Comprehensive Extractables Analysis of Medical Grade O-Ring

Dan Ewing,¹ Bill Hurley,² Andrew Feilden,³ Michael Creese,³ Kate Comstock,⁴ and John Schmelzel⁴ ¹Parker Hannifin O-Ring Division, Lexington, KY, USA; ²Darcoid Nor-Cal Seal, Oakland, CA; ³Simthers Rapra, Shrewsbury, UK; ⁴Thermo Fisher Scientific, San Jose, CA, USA



Q Exactive Plus MS HRAM Data Acquisition

The High Resolution Accurate Mass (HRAM) data acquisition on Q Exactive Plus MS using full scan/top3 ms/ms with polarity switching generated high quality data, ensuring the detection of structurally diversified compounds at all levels. Figure 1 shows high mass accuracy for pos/neg switching on the fly and the fine isotope pattern of A2. The Δ mass1.9954 between A0 and A2 indicate one sulfur present.





FIGURE 2. Base Peak Chromatographs of Full Scan WFI Extraction (ESI+)





FIGURE 3. Base Peak Chromatographs of Full Scan IPA Extraction (ESI+)



Data Analysis

SIEVE software for Component Extraction and Database Search

The data was processed using SIEVE 2.2 software for component extraction and differential analysis. The extracted components were filtered using the versatile and customizable filters and then searched against ChemSpider™ database for structure identification

Component Identification and Structure Elucidation

ChemSpider database searching generated multiple structures for each extracted components. HRAM data with 3 ppm threshold setting reduced the possible structures. To determine the correct structure(s), ms/ms fragments library search was carried out using "Mass Frontier" software, a small molecule structure analysis software. The "HighChem Fragmentation Library" in Mass Frontier software 7.0 has extensive published literature references. For each proposed structure, the "Fragments and Mechanisms" feature in Mass Frontier software was used to generate predicted "fragments and mechanisms" through HighChem Fragmentation Library search, see figure 4. A high degree of correlation between predicted and experimental fragments confirms the proposed structure. Mass Frontier software then automatically annotates the matching fragments based on library search results.

Figure 4. Fragment and Mechanism for Structure Elucidation



mzCloud High Resolution Spectral Database Searching

A search was conducted with "mzCloud". Figure 5 A and B show identification using the ms/ms spectrum search feature.



mzCloud[™] is a freely searchable high resolution spectral database at www.mzcloud.org. mzCLoud provides several search criteria for small molecule structure identification using tandem mass spectra, including spectra, fragments, precursor ions, etc, all of which can be very useful for unknown structure elucidation.

FIGURE 5-A. Copy MS/MS Spectrum to mzCloud for Substructure Identification







FIGURE 6. Base Peak Chromatogram of WFI Extraction of Sample A





Dook ID	вт	Managered (M + H)+	Calculated	Elemental	Error
Peak ID	RI	Measured (M+H)*	(IVI+H)+	Composition	(PPM)
1	1.0	127.0733	127.0723	C3H6N6	
2	2.0	133.0763	133.0761	C8H8N2	2.1
3	2.1	133.0763	133.0761	C8H8N2	2.1
4	3.7	179.0639	179.0638	C9H10N2S	0.8
5	3.8	179.0639	179.0638	C9H10N2S	0.8
6	4.9	193.0798	193.0794	C10H12N2S	2
7	5.0	193.0798	193.0794	C10H12N2S	1.9
8	5.1	221.0747	221.0743	C11H12ON2S	1.6
9	5.2	237.1058	237.1056	C12H16ON2S	0.7
10	5.3	251.1214	251.1213	C13H18ON2S	0.6
11	5.5	149.0713	149.0709	C8H8ON2	2.1
12	5.6	165.0484	165.0481	C8H8N2S1	1.9
13	5.7	165.0484	165.0481	C8H8N2S1	1.9
14	6.0	251.1214	251.1213	C13H18ON2S	0.7
15	6.6	251.1218	251.1213	C13H18ON2S	1.5
16	6.7	163.1331	163.1329	C8H18O3	0.97
17	6.9	221.1110	221.1107	C12H16N2S	1.3
18	8.5	235.1267	235.1264	C13H18N2S	1.6
19	10.0	265.1372	265.1369	C14H20ON2S	1.1
20	10.2	265.1372	265.1369	C14H20ON2S	1.2
21	10.7	219.1958	219.1955	C12H26O3	1.5
22	11.3	249.1698	249.1697	C12H24O5	1
23	16.0	233.1751	233.1747	C12H25O4	1.5
24	16.4	277.2011	277.2010	C14H28O5	0.2
25	20.7	261.2064	261.2060	C14H28O4	0.4
26	20.9	305.2324	305.2324	C16H32O5	0.1
27	21.6	325.1433	325.1434	C20H20O4	0.1
28	22.0	325.1438	325.1434	C20H20O4	0.3
29	23.7	399.2511	399.2506	C18H40O7P	1.4



