

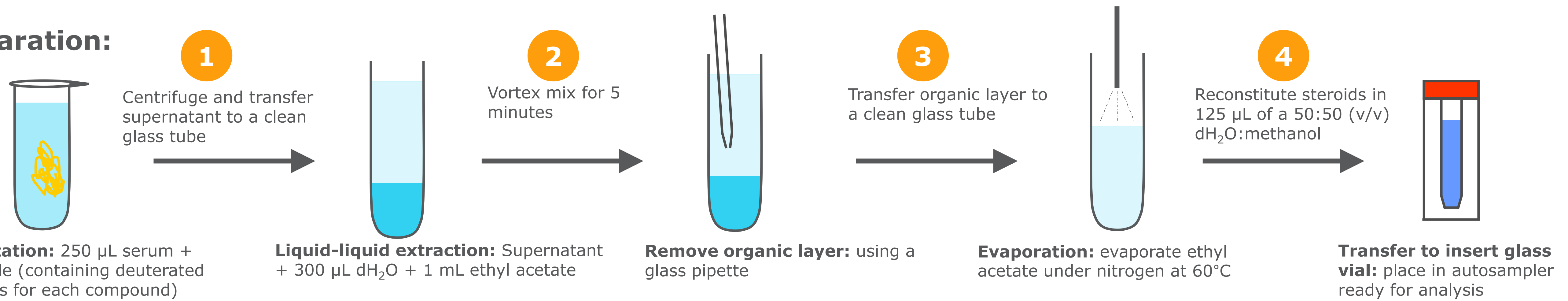
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## Introduction:

Analysis of serum steroids by LC-MS/MS is increasingly replacing immunoassay, especially for those most subject to cross-reaction. However, much more is possible. By using a cocktail of deuterated internal standards, multiple steroids can be simultaneously quantified to provide a 'serum steroid panel'. This also enables measurement of steroids not usually available, either due to low demand or lack of immunoassay specificity. Examples include 21-deoxycortisol, a more specific marker of 21-hydroxylase deficiency than 17-hydroxyprogesterone, and pregnenolone and 17-hydroxypregnenolone, steroid hormone precursors which may be increased in cases of adrenocortical carcinoma. In this study we describe a method for measurement of testosterone, progesterone, androstenedione, DHEAS, pregnenolone, 11-deoxycorticosterone, corticosterone, 17-hydroxypregnenolone, 17-hydroxyprogesterone, 11-deoxycortisol, 21-deoxycortisol, cortisol and cortisone from 250  $\mu$ L serum.

## Sample preparation:



• Schematic of sample preparation for LC-MS/MS. Each step has been extensively optimised to maximise recovery and minimise ion suppression. Combining protein precipitation with liquid-liquid extraction results in reproducible extraction across the range of the polarities of the steroids quantified.

## LC-MS/MS conditions:

LC-MS/MS analysis was performed using a TLX-II Transcend LC system and TSQ Vantage triple quadrupole mass spectrometer (both Thermo Scientific). Separation of steroids was achieved using an Accucore RP-MS column (100 mm x 2.1 mm, 2.6  $\mu$ m particle size). Mobile phases were (A) deionised water and (B) methanol, each containing 0.1% (v/v) formic acid. Steroids were eluted using the chromatography conditions shown in Table 1. Steroids were ionized using an APCI probe maintained at the conditions described in Table 2 and operated in positive ionisation mode. Parameters for each individual steroid quantified by the method are summarised in Table 3.

Start time (min)	Length (sec)	Gradient	% A	% B
0	30	Step	65	35
0.5	900	Ramp	20	80
15.5	150	Step	0	100
18	100	Step	65	35

