

# Evaluation of an automated SPE method for samples derived from capillary microsampling

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### Introduction

Alternatives to animal testing and the development of methods that help reducing the number of animals in preclinical studies are much sought after. In capillary micro sampling, a low volume of blood (for example 30 µL) is collected in a capillary, centrifuged and an exact volume of plasma (for example 10 µL) transferred into another capillary. For analysis, the plasma is washed or blown out into a sample tube and diluted to a volume, that can be handled reliably and reproducibly. In contrast to DBS techniques, plasma is processed and analyzed, thus avoiding investigation of critical parameters like effect of hematrocit and offering integration desting and the solution of the solution of the solution of tradefad precedures for addition of techniques. Investigation of critical parameters like effect of nematrocit and offering standard procedures for addition of stabilizers or internal standards during analysis. Even though necessary, dilution should be minimized as it directly affects the achievable limits of quantification. In this poster we describe an automated SPE procedure using small, single use cartridges in a modified CTC liquid handling auto sampler. Results from this approach are compared to results obtained from identical samples processed manually by protein precipitation.

# Experimental

MS-r

General: Samples were processed by dilution of spiked plasma with water containing the internal standard followed by online sample-preparation described below.

followed by online sample-preparation described below. <u>Working-solutions and sample preparation</u>: The analyte (MW 581) was dissolved in DMSO and diluted in ACN/DMSO (50:50, viv) to obtain working-solutions at concentrations twenty times higher than those of the final CAL and CC samples. Aliquots of the working-solutions were spiked into blank rat plasma and diluted with water containing the intermal standard in a ratio of 1:10 (v/v). The samples were vortexed, centrifuged and transferred to the ITSP sample-preparation plate. <u>Online-sample-preparation</u>: ITSP (ITSP Solutions Inc.) cartridges were conditioned with 80µL MeOH and 80µL 0.2% aqueous formic acid before loading 10µL sample. After drying the cartridge with 80µL air, the ITSP cartridges were washed twice with 80µl 0.2% aqueous formic acid and dried again. The compounds were eluted using 80µL EIOH and 10µL of the elutet was intecred onto the analytical cloums Sample-preparation.

eluted using 80µL EtOH and 10µL of the eluate was injected onto the analytical column. Sample-preparation of

eluted using 80µL EICH and 10µL of the eluate was injected onto the analytical column. Sample-preparation of each plasma sample was performed directly before the injection (see Figure 1 for the workflow and the results of the optimization process). <u>Chromatography:</u> 10 µL of the extracted samples were injected onto a Thermo Hypersil Gold (2.1 x 100 mm, 3 µm) analytical column. Eluent A consisted of 0.5% aqueous formic acid, eluent B of 0.5% formic acid in ACN and LC flow rate was 0.5 mL/min. The eluent composition was changed linearly from 70% to 5% A in 2.25 minutes. Eluent composition was kept at 5% B for one minute and then went back ballistically to starting conditions

Calibration range: 50.0 - 25'000 ng/mL (high-range, HR) and 5.00 - 2'500 ng/mL (low-range, LR). <u>Instrumentation and MS-method:</u> TSQ Quantum Ultra (Thermo Scientific), Rheos 2200 quartemary pump (Flux Instruments), HTX PAL autosampler (CTC Analytics). <u>Data-Processing:</u> Raw data were acquired with Xcalibur 2.0 software and processed with LCQuan 2.5 (Thermo Scientific)

Validation parameters: Intra- and inter-assay accuracy and precision, linearity, and carry-over









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# able 3. Carry-over.

