

Identification of the chemical shifts of a series of metabolites appearing in the ¹H-NMR spectrum of blood plasma by spiking

Bervoets Liene¹, Louis Evelyne¹, Mesotten Liesbet², Reekmans Gunter³, Thomeer Michiel⁴ and Adriaensens Peter³

¹Faculty of Medicine and Life Sciences, Hasselt University, Diepenbeek, Belgium
²Department of Nuclear Medicine, Ziekenhuis Oost-Limburg (ZOL), Genk, Belgium
³Institute for Materials Research (IMO), Hasselt University, Diepenbeek, Belgium
⁴Department of Pulmonary Medicine, Ziekenhuis Oost-Limburg (ZOL), Genk, Belgium

Background

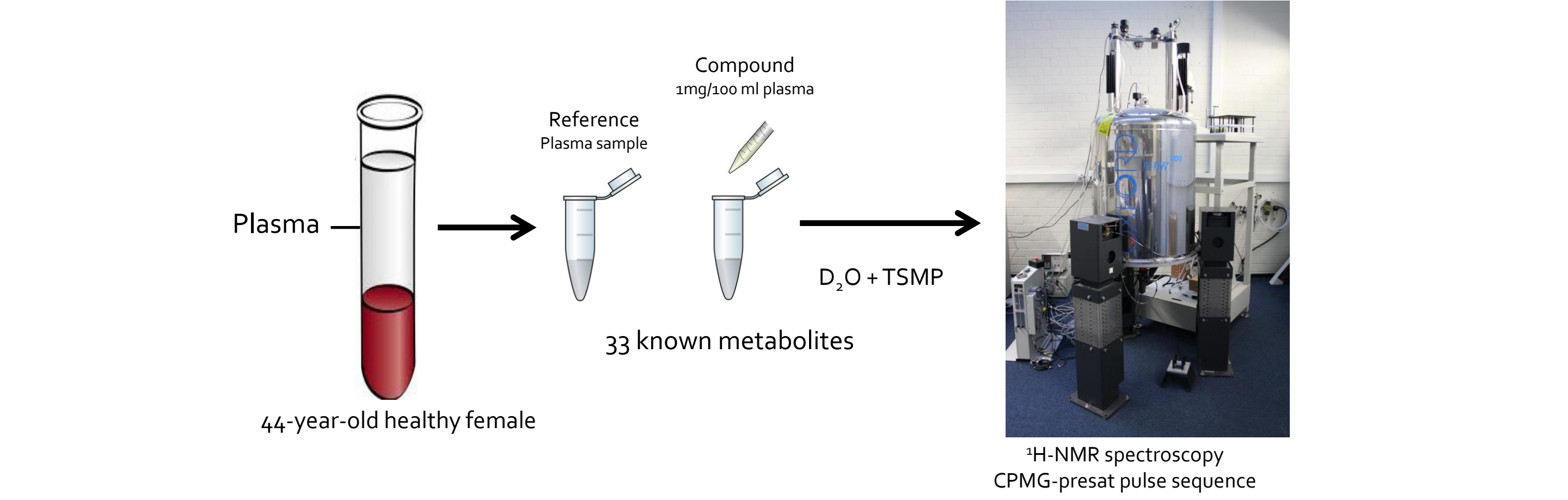
Instead of using reported chemical shift values of metabolites, which differ seriously from study to study due to differences in e.g. biofluid, temperature and pH, the chemical shifts of metabolites could be determined more accurately by spiking the biofluid itself.

Objective

To assign proton chemical shifts and J-coupling constants of known plasma metabolites measured with 400MHz ¹H-NMR spectroscopy and to compare the literature based on settings of integration regions (IR) in the ¹H-NMR spectra of plasma metabolites with those based on spiking experiments towards their power to discriminate between lung cancer patients and controls.

