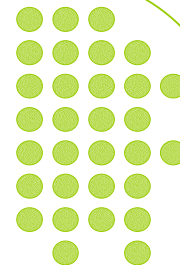


LC-MS based metabolomics and accurate mass measurements in complex extracts



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Introduction

Metabolomics represents the in-depth profiling of metabolites intrinsic to several organisms. An important feature of metabolomics is identifying differences in metabolite patterns, thus demanding accurate measurements in analytical devices. Here we discuss accurate mass measurement on a Q-TOF micro (Waters) equipped with a Lockspray device.

Aim

This part of our research investigates the possibility of accurate mass measurements in a metabolomic context. Our goal was to establish the mass accuracy of a Q-TOF micro (Waters), using the features available in the Masslynx software. A comparison was made between leucine-enkephalin as lockmass, and a mixture of compounds that covers the mass range 50-800.

Materials

HPLC Conditions:

Alliance 2695 (Waters®)
 Column:
 •Atlantis™ dC18, 2.1 x 150mm (Waters®)
 Mobile Phase:
 •Eluent A: 100% water + 0.1% formic acid
 •Eluent B: 90/10 acetonitrile/water + 0.1% formic acid
 Flow Rate: 200µl/min
 Injection Volume: 50µl

MS Conditions:

Mass Spectrometer: Q-TOF micro (Waters®)
 Ion Source: Lockspray™ in positive ion mode
 Software: Masslynx 4.0
 m/z-range: 50-800
 Capillary Voltage: 3000V
 Cone Voltage: 30V

Metabolites:

Amino acids, carbohydrates, nucleotides, plant hormones, steroids, fatty acids, polyamines, carotenoids and others were used from stock solutions at 1mg/ml

Lockspray solution:

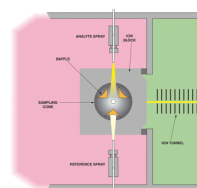
• Leucine-enkephalin 1ng/µl in 50/50 AcN/H₂O
 m/z-value: 556.2771

Lockmix:

• Acetanilide (m/z 136.0762)
 • Pentazocine (m/z 286.2171)
 • Trazodone (m/z 374.1747)
 • Dipyrindamole (m/z 505.3251)
 • Aconitine (m/z 646.3227)

Extraction procedure:

Arabidopsis thaliana leaves were homogenized with an Ultra-Turrax mixer (Ika) in 2:6:2 H₂O:MeOH:CHCl₃. Samples were centrifuged for 10 minutes and the supernatant (after spiking) was evaporated under nitrogen. Before injection, samples were dissolved in 75/25 H₂O/ACN + 0.1% FA.



The lockspray device (Waters®)

Methods

❖ A mixture of 5 compounds with lockmasses covering the typical mass range in metabolomic research from 50-800, is considered to give better accurate mass measurements than a single compound. Leucine-enkephalin is the standard product in accurate mass measurement using lockspray devices. Both lockspray compositions were tested to evaluate the best accurate mass measurement.

❖ Accurate mass measurement is an important feature in identifying metabolites in metabolomics. Subtle differences from multivariate data analysis can thus be attributed to specific metabolites, revealing complex biochemical regulations in e.g. plants.

Results

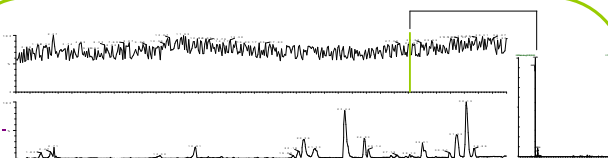


Figure 1: TIC for spiked extract, function 1 (sample) and function 2 (lockspray), using leucine-enkephalin as a lockmass; spectrum of leu-enk.

Name compound	Accurate mass (Da)	Mass accuracy (ppm; n=3)
leucine	132.1025	8.83 ± 1.58
phenylalanine	166.0868	11.24 ± 2.28
s-adenosylmethionine	399.1451	-2.92 ± 4.00
lactose	365.106	-4.93 ± 8.55
maltotriose (Na+)	527.1588	2.85 ± 1.71
uracil	113.0351	3.24 ± 5.03
cytidine	244.0933	2.59 ± 12.31
IMP	349.0594	6.11 ± 5.45
zeatin	220.1198	-3.03 ± 2.15
jasmonic acid	211.1334	-3.16 ± 7.28
abscisic acid	265.144	0.00 ± 5.07
epibrassinolide	481.3529	1.94 ± 3.72
spermidine	146.1657	-0.23 ± 3.77

Table 1: Several spiked metabolites with accurate mass (Da) and mass accuracy in ppm, using leucine-enkephalin as a lockmass (n=3)

Leucine-enkephalin (Figure 1) is presented as lockmass in accurate mass measurement. By means of the accurate mass measure tool in Masslynx, m/z correction throughout the entire chromatogram is possible. When analysing complex LC-MS matrices, data processing software bunches mass with retention time. In this perspective, masses are taken at most intense peak signal. Mass deviations up to 40ppm are obtained (results not shown). Such deviations are too large for identification purposes but adequate for multivariate data analysis where binning of masses is the rule. When mass correction is performed at a signal intensity (e.g. at the foothill of a peak) close to the intensity of the lockmass, however, mass differences lay within 10ppm (Table 1).

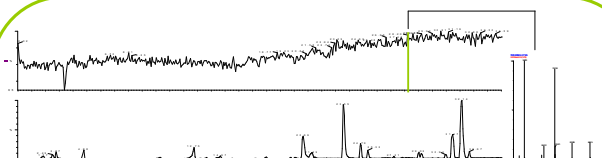


Figure 2: TIC for spiked extract, function 1 (sample) and function 2 (lockspray), using the lockmix for accurate mass measurement; spectrum of lockmix.

Name compound	Accurate mass (Da)	Mass accuracy (ppm; n=3)
leucine	132.1025	42.39 ± 9.66
phenylalanine	166.0868	45.96 ± 27.76
s-adenosylmethionine	399.1451	38.00 ± 16.20
lactose	365.106	37.07 ± 6.17
maltotriose (Na+)	527.1588	-1.83 ± 2.08
uracil	113.0351	49.24 ± 12.89
cytidine	244.0933	-36.87 ± 26.31
IMP	349.0594	11.27 ± 7.04
zeatin	220.1198	9.24 ± 3.22
jasmonic acid	211.1334	13.74 ± 5.76
abscisic acid	265.144	-2.39 ± 10.05
epibrassinolide	481.3529	16.20 ± 2.40
spermidine	146.1657	41.28 ± 9.29

Table 2: Several spiked metabolites with accurate mass (Da) and mass accuracy in ppm, using the lockmix for accurate mass measurements (n=3)

Via a tool in Masslynx, called secondary reference correction, a possibility is provided to correct masses using a mixture of compounds. Here we present a lockmix of 5 compounds covering the m/z range 50-800 (Figure 2). The secondary reference tool corrects masses with the lockmass closest to the m/z of the sample metabolite. Theoretically, better lockmass correction could be envisaged. Nevertheless, larger deviations are observed as can be seen in Table 2.

Conclusion

❖ We tried to obtain a better lockmass-correction in the m/z range 50-800 using a mixture of 5 compounds. Nevertheless, leucine-enkephalin seems the best solution for m/z-correction in a lockspray setting.

❖ Accurate mass measurements with a Q-TOF micro are feasible within a mass range of 10ppm, if the signal intensity of compound and lockspray are matched.