

Steroids analysis by GC-MS/MS and HPLC-HRMS with on-line SPE system

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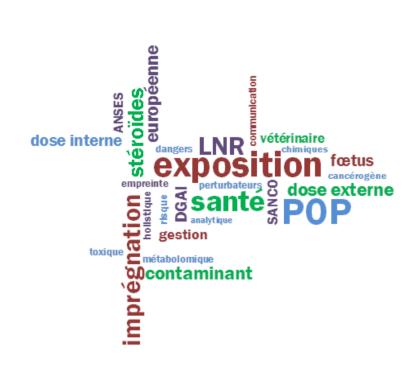
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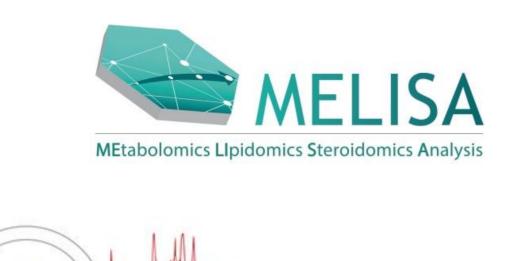
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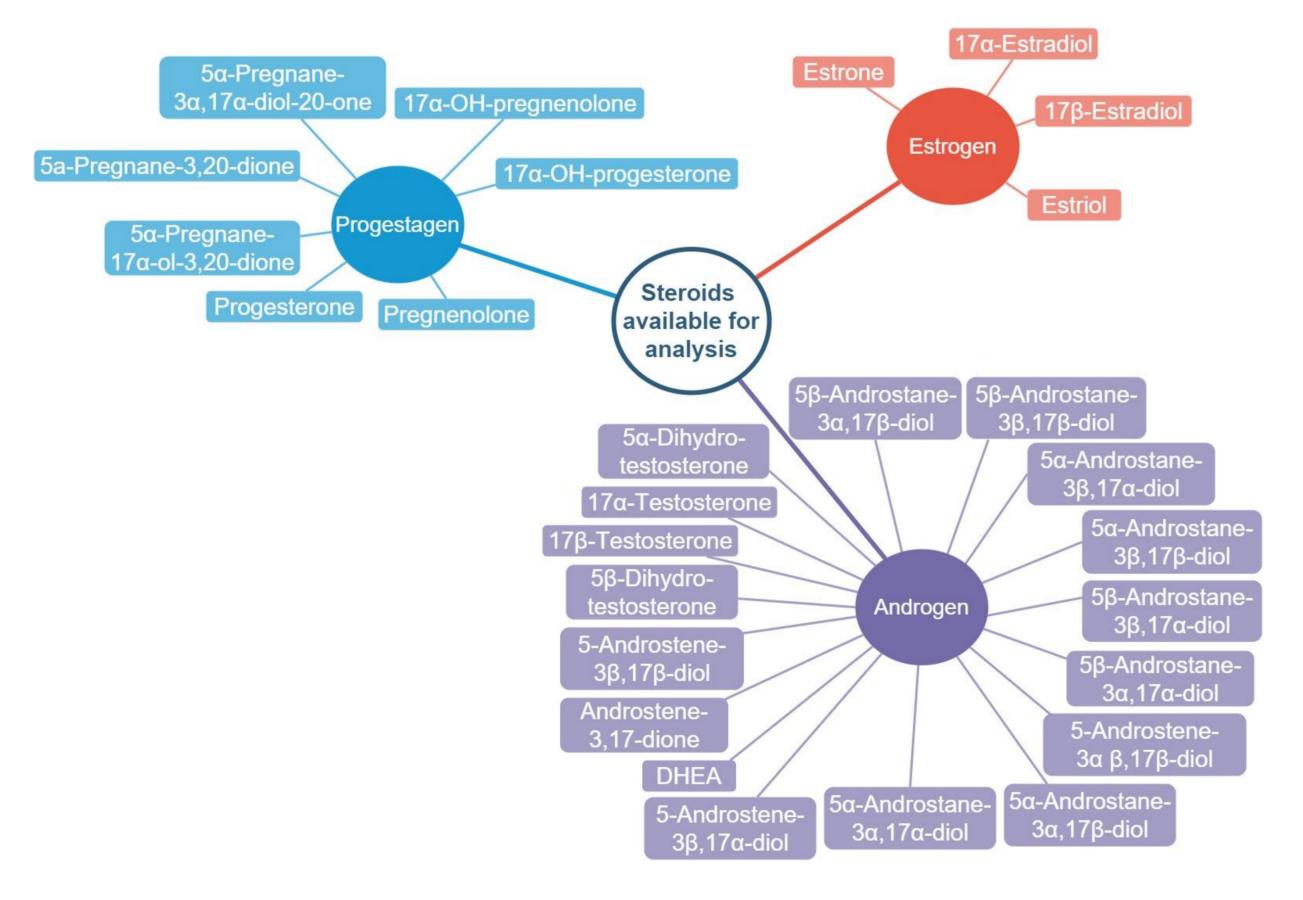
Introduction