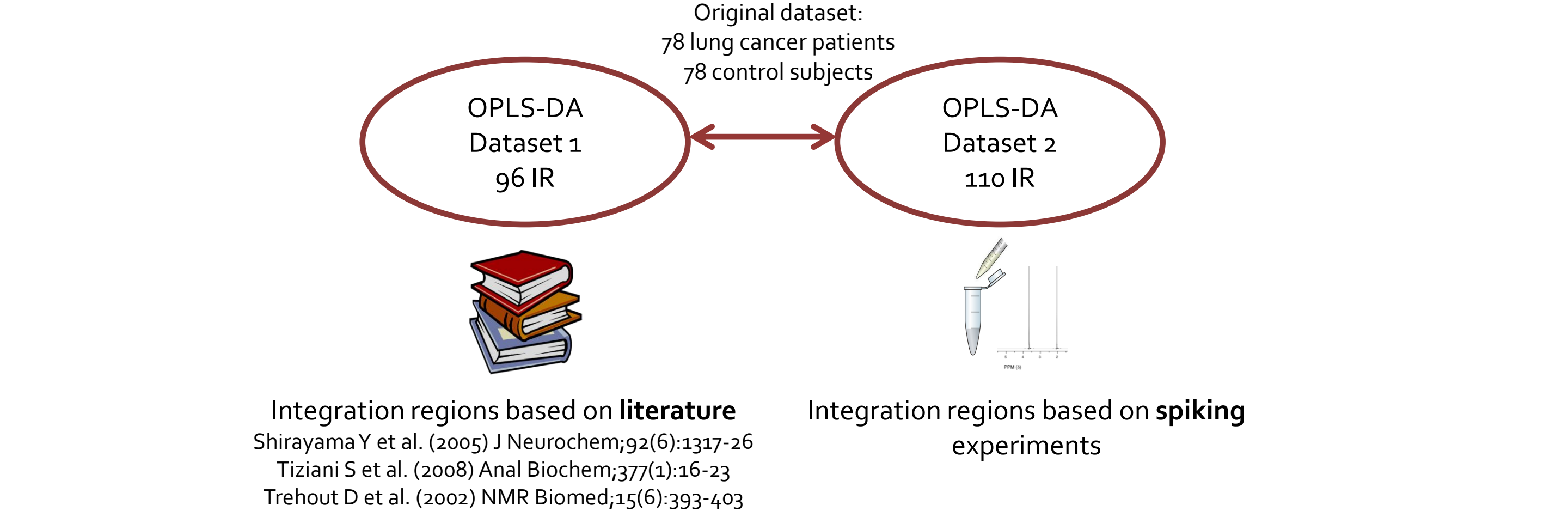
Methods

1. Spiking experiment



2. Multivariate data analysis

At first, the independent samples t-test (IBM SPSS version 20.0, Chicago, IL, USA) was implemented in order to evaluate differences in integration values of all defined IRs between lung cancer patients and control subjects. Additionally, Benjamini-Hochberg procedure was done in order to correct for multiple testing. Second, orthogonal partial least squares discriminant analyses (OPLS-DA) were performed on both datasets using SIMCA-P⁺ (version 12.0, Umetrics, Umea, Sweden).



Results

Chemical shifts and J-coupling constants of the 33 spiked metabolites are presented in Table 1 (see on the right). Figure 1 illustrates the difference of sensitivity and specificity between OPLS-DA of both datasets, i.e. based on literature or spiking experiments.

Figure 1 | OPLS-DA multivariate analysis carried out on 78 lung cancer patients (▲) and 78 controls (■): (A) based on 96 IR determined by literature chemical shift information and (B) based on 110 IR determined by spiking experiments

