

Metabolites as Biomarkers of Adverse Reactions Following Vaccination: A Pilot Study using Nuclear Magnetic Resonance Metabolomics



Bruce McClenathan, MD
Y. Sammy Choi, MD
Christina Spooner, MS

NMR and Multivariate Analysis

Delisha Stewart, PhD
Wimal Pathmasiri, PhD
Susan Sumner, PhD



“Medically Ready Force...Ready Medical Force”

Disclaimer



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Adverse Events Following Immunizations (AEFI)



- An Adverse Event Following Immunization (AEFI) is an adverse reaction to a vaccination that goes above and beyond the usual side effects that are known to be associated with vaccinations.
 - Vary in clinical severity from very mild to incapacitating
 - Rarely, an aberrant immune reaction from vaccination results in a potentially serious adverse event
 - A serious adverse event related to the smallpox vaccine is myocarditis and/or pericarditis (myopericarditis).

Metabolomics

- Metabolomics is the study of the small-molecule metabolite profile of a biological organism.
 - Functional view of the organism as determined by the sum total of DNA, RNA, proteins and environmental factors
 - More accurate picture of the actual phenotype of the organism
- Metabolomics may help identify a particular metabolic signature or “metabotype” in patients who are predisposed to developing AEFI such as a severe systemic reaction or myocarditis, that currently is difficult or impossible to identify prior to the development of the AEFI.

Study Goals



■ Exploratory Study Goals

- Use metabolomics to help determine if metabotypes of baseline samples could be used to predict AEFI
- Reveal potential biomarkers of AEFI by comparing case and control samples

Study Impact



- The ability to predict who may experience an adverse event following immunization (AEFI) based on metabolic profiles could significantly impact immunization health outcomes and help lead the way to personalized immunization healthcare.

Study Design

- Pre- and post-vaccine samples from 100 subjects were processed for metabolomics analysis across the following vaccine response groups:
 - **Group 1** : 5 subjects had an AEFI and developed clinically diagnosed myocarditis (**+MyoC**)
 - **Group 2** : 30 subjects had evidence of elevated troponins, but without symptoms following immunization (**+Trop - Sx**)
 - **Group 3** : 31 subjects had systemic symptoms following immunization (**SSFI**)
 - **Group 4** : 34 subjects had no symptoms and served as AEFI controls (**no AEFI**)

Methods- Sample Preparation



- 200 frozen serum samples were prepared for metabolomics analysis.
- 22 Quality Control (QC) samples were also generated from smaller aliquots of the source material.
- Methanol (60%) was added to each of the 200 experimental and 22 QC samples for extraction.
- Samples were vortexed, centrifuged and supernatants were transferred to new tubes and lyophilized to dryness.
- Samples were reconstituted in phosphate-buffered D₂O master mix, vortexed and centrifuged.
- A 600 μL aliquot of the supernatants was transferred into NMR tubes for data acquisition on a 700 MHz spectrometer.

Data Acquisition and Analysis



- ^1H NMR spectra of individual and pooled samples were acquired on a Bruker Avance 700 MHz NMR spectrometer using standard data acquisition and processing methods.
- NMR spectra were processed using intelligent binning. The binned data and associated metadata were transferred to Umetrics SIMCA-P-14.1 for multivariate analysis by Principal Components Analysis (PCA) and Orthogonal Partial Least Squares-Discriminant Analysis (OPLS-DA).
- The bins important to the differentiation of phenotypes were determined through inspection of Variable Influence on Projection (VIP) plots (SIMCA), statistical tests, and fold changes (SAS).
- Bins that were found to be important for group separation ($\text{VIP} \geq 1$, $p\text{-value} < 0.10$ and fold change ≥ 2) were library-matched to metabolites using Chenomx NMR Suite 8.1 Professional.