Steroids hormones are synthesized in several tissues (e.g. adrenal glands, brain, skin) and regulate essential biological functions including growth and reproduction. Disruptions in steroid homeostasis can lead to serious physiological problems. It is a real challenge to be able to quantify them rapidly in various matrices.

In this work, protocols have been developed to measure steroids in various human matrices such as follicular liquid or periprostatic adipose tissue with GC-MS/MS. These methods are very efficient in terms of sensitivity but remain long and expensive. Thus, a new method was developed aiming at providing a faster and cost effective method that allows to enlarge the panel of monitored steroids available for analysis with the detection of molecules belonging to the corticoid family by HPLC-HRMS with online SPE system. These two techniques are discussed and evaluated.

Sample preparation

Steroids are synthesized in several tissues and play a critical role in several biological processes. In order to be able to quantify steroids in various matrices, our sample preparation methods are systematically re-evaluated according to the matrix in order to adapt to the constraints of expected concentration, quantity of matrix available in order to have access to the thirty or so steroids available for analysis.



✓ Several matrices are studied including, for exemple, follicular fluid and adipose tissue :

Grinding of the adipose tissue in chloroform : methanol Phase separation by adding 0.5% NaCl solution

Adipose Organic phase is taken and evaporated

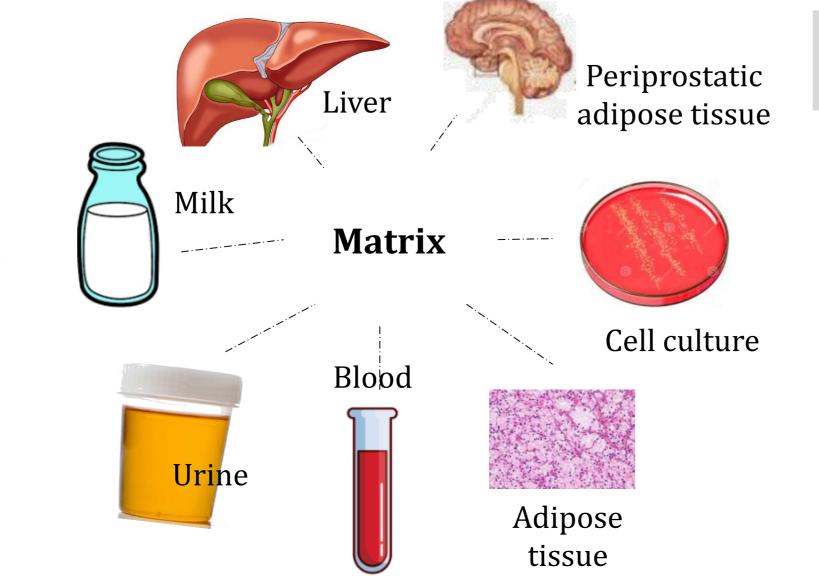
Removal of lipids: addition methanol: water (centrifugation/separation of fat layer/evaporation)

Gel Permeation Chromatography (GPC)