ICPMS Analyses

The samples were prepared by placing the O-rings in 25 ml DI water and 25 ml 2% nitric acid and soaked at RT for 24 hours. The analyses were conducted on Thermo Scientific iCAP Q ICP-MS with He KED (Kinetic Energy Discrimination) interference reduction mode setting. The instrument was standardized at 10 ppb.

To determine if trace and potentially toxic metals were leached from the O-rings, the USP<232> Class1 & 2 elements and additional elements which are commonly analyzed by ICP-MS were determined.

The analyses results for the four types of O-rings showed that they are clean of all Class 1 & 2 elements, see Figure 7 for the ICPMS results for sample 1A and B. The system control software Qtegra provides full 21CFR Part 11 tool set to operate under compliant environments.

FIGURE 7. ICPMS Results for O-Rings Sample A and B (C & D not shown)



Conclusion

This study demonstrated a workflow for rubber O-ring extractable analysis using HRAM data acquisition, data-process software, and database search.

Thermo Scientific™

QICP-MS

The UHPLC/ HRAM full MS/HCD MS² with polarity switching data acquisition on Q Exactive Plus MS, coupled with effective process software and database search using SIEVE, Mass Frontier, and mzCloud, significantly increased the confidence and throughput of routine extractable analysis, particularly for unknown components identification and structure characterization.

WFI and IPA extraction profiles of the four types of medical grade O-rings were quickly established by using this workflow. Data not show for sample B, C, and D.

The ICPMS results show that the four samples have none or very low level trace element present. GCMS analysis was carried out but the data has not been reported.

References

- 1. ISO10993-5 and -10.
- 2. USP <1663>
- 3. PQRI "L/E Recommendations to the FDA"
 - http://www.pqri.org/publications/index.asp

Acknowledgements

The authors would like to thank Parker O-ring and Darcoid Nor-Cal Seal for providing the O-ring samples, Smithers Rapra for the extractions, and Thermo Fisher Scientific for the MS analyses.

www.thermofisher.com

©2016 Thermo Fisher Scientific Inc. All rights reserved.

All trademarks are the property of Thermo Fisher Scientific and its subsidiaries. This information is presented as an example of the capabilities of Thermo Fisher Scientific products. It is not intended to encourage use of these products in any manners that might infringe the intellectual property rights of others. Specifications, terms and pricing are subject to change. Not all products are available in all countries. Please consult your local sales representative for details.

 Africa
 +43 1 333 50 34 0

 Australia
 +61 3 9757 4300

 Austria
 +43 810 282 206

 Belgium
 +32 53 73 42 41

 Canada
 +1 800 530 8447

 China
 800 810 5118 (free call domestic) 400 650 5118

 PARKER-EN 0616S

Japan +81 45 453 9100 Korea +82 2 3420 8600 Latin America +1 561 688 8700 Middle East +43 1 33 50 34 0 Netherlands +31 76 579 55 55 New Zealand +64 9 980 6700 Norway +46 8 556 468 00 Russia/CIS +43 1 333 50 34 0 Singapore +65 6289 1190 Spain +34 914 845 965 Sweden +46 8 556 468 00 Switzerland +41 61 716 77 00 UK +44 1442 233555 USA +1 800 532 4752

