Combining Accurate Mass from High Resolution and Spectral Accuracy from Lower Resolution towards Unique Elemental Composition Determination

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Introduction

Unknown compound identification benefits greatly from the ever-increasing mass accuracy capabilities on high resolution (HiRes) MS systems. Unfortunately, due to various hardware/firmware/software factors, the holy grail of uniquely determining the elemental composition of a real unknown remains elusive except in limited cases. While high resolution MS is known to readily achieve measurements within 1-5ppm or even better mass accuracy, these instruments have been found to lack spectral accuracy (SA) which could help further eliminate incorrect elemental compositions (Ref 1-2). Paradoxically, low or lower resolution (LowRes) MS lends itself to higher spectral accuracy but is typically associated with lower achievable mass accuracy. In this paper, we demonstrate the feasibility of combining high- and low- resolution measurements into one analysis to achieve unique but also high confident elemental composition determination, all within the same single injection by taking advantage of both HiRes and LowRes scanning capability available on an Orbitrap LC/MS system!

Method

Thermo Orbitrap LC/MS system

Sample and sample preparation

LC column and mobile phase

MS Data Acquisition: ESI+ mode

- Full MS scan, HiRes 120K resolving power (RP), AGC target 1e6, 50-500 Da
- DDA Full MS2 scan: 10 ions, 15K RP, 0.50Da window, AGC target 1e5
- Full MS scan, LowRes 15K RP, AGC target 1e6, 50-500 Da

Thermo Xcalibur Software for Post Processing

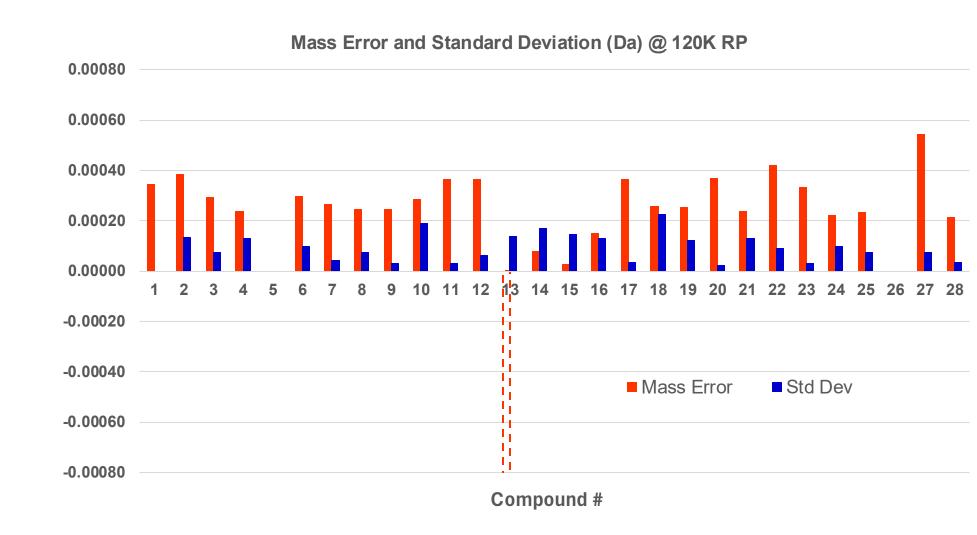
Cerno MassWorks software for sCLIPS (self Calibrating Line-shape Isotope Profile Search) Spectral Accuracy analysis

Results and Discussion

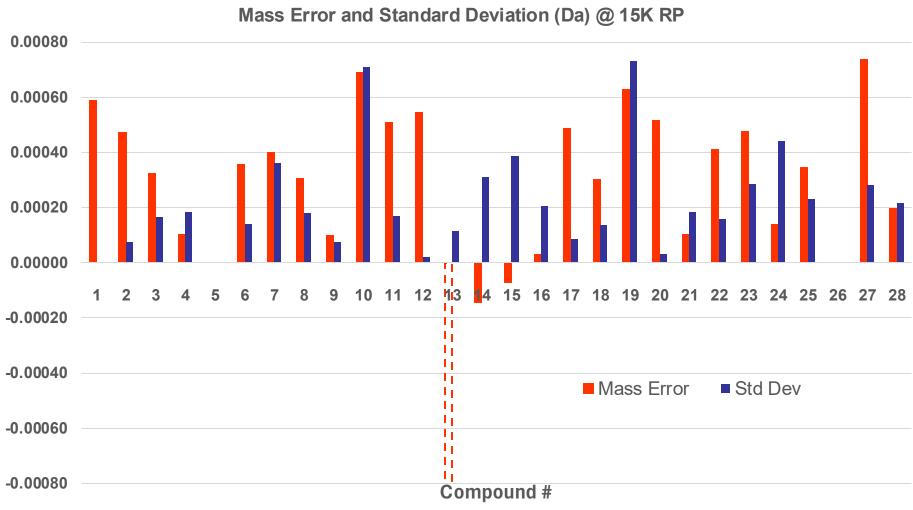
Using the Xcalibur software and the accurate mass XIC confirmed 26 of 28 expected compounds in the run data acquired, with their expected RT location identified as shown in the summary table below along with other analysis results.

