Differential mobility analysis (DMA) is a technique that enables separation of species in space based on their difference in ion mobility. Since the movement of a molecule can have a significant effect on its mobility, this technique could assist in eliminating isobaric interferences. In essence, a DMA can be used to selectively detect each species, there is a common fragment (MRM 316-159 @ 45eV) that can be used to improve selective detection of the metabolite OR ensure discrimination from source-CID fragmentation of the metabolite and the parent drug.

RESULTS

The DMA has been designed to provide a very low level of turbulence in the region between the slit (on sampling from source) and the orifice (on sampling into the MS vacuum). The desirability of the DMA ensures that laminar flow can be maintained through the chamber even for Reynolds numbers well beyond the usual threshold for turbulent transition. Molecular ions or clusters from the ion spray enter through a slit into the shear gas region. The second plate is provided with an outlet orifice that is located approximately 25 mm downstream of the inlet slit. A potential difference is applied between the first and second plate which causes the flow of ions, introduced via the inlet slit, to migrate towards the orifice. The laminar gas flow displaces ion trajectories from the slit and carries them out through the second plate outlet orifice, thus allowing a specific value reach the second plate close enough to the orifice to be sampled through it.

The particle mobility varies at the speed of the gas flow, so that particles with low mobility are carried further downstream and particles with higher mobility cross the chamber quickly. The particles are then subjected to sheath gas flow. The DMA device tested in this work was built by SEADM (Sociedad Europea de Analisis by LC-MS/MS System is registered trademark of Applied Biosystems|MDS Sciex). All chemicals were obtained from Sigma (St Louis, MO) or from Cambridge Isotope (Andover, MA) and used without further purification. Urine samples were obtained from internal volunteers and typically diluted 2:1 or 1:1 prior to being spiked with analytes of interest. No additional sample preparation was performed prior to LC separation.

Chromatography was performed using a Luna C18(2) column (250×5.0 mm) from Phenomenex, CA with gradient elution. Samples were prepared using Phosmax Ethyl series 200 staircase and micro pumps. For MRM acquisition, optimal DMA voltage and collision energy (CE) conditions were used for all fragment ions monitored.

**DISCUSSION AND CONCLUSION**

Discordance and conchordance are isobaric species at m/z 216. Though specific fragment ions can be used to selectively detect each species, there is a common fragment (MRM 316-159 @ 45eV) for both species that could be used to reduce the presence of interference in controlled fashion. This approach was used to assess the effectiveness of the DMA at reducing interferences. Figure 4 shows the high optimisation between hydrobromide and oxycodone when operated with the TurboSpray at 45°C (condition for LC at 40μL/min). The optimum value was used for each transition. Figure 5 shows the LC-MSMS separation with the DMA device, showing that each compound interferes in the analysis of the other. However, when the acquisition is performed at the DMA voltage specific to oxycodone (Figure 6) and oxycodone (Figure 7), the respective interferences are reduced significantly (>98%). Further reduction could be obtained if this high voltage could then be used to achieve interference completely, with a small reduction for both analyte interference.

**MATERIALS AND METHODS**

The DMA device tested in this work used a Biomedical (Societate European de Analisis Bioanalitical) Corporation model to provide mobility discrimination of ions prior to MS/MS analysis. A variety of samples have been tested to show the resolving power of the DMA, and to demonstrate the improved signal-to-noise provided by this system. DMA-MSMS combination was evaluated in terms of terms of its performance in the analysis of different species through isolation experiments. Further tests were performed on samples spiked in biological matrices to assess the improvement of IMS when the technique is coupled to LC and MSMS.

**REFERENCES**


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