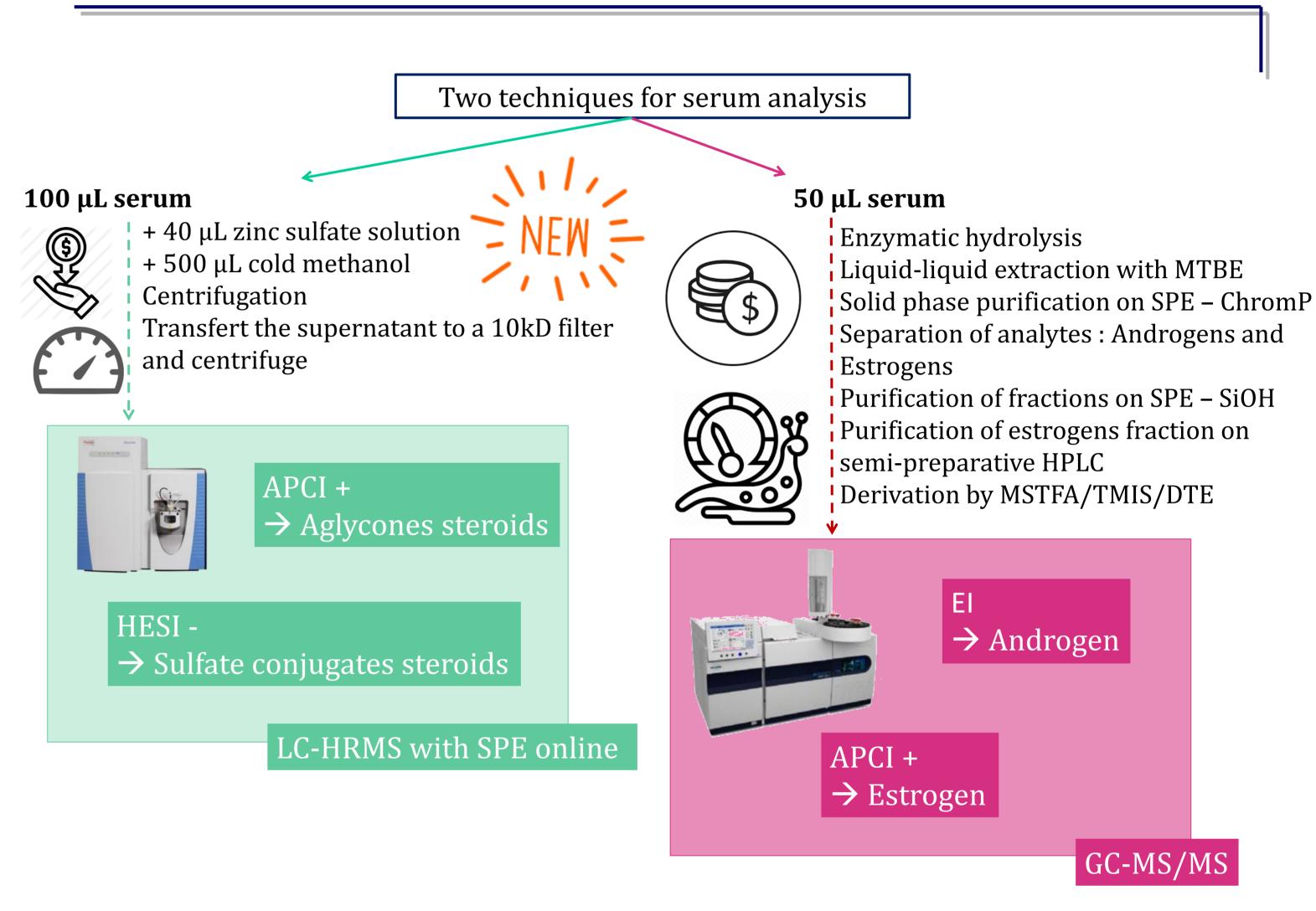
Derivation by MSTFA/TMIS/DTE Injection by GC-EI-MS/MS