Calibration Range	Ourly Over	Ourly Over
	[% of CAL8]	[% of Cal1]
Low-Range [1st Blank after Cal8]	0.6 **	229.7 **
Low-Range [2 <sup>nd</sup> Blank after Cal8]	0.2 **	80.3 **
High-Range [1st Blank after Cal8]	0.7	278.6
High-Range [2 <sup>nd</sup> Blank after Cal8]	0.3	108.5
* Standard-Wash-solution; Wash 1: H <sub>2</sub> O/EtOH (50:50, v/v); Wash 2 ACN/MeOH/i-Prop (1:1:1, v/v/v)		
** Carry-Over can be significantly reduced using 0.3% Tween in Wash-solution 1 (below 30% of Cal1 for the 2 <sup>nd</sup> Blank after Cal8)		

on: SPE Sample Tray [MT1-Frnt] on: Filtration Sample Tray [MT2-Rear / ITSPsmpl on: ITSP Cartridge Tray [ITSPprop] on: Eluate & Filtrate Tray [MT2-Rear / ITSPelut] ar / ITSPsmoll 2: TrayHolder 2 reat Position: Eluate & Filtrate Tray [M] Position1: MeOH Position2: 0.2% aq. HFo Position3: EIOH Wash1: H2O/EIOH (50:50 v/v) Wash2: ACN/MeOH/i-Prop (1/1/1 v/v) 3: Solvent Reservoi

5: Injection Valve

#### Results

Blank rat plasma was spiked with the analyte and diluted with water containing the internal standard in a ratio of 1:10 (viv). CALs and QCs were prepared to cover concentrations of 5.0. - 25000 ng/mL in the high-calibration range and 5.00 - 2'500 ng/mL in low calibration range. The diluted plasma samples were transferred to the ITSP sample-preparation plate and automatically extracted directly before analysis. Sample preparation and LC-MS/MS measurements were performed in parallel using the "Prep Ahead Function" of the CTC autosampler (Figure 4). Chromatograms of the lowest calibration standard Cal1 are presented in Figure 2 and compared with the chromatograms of the calibration transfer presented for both calibration transfer presented in Table 2. An example of a typical calibration curve for each range is presented in Figure 3. Both assays gave very similar results and the intra- and inter-run performance is equivalent to the data obtained using a standard protein-precipitation method. Blank rat plasma was spiked with the analyte and diluted with

data obtained using a standard protein-precipitation method. The carry-over in the analytical assay does not meet the acceptance

criteria of the EMA guideline but can be significantly reduced by using 0.3% Tween as an additive in the aqueous wash-solution (see Table 3).

The influence of the amount of (diluted) plasma loaded onto The initial control of the amount of (alluted) plasma loaded onto the cartridge and the volume of the extraction solvent is presented in Figures 6 and 7. Elution from the ITSP cartridge is complete with as little as 20 µL of extraction solvent (Figure 7) resulting in a factor 4 higher concentration of the analyte in the eluate compared to the standard-elution method. The capacity of the cartridges has been tested between 2 to 40 µL diluted plasma (Figure 6). The area ratio of analyte to internal standard is constant

The area ratio of analyte to internal standard is constant across this range and demonstrate excellent performance of the method across a wide range of sample volumes. The sample-preparation time and the overall run-time of the automated and manual method are compared in Figure 5. Since only minimal manual intervention is required for the automated approach, this workflow offers significant advantages by high sample-workload and longer LC-MS/MS run-times.



## Conclusions

•The automated workflow described above gave equivalent results (LLOQ, precision, accuracy) compared to samples results (LLOQ, precision, accuracy) compared to samples processed manually by protein precipitation. The overall time/sample is slightly higher for the automated protocol. However, since only minimal intervention is required, process safety is supprior and human resources are freed up for other tasks. •The automated protocol may be further optimized in several aspects. As shown in Figure 7, a volume of 20 µL is sufficient for complete elution of the analyte from the cartridge. Figure 6 indicates that an loading volume of 25 µL diluted lagena is

for complete elution of the analyte from the cartnage. Figure 6 indicates that an loading volume of 2-5 LL diluted plasma is sufficient allowing the use of low-volume samples. Body analysis of samples originating from studies using microsampling techniques. -Wethods for the automated optimization of the SPE conditions exist and will be applied in future studies.

Reference: Nilsson LB, Ahnoff M, Jonsson O; Bioanalysis (2013) 5(6), 731-738