| Compound # | Name | Elemental Composition (M) | Exact Mass [M+H]+ | MS1 | MS1 RT (Min) | 120K RP Only | | | | 120K & 15K RP | | | | | |
|---------------|------------------|------------------------------|----------------------|--------------|-----------------|--------------|------|-------|--------------------|---------------|------|-------|--------------------|------|-----------------|
| | | | | | | SA% | Rank | Total | SA Breakout (%) | SA% | Rank | Total | SA Breakout (%) | ΔSA% | Notes |
| 1 | Bitertanol | C20H23N3O2 | 338.18630 | ~ | 14.18, 14.26 | 98.3 | 1 | 33 | 0.2 | 99.7 | 1 | 33 | 2.8 | 1.4 | |
| 2 | Bromuconazole | C13H12BrCl2N3O | 375.96136 | \checkmark | 12.58 | 96.3 | 3 | 940 | -0.5 | 98.4 | 1 | 940 | 1.3 | 2.0 | |
| 3 | Cyproconazole | C15H18ClN3O | 292.12112 | ✓ | 12.18, 12.30 | 96.6 | 1 | 43 | 1.5 | 97.7 | 1 | 43 | 2.0 | 1.1 | |
| 4 | Dichlorobutrazol | C15H20ClN3O | 294.13677 | ~ | 11.90 | 83.3 | 1 | 31 | 0.2 | 94.2 | 1 | 31 | 0.7 | 10.9 | interference |
| 5 | Difenoconazole | C19H17Cl2N3O | 374.08214 | | | | | | | | | | | | |
| 6 | Diniconazole | C15H17Cl2N3O | 326.08214 | \checkmark | 14.49 | 97.5 | 1 | 151 | 1.1 | 98.8 | 1 | 151 | 1.6 | 1.3 | |
| 7 | Epoxiconazole | C17H13ClFN3O | 330.08039 | \checkmark | 13.15 | 97.2 | 1 | 159 | 0.3 | 98.9 | 1 | 159 | 0.1 | 1.7 | |
| 8 | Etaconazole | C14H15Cl2N3O2 | 328.06141 | \checkmark | 12.95, 13.57 | 97.2 | 1 | 208 | 0.1 | 99.2 | 1 | 208 | 2.0 | 2.0 | |
| 9 | Ethirimol | C11H19N3O | 210.16009 | \checkmark | 0.80 | 99.1 | 1 | 2 | 2.4 | 99.5 | 1 | 2 | 2.4 | 0.4 | |
| 10 | Etaxazole | C21H23F2NO2 | 360.17696 | \checkmark | 17.24 | 98.2 | 1 | 69 | 3.4 | 99.0 | 1 | 69 | 1.5 | 0.9 | |
| 11 | Fenarimol | C17H12Cl2N2O | 331.03995 | \checkmark | 12.63 | 97.8 | 1 | 304 | 0.1 | 97.9 | 1 | 304 | 1.3 | 0.1 | |
| 12 | Fenbuconazole | C19H17ClN4 | 337.12145 | \checkmark | 14.09 | 98.0 | 1 | 118 | 0.3 | 98.2 | 1 | 118 | 0.6 | 0.2 | |
| 13 | Fluquinconazole | C16H8Cl2FN5O | 376.01627 | \checkmark | 13.42 | 96.2 | 3 | 940 | -0.8 | 99.0 | 1 | 940 | 2.2 | 2.8 | |
| 14 | Flusilazole | C16H15F2N3Si | 316.10761 | \checkmark | 13.90 | 93.0 | 17 | 89 | -3.7 | 98.9 | 1 | 89 | 0.2 | 5.9 | |
| 15 | Flutriafol | C16H13F2N3O | 302.10995 | \checkmark | 9.92 | 98.6 | 1 | 64 | 0.5 | 99.2 | 1 | 64 | 0.2 | 0.5 | |
| 16 | Fuberidazole | C11H8N2O | 185.07094 | \checkmark | 0.78 | 99.1 | 1 | 12 | 3.4 | 99.0 | 1 | 12 | 3.2 | -0.1 | |
| 17 | Hexaconazole | C14H17Cl2N3O | 314.08214 | \checkmark | 14.00 | 97.3 | 1 | 124 | 0.4 | 98.5 | 1 | 124 | 2.1 | 1.3 | |
| 18 | Ipconazole | C18H24ClN3O | 334.16807 | \checkmark | 15.27, 15.46 | 97.0 | 1 | 47 | 1.6 | 99.3 | 1 | 47 | 3.0 | 2.3 | |
| 19 | Metconazole | C17H22ClN3O | 320.15242 | \checkmark | 14.04, 14.24 | 97.2 | 1 | 48 | 1.2 | 99.1 | 1 | 48 | 2.9 | 1.9 | |
| 20 | Nuarimol | C17H12ClFN2O | 315.06950 | \checkmark | 11.26 | 98.6 | 1 | 167 | 0.4 | 99.2 | 1 | 167 | 2.5 | 0.7 | tied for top hi |
| 21 | Paclobutrazol | C15H20ClN3O | 294.13677 | \checkmark | 11.89 | 66.6 | 1 | 30 | 1.4 | 94.2 | 1 | 30 | 0.9 | 27.6 | interference |
| 22 | Penconazole | C13H15Cl2N3 | 284.07158 | \checkmark | 13.98 | 98.7 | 1 | 82 | 1.1 | 98.5 | 1 | 82 | 1.1 | -0.2 | |
| 23 | Propiconazole | C15H17Cl2N3O2 | 342.07706 | \checkmark | 14.48, 14.58 | 97.3 | 1 | 206 | 0.1 | 99.0 | 1 | 206 | 1.8 | 1.7 | |
| 24 | Tebuconazole | C16H22ClN3O | 308.15242 | \checkmark | 13.62 | 97.2 | 1 | 31 | 7.9 | 98.6 | 1 | 31 | 3.0 | 1.5 | |
| 25 | Tetraconazole | C13H11Cl2F4N3O | 372.02881 | ✓ | 13.74 | 98.2 | 1 | 565 | 0.2 | 99.3 | 1 | 565 | 0.1 | 1.1 | tied for top hi |
| 26 | Triadimenol | C14H18ClN3O2 | 296.11603 | | | | | | | | | | | | |
| 27 | Triflumizole | C15H15ClF3N3O | 346.09285 | ✓ | 13.99 | 98.1 | 1 | 181 | 0.3 | 98.8 | 1 | 181 | 0.1 | 0.8 | |
| 28 | Triticonazole | C17H20ClN3O | 318.13677 | ~ | 12.26 | 97.5 | 1 | 60 | 1.0 | 98.4 | 1 | 60 | 1.0 | 0.9 | |

