MS)
⇒ LC-MS as valuable alternative

Objectives: fast and easy analysis

Simple sample preparation:

✍ **Enrichment:**


- ✍ Not strictly necessary
- LC-MS is very sensitive

✍ **Purification:**


- ✍ Saliva is relatively clean

⇒ LC-ESI-MS with protein precipitation

Amphetamines







-  Amphetamine, Methamphetamine,
MDA (3,4-Methylenedioxyamphetamine)
MDMA (3,4-Methylenedioxymethylamphetamine)
MDEA (3,4-Methylenedioxyethylamphetamine)

Opiates

-  Morphine
Codeine
6-MAM (6-monoacetylmorphine)

Cocaine and Benzoylecgonine

Internal standards:

-  Amphetamines
 -  MDMPA (Methylenedioxypropylamphetamine)
-  Opiates
 -  Butorphanol
-  Cocaine and Benzoyllecgonine
 -  2'-methylcocaine

Overview of the experiments:

Sample preparation:

200 µL saliva (frozen/thawed)

100 µL of 55% MeOH in water

- containing IS and standard

50 µL formic acid

vortexing - centrifugation

supernatant pH adjusted with NH_4OH

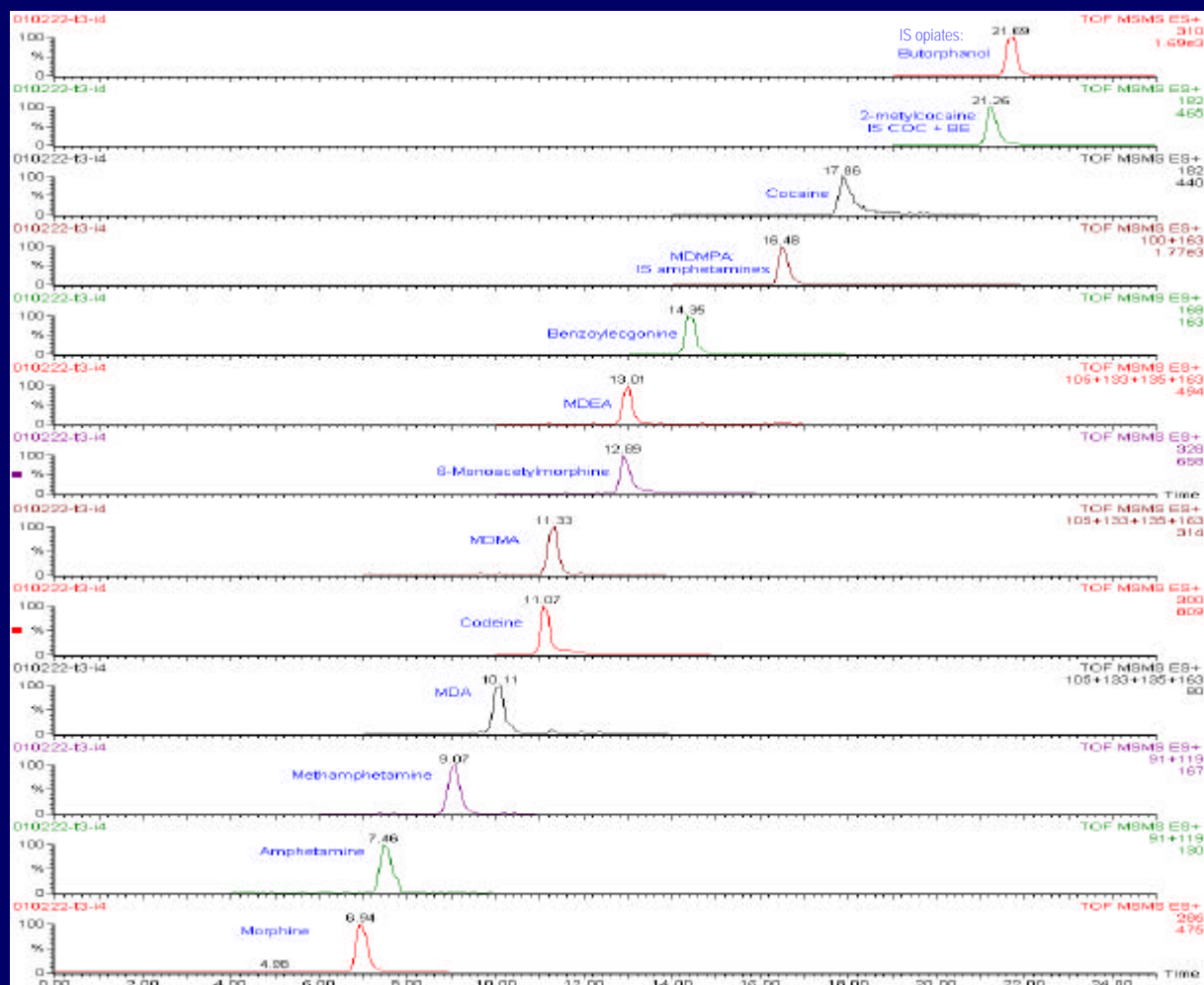
50 µL injected

Chromatographic parameters:

