

Retention Index Prediction Combined with *In Silico* Fragmentation Spectra Comparisons for Increasing Confidence in Structural Elucidation using Non-Targeted Gas Chromatography coupled with High Resolution Mass Spectrometry

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"P.A. Guy, E. Dossin, E. Martin, P. Diana, P. Pospisil, M. Bentley"

Philip Morris International R&D

- > Generation of aerosol sample / chemical complexity / GC-HR-MS analysis
- > Building linear retention index (LRI) prediction models
 - RapidMiner Dragon software (RM)
 - □ ACD/ChromGenius software (CG)
 - LRI modeling assessment & usage to characterize aerosol constituents (library database)
- > Non-targeted screening workflow for aerosol characterization
- Case studies
- Conclusion and next steps



PMI Science

• PMI is working on various Reduced Risk Products (RRP) delivering nicotine containing aerosols.



Tobacco Heating System (THS) 2.2

- In this context, it is important to fully characterize the chemical composition of RRP aerosols in comparison to smoke produced from cigarettes.
- For analytical method development purposes we use a reference cigarette (3R4F).



Generation of Smoke Samples from a Reference Cigarette



- Cambridge filter is combined with the impingers Whole smoke
- Addition of retention index chemical markers (n-alkanes) & isotopically labeled internal standards



Unique Compounds & Spectra Database (UCSD)

11,567 molecules are registered in our in-house database:

- □ Over 7,000 chemicals reported as present in tobacco and tobacco smoke¹
- Over 3,000 molecules associated with flavor properties²⁻³







² Leffingwell, J. C. *et al.* Tobacco flavoring for Smoking Products, R. J. Reynolds Tobacco Company, Winston-Salem, NC, **1972**.

³ EFSA flavoring substances database.



Martin, E. et al. 2012. J. Chemoinform., 4, 1, 1-14.

Analytical Technique: GC-High Resolution (GC-HR-MS)

GC-HR-MS_2 (7200B Agilent Q-TOF-MS)

Apolar and polar From LRI of 1,000 to 3,000 (HP-5ms GC column)



GC-HR-MS_1 (7200A Agilent Q-TOF-MS)

Volatile and semi-volatiles From LRI of 500 to 1,900 (DB-624 GC column)



Goal is to screen the broadest range of smoke constituents in a "non-targeted screening" approach.



Building Linear Retention Index Models using QSPR



Accuracy Data for Predicted versus Experimental LRI Values



 \triangle n=23 reference standards (Validation set)

LRI Prediction for the Complete UCSD Compound Library



Non-targeted Screening Workflow for Aerosol Characterization



Case Study 1: Compound Identification with Accurate Mass Library



Easy compound confirmation if reference standard is already present within our Personal Compound Database accurate mass Library (PCDL, n~700)

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Case Study 2: Problematic Hit Proposals



There is a need to develop alternative approaches when compounds are not registered in existing MS libraries



PHILIP MC

Case Study 2: GC-HR-MS in Chemical Ionization Mode & MS/MS

GC-HR-MS (Full Scan MS) Positive Chemical Ionization (PCI)



Determination of elemental formula (adduct ion species)



GC-HR-MS (Full Scan MS/MS) PCI data acquisition CID of 191.1184



MS/MS data processed using a larger chemical database with *in silico* predicted fragmentation software



In Silico Theoretical Fragmentation Software Evaluation: MetFrag



Wolf, S. et al. BMC Bioinformatics 2010, <u>11</u>, 148. http://msbi.ipb-halle.de/MetFrag/

Met Frag

In Silico Theoretical Fragmentation Software Evaluation: Molecular Structure Correlator (MSC)





Hill, A.W. & Mortishire-Smith, R.J. Rapid Commun. Mass Spectrom. 2005, 19, 3111.