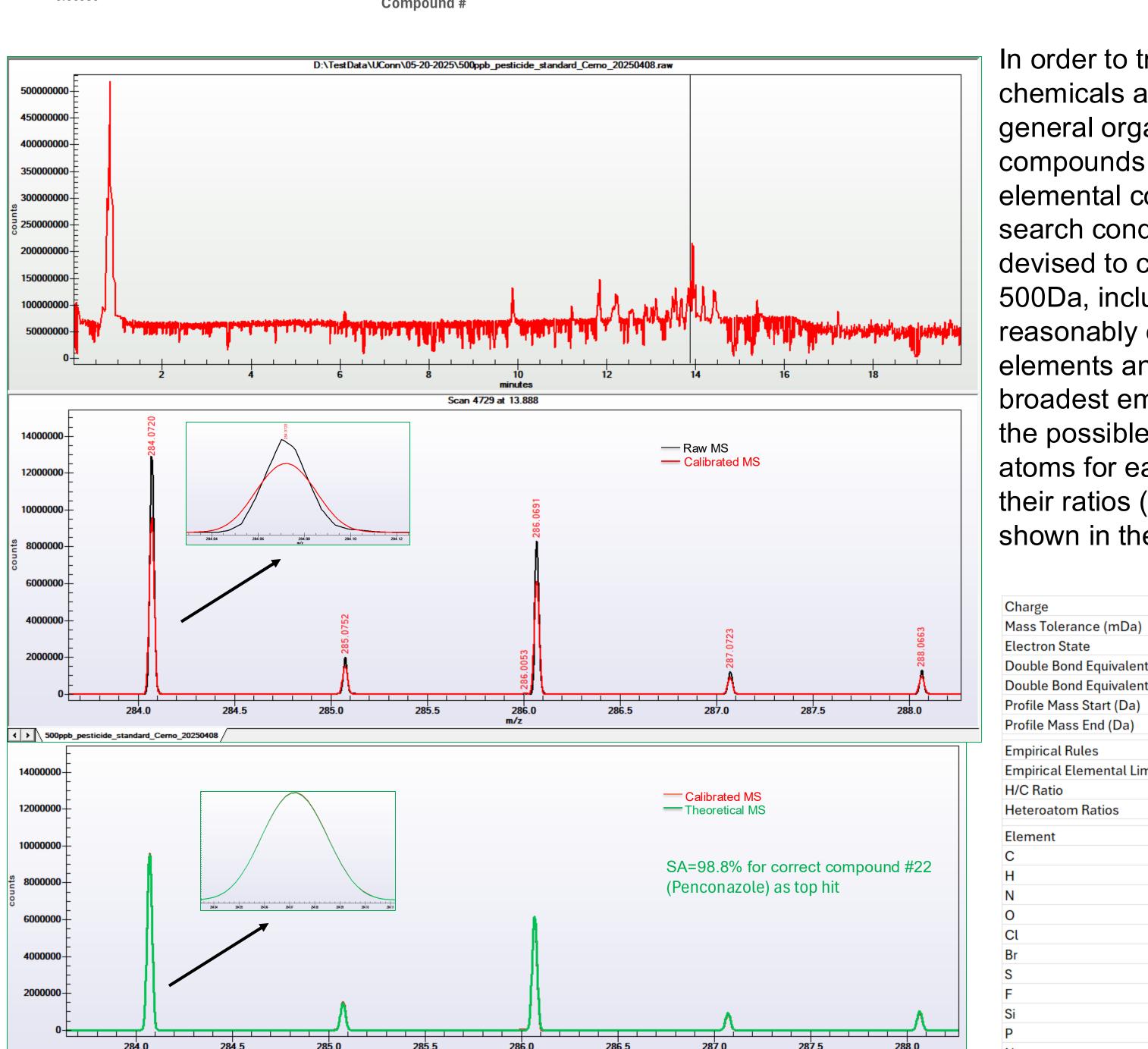
Within each RT window identified, up to 3 most abundant full MS scans at 120K and 15K RP were used to report up to 3 accurate monoisotopic mass values at each RP, from which an average accurate mass was calculated and compared to the exact mass to compute a mass error (bias) along with the corresponding standard deviation at each RP, as shown in the below graphs.