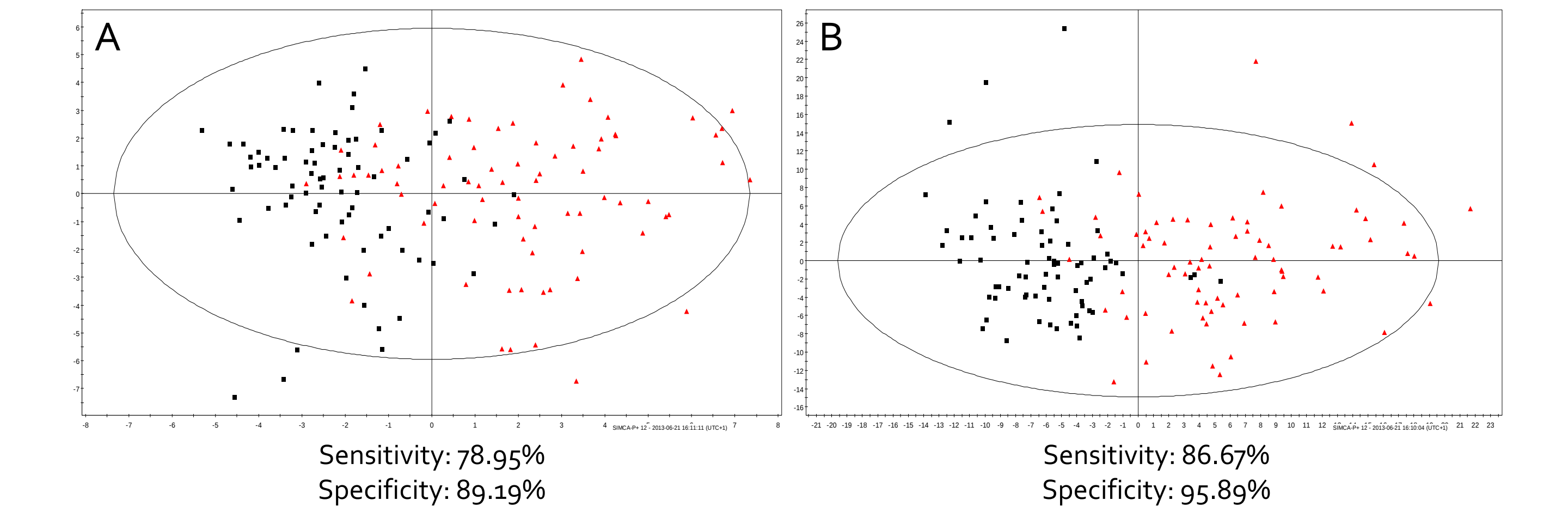


Table 1 | Proton chemical shifts (δ in ppm) and coupling constants (J in Hz) for low-molecular-weight plasma metabolites. Chemical shifts are reported with reference to TSMP singlet resonance at 0.015 ppm and multiplicity definitions are: s, singlet; d, doublet; dd: double doublet; t, triplet; dt, double triplet; q, quartet; p, pentaplet; o, octaplet; m, multiplet. Assignments of the molecular groups follow the IUPAC-IUB nomenclature. br: broad peak area, difficult J-coupling assignment. The multiplicity given here was observed in conventional 1D-spectra recorded at 400 MHz (Varian Inova spectrometer).