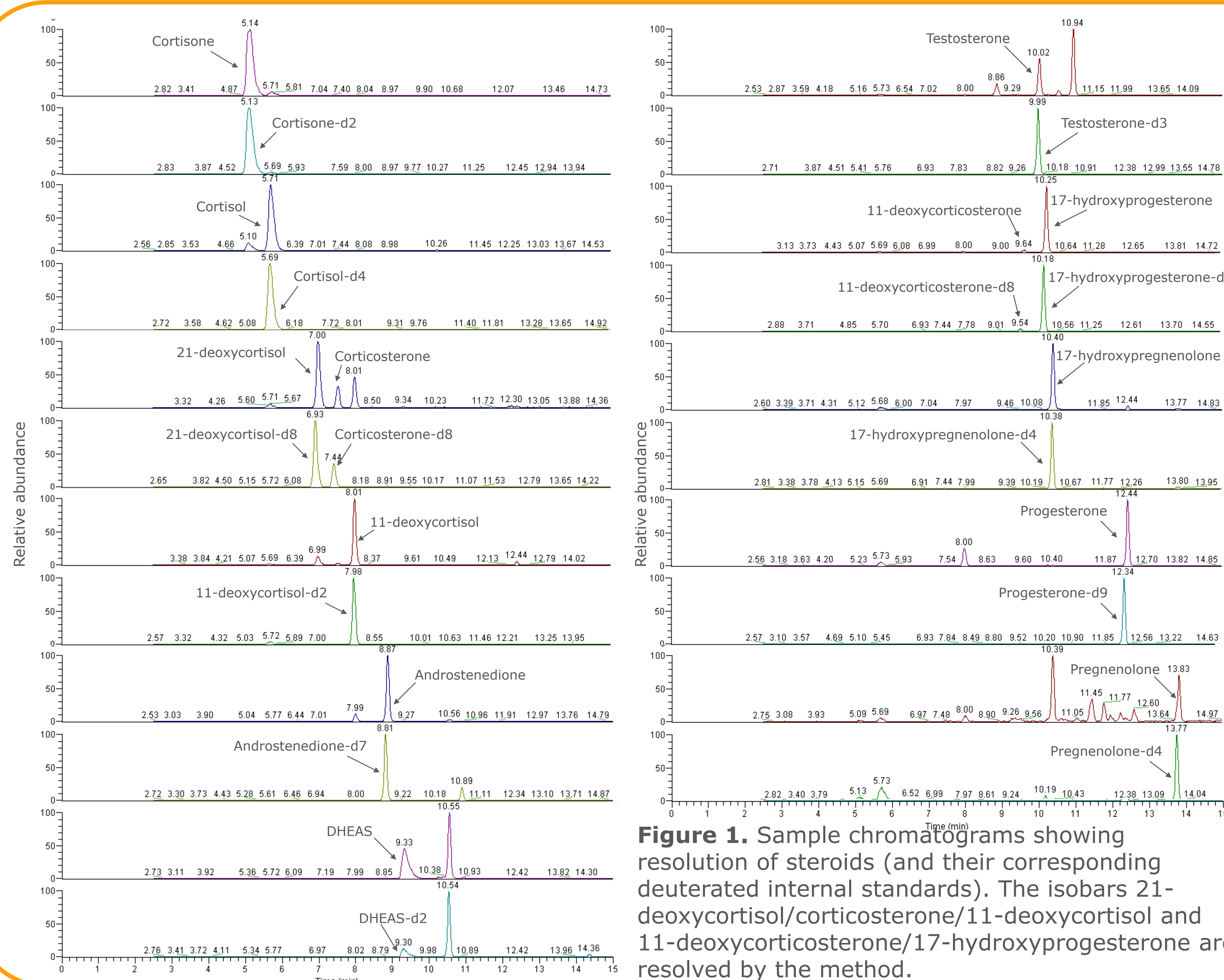
**Table 1.** Chromatography gradient conditions. Flow rate was kept constant at 0.4 mL/min throughout.