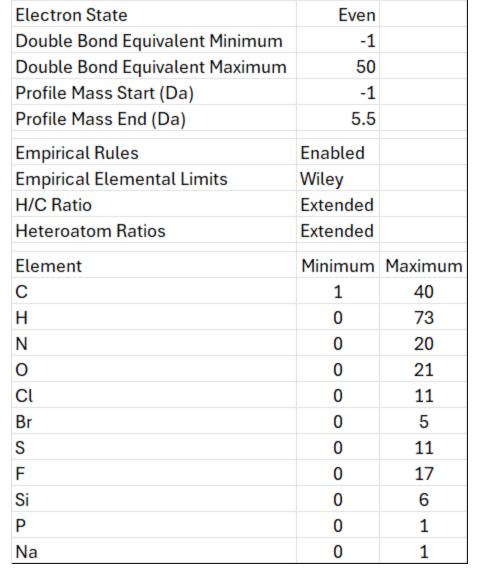
At 120K RP, all mass errors are positive and <0.6 mDa (except for the mistaken compound #13) whereas the standard deviation is 2-3x smaller or <0.2mDa, indicating that the systematic mass error dominates at 120K RP and further improvement is likely limited if not impossible. Nonetheless, this makes it feasible to search for unknown elemental composition within a tight 1mDa mass window, which in and by itself would not be enough to get even close to unique identification (medium # total hits = 86 from the summary table on the left).