Assessment for MetFrag In Silico Fragmentation

Alone	PNG_Image	e Comment	ChemSpider ID	Mass	MetFrag Score	Rank	PNG_Image	LRI_pred CG	LRI_pred RM	LRI_exp	MetFrag & LRI_pred. SCORE	Rank	+
		unspecified stereochem.	1221410 (2z & 2E) 1221411 (2Z form 4603758 (2E form	190.1106	1.0000	1 st		1701.97 ∆LRI=-82.3	1763.39 ∆LRI=-20.9	1'784	0.930	1 st	LRI Prediction
		unspecified stereochem.	2045246	190.1106	1.0000	2 nd		1793.5298 ∆LRI=+9.3	1898.80 ∆LRI=+114.55	1'784	0.920	2 nd	
5 th propo confirm (ref. stand	osal ed dard)		1259330	190.1106	0.9860	3 rd		1811.87 ∆LRI=+27.6	1891.95 ∆LRI=+107.7	1'784	0.916	3 rd	
			1256481	190.1106	0.9860	4 th		1820.33 ∆LRI=+36.1	1893.98 ∆LRI=+109.7	1'784	0.910		1 st proposal confirmed
			3716473	190.1106	0.9840	5 th		1637.96 ∆LRI=-146.3	1702.82 ∆LRI=-81.4	1'784	0.884	5 (r	ef. standard)
			963178	190.1106	0.9840	6 th		1634.80 ∆LRI=-149.5	1699.52 ∆LRI=-84.7	1'784	0.881	di	scriminatory power

Usefulness to combine LRI prediction with MetFrag score



Interpretation of (1-Methyl-3-pyrrolidinyl)(3-pyridinyl)methanone MS/MS Spectrum Using MetFrag Software



MetFrag vs. Molecular Structure Correlator Software

TRUE COMPOUND	(R,S)-1-methyl-3-nicotinoylpyrrolidine		2,3-pentanedione	2-pentanone	3-penten-2-one	
Formula	G	C ₁₁ H ₁₄ N ₂ O	$C_5H_8O_2$	$C_5H_{10}O$	C₅H ₈ O	
RANKING NIST14 nominal classical search	+EI	not registered	Not present in hit list	1 st	Not present in hit list	
RANKING NIST14 with formula constraint		-	2 nd	1 st	Not present in hit list	
# Cpds NIST14		38	50	55	34	

# Cpds ChemSpider	3,651		243	125	120	
# of Fragment ions (above 10%)	g	6	3	4	7	
RANKING MetFrag	CI full scan	5 th ranking	15 th ranking	17 th ranking	12 th ranking	
RANKING MSC	MS/MS	43 th ranking	34 th ranking	6 th ranking	15 th ranking 792	
LRI expt		1'783	738	730		
LRI (RM)	1763 (∆LRI=-20)		842 (∆LRI=+104)	714 (∆LRI=-16)	746 (∆LRI=-46)	
LRI (CG)	1702 (∆LRI=-81)		771 (∆LRI=+33)	732 (∆LRI=+2)	770 (∆LRI=-22)	
RANKING MetFrag & LRI pred.	1 st		7 th	3 rd	4 th	



Conclusions & Next Steps

Advantageous to combine state-of-the-art instrumentation with advanced chemoinformatic tools

- LRI prediction models using both RM & CG software (algorithms) showed great results
- Low differences between the two LRI models enhanced the confidence level for compound identification
- Existing MS libraries are not exhaustive and additional strategies need to be developed
- Targeted MS/MS combined with software to predict in silico fragmentation is mature
 - □ MetFrag software seems to be more reliable than Molecular Structure Correlator
 - Addition of LRI prediction values demonstrated a greater potential to correctly rank putative hits than *in silico* fragmentation alone



Conclusions & Next Steps (continued)

This combined approach significantly reduces the amount of compounds purchased for absolute confirmation

- □ Reducing the overall time for compound identification
- Reducing the cost for purchasing chemicals
- □ Minimizing the rate of false positive compound identification
- Complete automated data-processing has to be developed and validated in order to reduce the workload for Non-Targeted Screening applications
 - Final Ranking SCORE to be calculated on the fly (accurate mass results LRI predictions)
 - Data fusion across volatile semi-volatile & polar apolar methods



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22