Discharge current ( $\mu$ A)	5
Vaporiser temperature ( $^{\circ}$ C)	500
Sheath gas pressure (Arb)	20
Aux gas pressure (Arb)	5
Capillary temperature ( $^{\circ}$ C)	400

**Table 2.** APCI source conditions. Sheath and aux gas was nitrogen.

Steroid	Q1 m/z	Q3 quantifier m/z (Collision energy, V)	Q3 qualifier m/z (Collision energy, V)	S lens (Arb)	Low standard (nmol/L)	High standard (nmol/L)	LLOQ (nmol/L)	Internal standard
Testosterone	289.2	97.0 (20)	109.0 (25)	61	0.17	69.0	0.17	Testosterone-d3
Androstenedione	287.1	97.0 (22)	109.1 (21)	57	1.75	698.0	0.88	Androstenedione-d7
DHEAS	271.1	105.0 (30)	91.0 (38)	30	35.0	13580.0	35.0	DHEAS-d2
Pregnenolone	299.2	105.1 (33)	91.0 (43)	58	8.00	316.0	4.00	Pregnenolone-d4
17-hydroxypregnenolone	297.1	105.0 (34)	91.1 (45)	60	3.00	1203.0	1.50	17-hydroxypregnenolone-d3
Progesterone	315.1	97.0 (20)	109.0 (26)	66	0.40	159.0	0.40	Progesterone-d9
17-hydroxyprogesterone	331.2	97.0 (26)	109.0 (26)	67	2.30	908.0	1.15	17-hydroxyprogesterone-d8
11-deoxycorticosterone	331.2	97.0 (26)	107.0 (26)	67	0.30	30.0	0.30	11-deoxycorticosterone-d8
Cortisol	363.2	121.0 (26)	91.0 (47)	65	3.45	1379.0	3.45	Cortisol-d4
Cortisone	361.1	163.1 (21)	121.0 (30)	74	0.69	277.0	0.69	Cortisone-d2
11-deoxycortisol	347.1	109.0 (27)	97.0 (25)	72	0.72	289.0	0.36	11-deoxycortisol-d2
21-deoxycortisol	347.1	105.1 (27)	121.1 (41)	66	0.72	289.0	0.36	21-deoxycortisol-d8
Corticosterone	347.1	105.1 (27)	121.1 (41)	66	0.72	289.0	0.72	Corticosterone-d8

**Table 3.** Optimised method parameters for each steroid in the panel. Calibration range, lower limit of quantification (LLOQ) and deuterated internal standard used for each steroid are also listed.



**Figure 1.** Sample chromatograms showing resolution of steroids (and their corresponding deuterated internal standards). The isobars 21-deoxycortisol/corticosterone/11-deoxycortisol and 11-deoxycorticosterone/17-hydroxyprogesterone are resolved by the method.

## Results:

- The described method allows quantification of 13 steroids from a single 250  $\mu$ L aliquot of serum. Several of the steroid are not currently routinely quantified in the UK.
- Increasing the percentage of methanol slowly from 35% to 80% (v/v) over 15 minutes allows complete resolution of steroid isobars (21-deoxycortisol/corticosterone/11-deoxycortisol and 11-deoxycorticosterone /17-hydroxyprogesterone, Figure 1). This cannot be achieved using shorter analysis time.
- The method is linear for all steroids over the calibration ranges used, with good LLOQ obtained for each steroid (Table 3).
- Intra- and inter-batch precision and UKNEQAS comparison to LC-MS groups were excellent where available (data not shown).
- No ion suppression was noted following the extensive sample clean-up (data not shown).

## Conclusion:

- This method will allow specific panels to be targeted for individual diseases with disordered steroidogenesis.
- Examples include:
  - **CAH panel:** 17-hydroxyprogesterone and 21-deoxycortisol (21-hydroxylase deficiency), 11-deoxycortisol and 11-deoxycorticosterone (11 $\beta$ -hydroxylase deficiency), 17-hydroxypregnenolone (3 $\beta$ -HSD deficiency), 11-deoxycorticosterone and corticosterone (17 $\alpha$ -hydroxylase deficiency) plus cortisol, DHEAS and androstenedione
  - **Hirsutism panel:** Testosterone, DHEAS, androstenedione and 17-hydroxyprogesterone.
  - **Adrenocortical carcinoma:** Adrenocortical carcinoma typically produces excess steroid precursors. As such (and consistent with our experience from urine steroid profiling) preliminary data shows steroids such as pregnenolone, 17-hydroxypregnenolone, corticosterone and 11-deoxycortisol may be useful markers of malignant transformation, in addition to more established markers such as androstenedione, DHEAS and 17-hydroxyprogesterone.