Compound	Group	δ (ppm) in plasma	Multiplicity	J (Hz)	Connectivity	Compound	Group	δ (ppm) in plasma	Multiplicity	J (Hz)	Connectivity	
Amino acid metabolism												
Histidine (His)	^oCH	4,012	dd	8	α - β	Tyrosine (Tyr)	^oCH	3,954	dd	5	α - β	
	$^\beta\text{CH}_2$	3,150	dd	4,9	α - β'		$^\beta\text{CH}_2$	3,230	dd	7,6	α - β'	
		3,260	dd	15,5	β - β'			3,075	dd	14,2	β - β'	
	$^\gamma\text{CH}$	7,802	s	none			$^\gamma\text{CH}$	6,924	d	8,5	γ - γ'	
Arginine (Arg)	^oCH	7,086	s	none		Asparagine (Asn)				8,4	δ' - γ'	
	^oCH	3,690	t	6,1	α - β		^oCH	7,222	d	8,5	δ - δ'	
	$^\beta\text{CH}_2$	1,700	m	br	β - β'		$^\beta\text{CH}_2$	3,999	q	7,8	α - β	
	$^\gamma\text{CH}_2$	1,875	m	br	β - γ			2,962	dd	4,3	α - β'	
Methionine (Met)			br	β - γ'			2,845	dd	16,7	β - β'		
	$^o\text{CH}_2$	3,266	t	6,9	δ - γ	Threonine (Thr)	^oCH	3,596	d	4,9	α - β	
	^oCH	3,885	dd	5,4	α - β		^oCH	4,276	o	6,6	β - γ	
				1,5	α - β'		$^\gamma\text{CH}_2$	1,358	d			
$^\beta\text{CH}_2$	2,230	m	br	β - β'	Aspartate (Asp)		^oCH	3,930	dd	3,7	α - β	
$^\gamma\text{CH}_2$	2,673	t	7,6	β - γ , β - γ'		$^\beta\text{CH}_2$	2,850	dd	8,9	α - β'		
$^\delta\text{CH}_2$	2,167	s	none				2,702	dd	17,5	β - β'		
Glutamine (Gln)	^oCH	3,786	t	6,2		α - β	Glutamate (Glu)	^oCH	3,788	dd	7,1	α - β
	$^\beta\text{CH}_2$	2,160	m	5,9	α - β'	$^\beta\text{CH}_2$		2,162	m	4,9	α - β'	
				14,5	β - β'				14,7	β - β'		
	$^\gamma\text{CH}_2$	2,480	m	6,3	β - γ	$^\gamma\text{CH}_2$		2,388	m	8,41	β - γ'	
			9,2	β - γ'				6,88	β - γ'			
			9,2	β - γ'				6,4	β - γ			
			6,4	β - γ'				8,4	β - γ			
			15,3	γ - γ'				15,9	γ - γ'			
Lysine (Lys)	^oCH	3,760	t	6,0	α - β	Creatine	$^o\text{CH}_2$	3,068	s	none		
	$^\beta\text{CH}_2$	1,900	m	br	β - β'			3,962	s	none		
	$^\gamma\text{CH}_2$	1,500	m	br	β - γ , β - γ'		Creatinine	$^o\text{CH}_3$	3,075	s	none	
	$^\delta\text{CH}_2$	1,751	p	7,5	γ - δ			$^\beta\text{CH}_2$	4,087	s	none	
$^\epsilon\text{CH}_2$	3,030	t	7,5	δ - ϵ								
Glycine (Gly)	$^o\text{CH}_2$	3,586	s	none	Glucose metabolism							
	Isoleucine (Ile)	^oCH	3,968	d	4,0	α - β	Glucose					
$^\beta\text{CH}$		2,020	m	br	β - δ	α -anomer	^oCH	5,216	d	3,8	α - β	
$^\gamma\text{CH}_2$		1,040	d	7,0	β - γ		$^\beta\text{CH}$	3,519	dd	9,6	β - γ	
$^\delta\text{CH}_2$		1,504	p	7,4	γ - δ		$^\gamma\text{CH}$	3,698	t	9,4	γ - δ	
$^\epsilon\text{CH}_2$	0,970	t	7,4	δ - ϵ	$^\delta\text{CH}$		3,395	t	9,9	δ - ϵ		
Leucine (Leu)	^oCH	3,769	dd	7,0	α - β	β -anomer	$^\epsilon\text{CH}$	3,822	m	1,5	ϵ - ζ	
				1,5	α - β'		$^\zeta\text{CH}$	3,826	dd	6	ϵ - ζ'	
	$^\beta\text{CH}_2$	1,742	m	br	β - γ		$^\delta\text{CH}$	3,749	dd	12,1	ζ - ζ'	
	$^\gamma\text{CH}$	1,742	m	br	β - γ		^oCH	4,630	d	8	α - β	
Alanine (Ala)	$^\delta\text{CH}$	1,003	d	4,7	γ - δ	β -anomer	$^\beta\text{CH}$	3,230	dd	9,1	β - γ	
		0,987	d	4,7	γ - δ'		$^\gamma\text{CH}$	3,473	t	9,4	γ - δ	
	^oCH	3,790	q	7,2	α - β		$^\delta\text{CH}$	3,387	t	8,9	δ - ϵ	