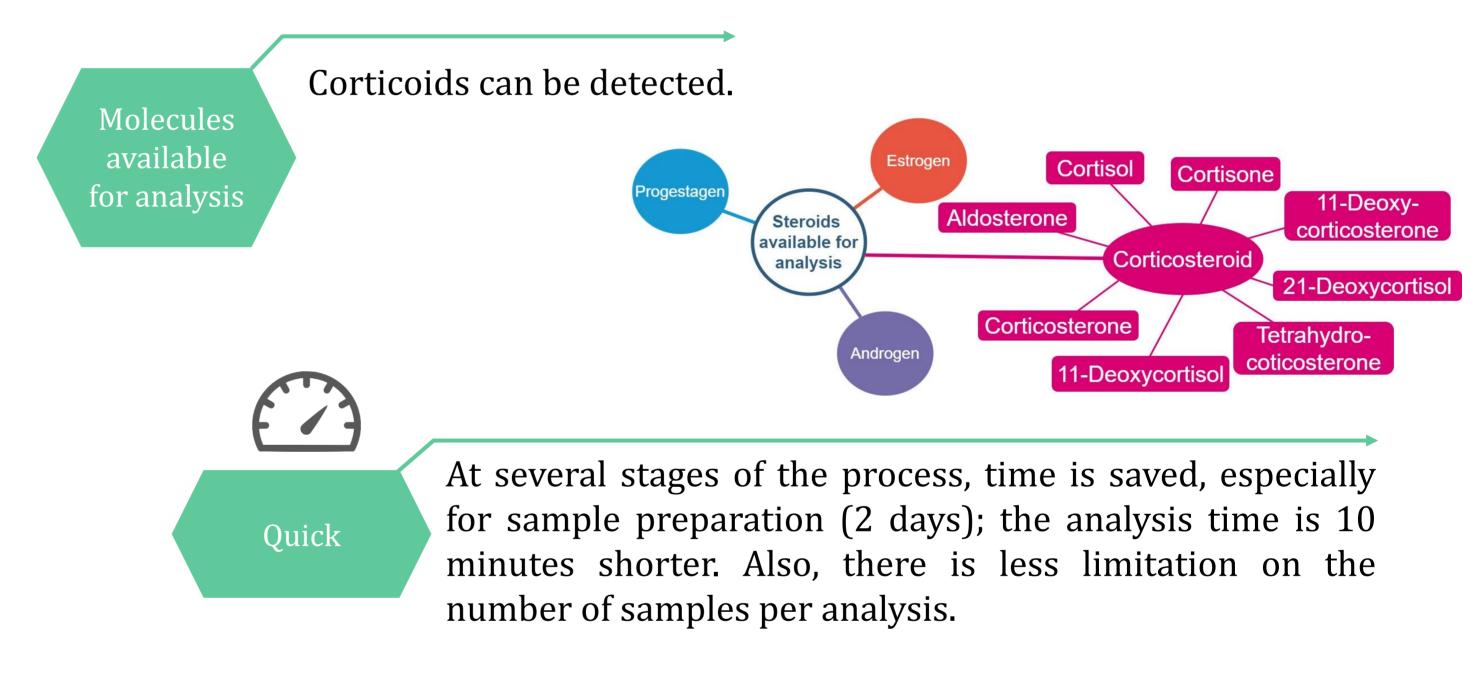
✓ The different matrices already analyzed:

Enzymatic hydrolysis
Liquid-liquid extraction with MTBE
Solid phase purification on SPE – ChromP
fluid
Solid phase purification on SPE – SiOH
Derivation by MSTFA/TMIS/DTE
Injection by GC-EI-MS/MS



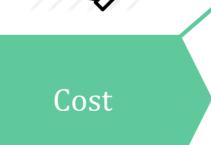
Comparaison of two methods





The limit of detection are better, they allow to quantify with precision all the molecules. Contrary to the on-line SPE method, which allows to detect more molecules but with a less good sensitivity.

Limit of detection



This method is 10 times cheaper.

Safe

This method is more respectful of the environment by using less consumable and less chemical products.





Sample preparation steps are less complicated to apply and they are fewer.



Conclusion

Several sample preparation procedures have been developed to answer to the need of different studies.

The new proposed method appears to correctly answers several requirements in term of high throughput capacity and cost effectiveness. The perspectives would be to transfer this new method on a more sensitive instrumentation and allowing to realize MS/MS for better sensitivity and specificity performances.

tissue