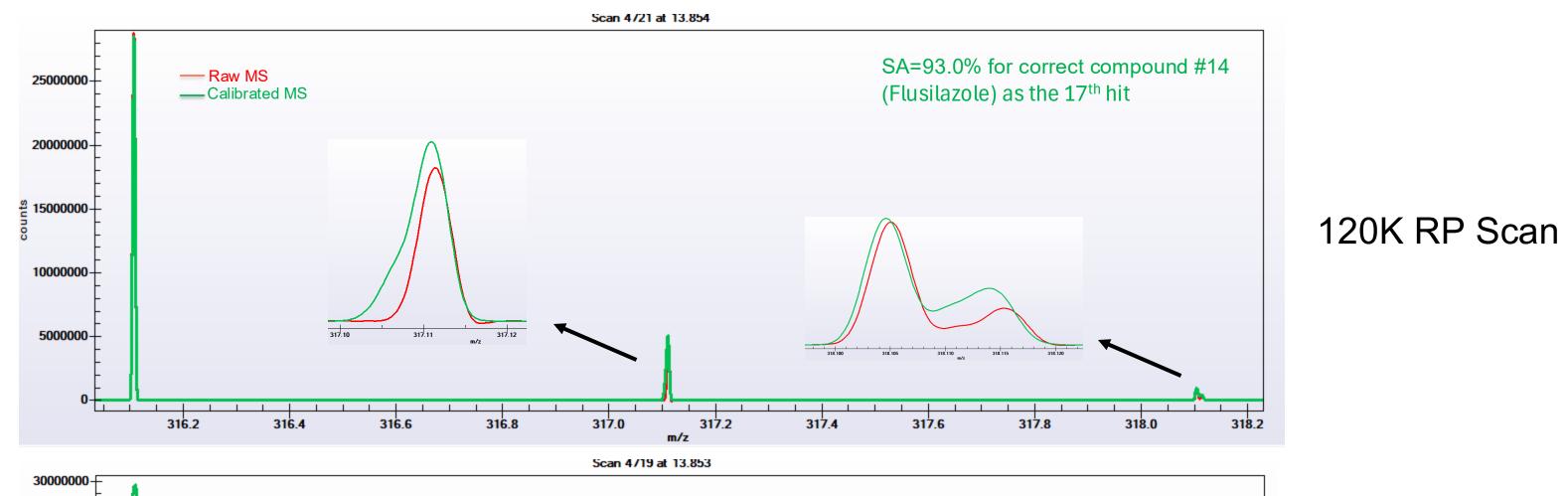
At 15K RP, both the mass error and the standard deviation increase and there are now negative mass errors due likely to the larger standard deviation. It would not be feasible to use the tight 1mDa mass window for confident unknown elemental composition search at 15K RP, unless a more accurate 120K RP mass measurement is available and utilized.



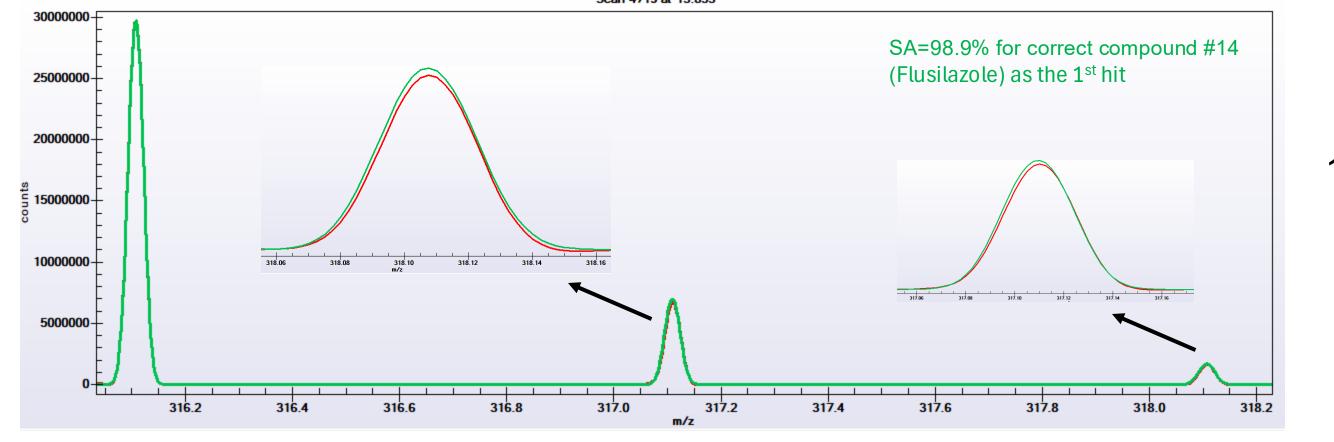
In order to treat these test chemicals as true unknown general organic compounds, a generous elemental composition search conditions were devised to cover m/z up to 500Da, including all reasonably expected elements and using the broadest empirical rules on the possible number of atoms for each element and their ratios (Ref 3), as shown in the table below.