- Phenyl type column
Narrow bore, Hypersil BDS
- Gradient elution
50 mM NH₄Formate pH 4
Gradient from 6 to 50% MeOH
Flow: 200 µL/min Run time: 24'

Mass spectrometric analysis: MS/MS

Quantification on fragment ions
Except opiates: extensive fragmentation






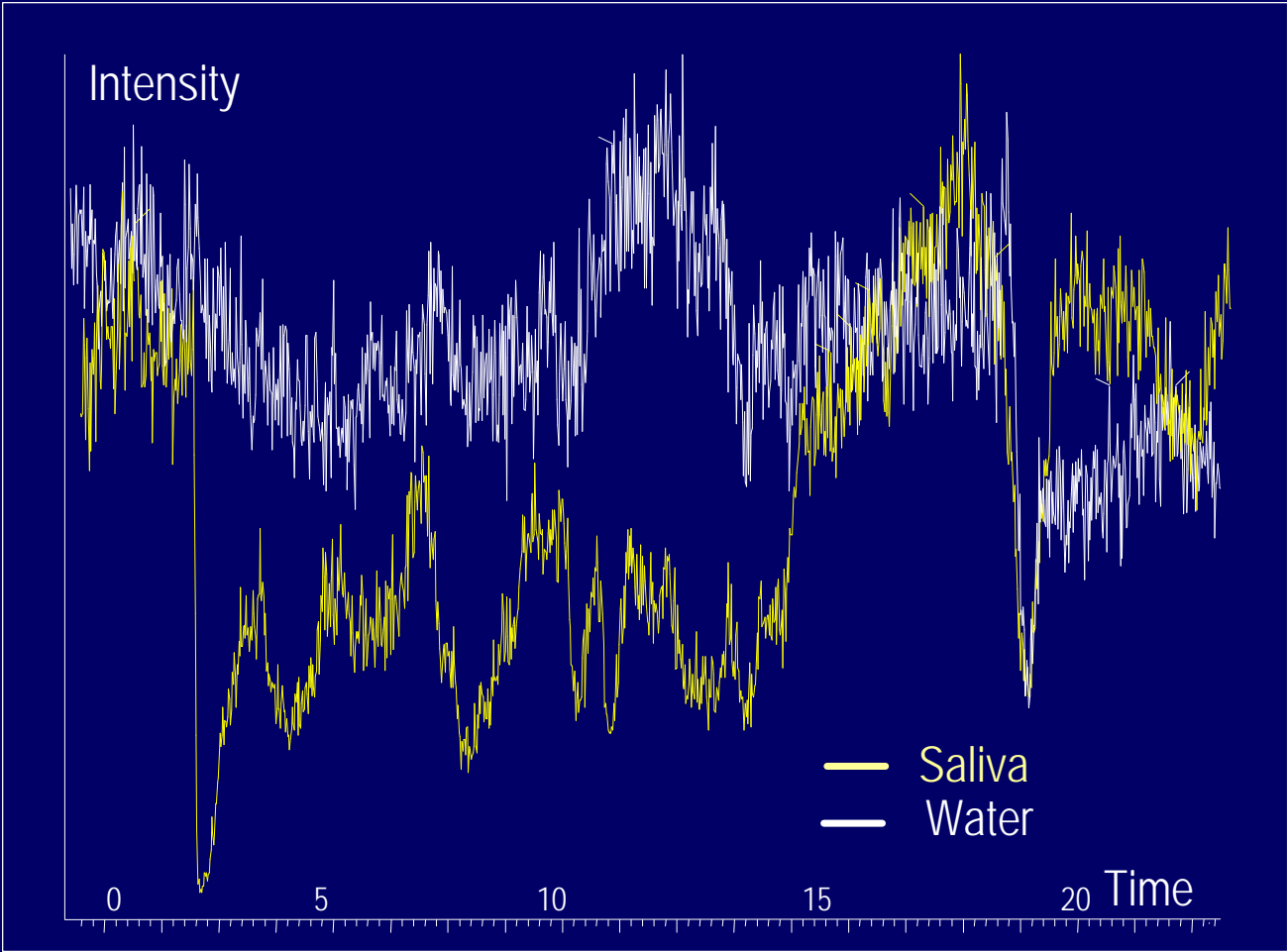
Validation parameters:

- Linearity (n=4): 5 - 500 ng/mL
7 points - $R^2 > 0.995$
- Within Day Precision (n = 7):
at 25 ng/mL
CV% < 10 except MDA = 12.5
- Total Precision (n = 4):
For all concentrations
CV% < 15 except for lowest point
- Stability: all components stable
- Accuracy: not acceptable
sometimes > 20% deviation

Problems and explanation:

Validation parameters:

- Matrix suppression: decreased ionization efficiency in ESI
 -  saliva of different individuals spiked after sample preparation
 -  variable suppression
- Confirmation of matrix effect
 -  post-column introduction of MDMA

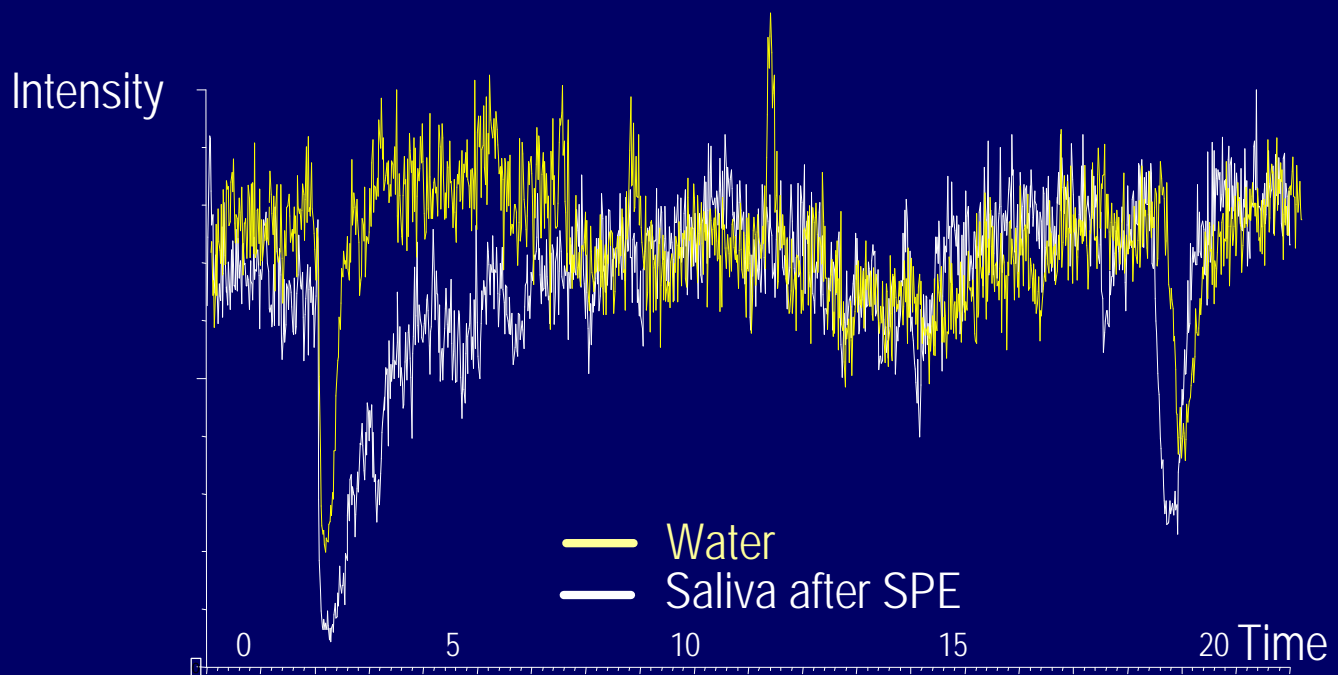


More aggressive protein precipitation

1. 100 μL saliva (frozen/thawed)
100 μL of pure MeOH
 - containing IS and standard500 μL Acetonitrile
20 μL Methanolic hydrochloric acid
vortexing - centrifugation - evaporation
residue redissolved in eluent
50 μL injected
2. Extra Ultrafiltration step (3000 Da filter)

Explanations and tips

✍ Same problems with SPE?



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- ✍ More thorough sample clean-up
(e.g. SPE)
- ✍ Use of APCI ?
- ✍ Use of labelled internal standards?
 - ✍ Same retention time
 - ✍ Same matrix suppression

Conclusion:

 Pitfall associated with ESI combined with MS/MS

 You only see what you are looking for!