	$^\beta\text{CH}_3$	1,509	d	14,3	β - β' , β''		$^\epsilon\text{CH}$	3,450	m	1,6	ϵ - ζ	
			14,3	β - β''	Inositol	$^\zeta\text{CH}$	3,882	dd	5,4	ϵ - ζ'		
Serine (Ser)	^oCH	3,845	dd	5,3		α - β	$^\gamma\text{CH}$	3,707	dd	12,3	ζ - ζ'	
	$^\beta\text{CH}_2$	3,982	dd	4,1		α - β'	^oCH	3,563	dd	2,9	α - β	
		4,002	dd	12,2		β - β'	$^\beta\text{CH}$	4,097	t	10	α - ζ	
	Proline (Pro)	^oCH	4,162	dd	6,3	α - β	$^\gamma\text{CH}$	3,563	dd	2,9	β - γ	
				8,9	α - β'	$^\delta\text{CH}$	3,655	t	9,8	γ - δ		
$^\beta\text{CH}_2$		2,382	m	br	β - β'	$^\epsilon\text{CH}$	3,306	t	9,3	δ - ϵ		
$^\gamma\text{CH}_2$		2,060	m	14,0	γ - β	$^\zeta\text{CH}$	3,655	t	9,3	ϵ - ζ		
			7,0	γ' - β , γ - β' , γ - β''	Glycolyse							
Phenylalanine (Phe)	$^\delta\text{CH}_2$	3,365	dt	14,1	δ - γ	Lactate	^oCH	4,138	q	6,9	α - β	
		3,444	dt	7,0	δ' - γ , δ - γ' , δ' - γ'		$^\beta\text{CH}_2$	1,354	d			
				7,0	δ - δ'		$^o\text{CH}_3$	2,402	s	none		
	Cysteine (Cys)	^oCH	3,955	dd	5,2	α - β	Krebs Cycle					
$^\beta\text{CH}_2$		3,310	dd	7,7	α - β'	Citrate	$^{\alpha\beta}\text{CH}_2$	2,642	q	15,7	α - β	
		3,140	dd	14,4	β - β'				60,2	α - α' , β - β'		
$^\gamma\text{CH}$		7,351	d	7,2	γ - δ		α -ketoglutarate	$^o\text{CH}_2$	3,040	t	6,9	α - β
$^\delta\text{CH}$	7,454	t	7,2	δ - ϵ	$^\beta\text{CH}_2$	2,470		t				
$^\epsilon\text{CH}$	7,397	t			Succinate	$^o\text{CH}_2$		2,439	s	none		
Valine (Val)	^oCH	3,973	dd	5,7		α - β	$^\beta\text{CH}_2$	2,439	s	none		
	$^\beta\text{CH}_2$	3,112	dd	4,3	α - β'	Malate	^oCH	4,300	dd	10,2	α - β	
		3,052	dd	14,7	β - β'		$^\beta\text{CH}_2$	2,700	dd	3	α - β'	
	^oCH	3,635	d	4,3	α - β			2,400	dd	15,4	β - β'	
Tryptophan (Trp)	$^\beta\text{CH}$	2,305	o	7,1	β - γ	Lipid metabolism						
	$^\gamma\text{CH}_2$	1,074	d	7,1	β - γ'	Acetate	CH ₃	1,948	s	none		
	$^\delta\text{CH}_3$	1,021	d				CH ₃	2,319	s	none		
	^oCH	4,085	dd	5,2	α - β		β -hydroxybutyrate	^oCH	2,400	dd	7,3	α - β
$^\beta\text{CH}_2$	3,340	dd	8,1	α - β'	$^\beta\text{CH}_2$			2,300	dd	14,4	β - β'	
			15,3	β - β'	$^\gamma\text{CH}_2$			1,200	d	6,3	β - γ	
$^\gamma\text{CH}$	7,351	s	none									
	^oCH	7,770	d	7,8	δ - ϵ							
	$^\epsilon\text{CH}$	7,229	t	7,8	ϵ - ζ							
	$^\zeta\text{CH}$	7,310	t	7,8	ζ - η							
	^oCH	7,570	d									

Conclusion

Instead of relying on chemical shifts of metabolites derived from literature, spiking experiments seem to be a better approach in order to more accurately assign the chemical shifts of plasma metabolites in a ¹H-NMR spectrum. Consequently, it could lead to an enhancement of the discriminative power of the cluster analysis and a better understanding and/or explanation of the clinical relevance of study findings.

Acknowledgements

This study is part of the Limburg Clinical Research Program (LCRP) UHasselt-ZOL-Jessa, supported by the foundation Limburg Sterk Merk, Hasselt University, Ziekenhuis Oost-Limburg and Jessa Hospital.