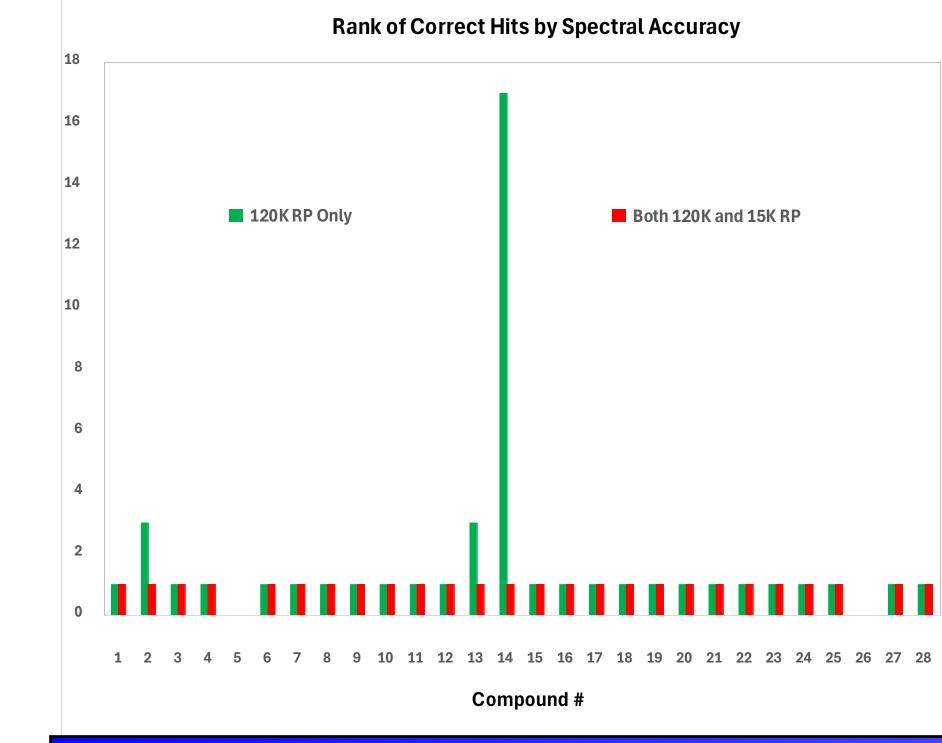


For each compound detected, the most abundant scans from 120K and 15K RP were selected for sCLIPS elemental composition determination. For the 120K scan, its own accurate mass was used whereas for the 15K scan, the accurate mass from the 120K scan was adopted instead to search for all possible elemental compositions, with the list of hits sorted by SA from high to low. The SA for the correct compound, its rank among the total number of hits, and the SA breakout from the 2nd best hit when the correct compound is the top hit are all listed in the summary table on the left. When the correct compound is not the top hit, the SA breakout is calculated as the SA difference between the correct compound and that of the top hit (a negative value). For all compounds, there is a significant increase from 120K to 15K RP scan in SA itself (median 97.4% vs 98.9%) and/or SA breakout (median 0.4% vs 1.6%), resulting in better ranking while increasing identification confidence. It should be noted that 1.0% in SA often means the difference between unique and ambiguous identification.



15K RP Scan





Using sCLIPS and SA for unknown elemental composition at 120K RP, 23 out of the 26 compounds are found as the top SA hits, an impressive feat from a median # of 86 hits.

The most remarkable results are obtained by using both 120K and 15K RP scans, where all 26 compounds are determined as the top SA hit with high confidence due to the better SA and/or larger SA breakout, achieving unique unknown elemental composition on a commercially available MS as is.

Conclusion

This study with 26 small molecule compounds demonstrated that it is feasible to achieve unique elemental composition determination of true unknowns by using both HiRes and LowRes scans in the same data acquisition and taking advantage of the high mass accuracy from HiRes scan and high spectral accuracy from the LowRes scan on an Orbitrap MS system.

References

- 1. Wang SA
- 3. John Erve
- 3. T. Kind

Conflict of Interest (COI) Statement