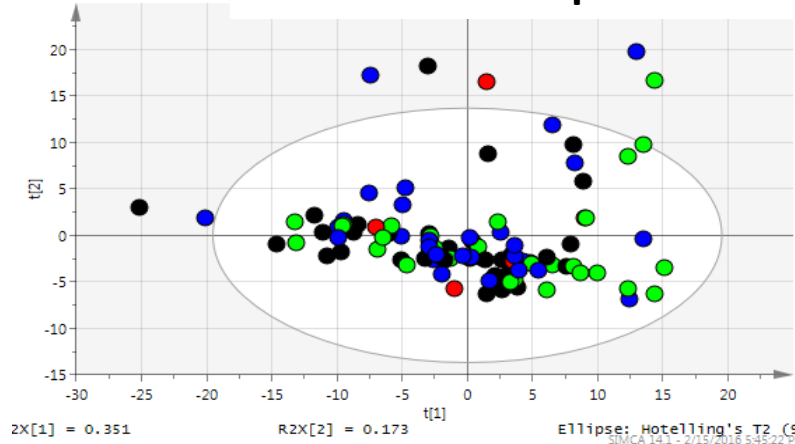
Subject Characteristics

Characteristic	+MyoC (n= 5)	+Trop – Sx (n= 30)	SSFI (n= 31)	no AEFI (n= 34)
Age, years (Mean, SD)	26.6 (6.9)	21.7 (3.3)	24.4 (7.4)	23.2 (6.5)
Male	4 (80%)	29 (96.7%)	27 (87.1%)	30 (88.24%)
Race				
White	5 (100%)	21 (70%)	23 (74.2%)	23 (67.7%)
Black	0	1 (3.3%)	3 (9.7%)	5 (14.7%)
Hispanic	0	3 (10%)	4 (12.9%)	2 (5.9%)
Asian	0	3 (10%)	0	2 (5.9%)
Other	0	2 (6.7%)	1 (3.2%)	2 (5.9%)
Non-Smoker*	2 (40%)	22 (73.3%)	13 (41.9%)	21 (61.8%)
Excellent Health (pre-vaccine)	3 (60%)	23 (76.7%)	16 (51.6%)	28 (82.4%)
Family History of CAD	1 (20%)	2 (6.9%)	2 (6.5%)	6 (17.7%)

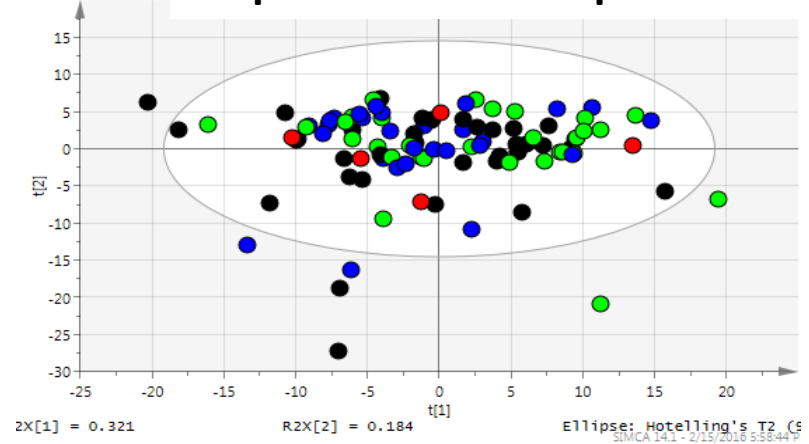
*never smoker, former (>1 year)

How do baseline or post-vaccine only samples separate across the 4 Groups?

All baseline samples



All post-vaccine samples

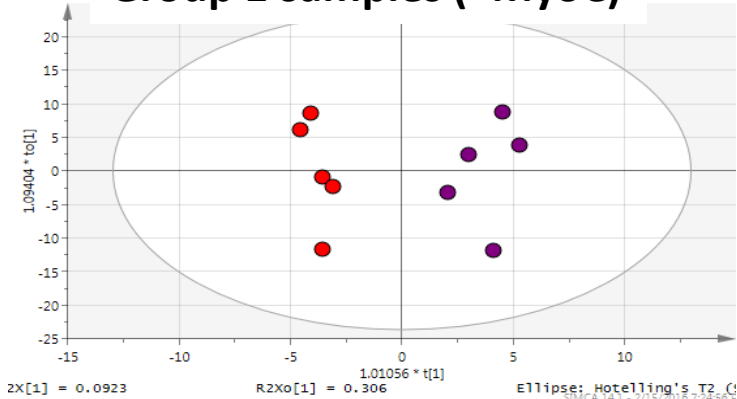


- Group 1 (+MyoC)
- Group 2 (+Trop - Sx)
- Group 3 (SSFI)
- Group 4 (no AEFI)

In PCA there were no clear patterns of separation based on Group categorization.

How do samples from subjects that developed MyoC compare at baseline versus post-vaccination?

Group 1 samples (+MyoC)



● **Baseline**
● **Post-vaccine**

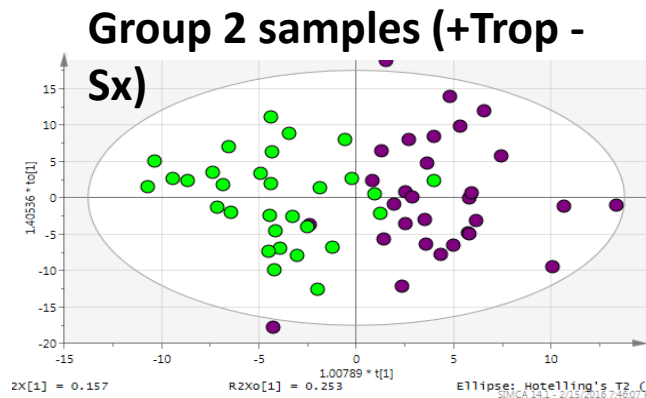
Significant metabolites identified by group-differentiating bins

Metabolite names	VIP	p-value*	Fold Change**
2-oxoisocaproate	0.5	0.063	1.1
3-Methyl-2-oxovalerate	0.6	0.063	-1.1
Acetate Lysine Arginine	1.8	0.063	-1.1
Creatine Creatine Phosphate Tyrosine	1.3	1	-1.3
Creatinine Creatine Creatine phosphate Lysine	2.7	0.063	-1.3
Fructose Histidine Phenylalanine Serine	1.4	1	-1.2
Glucose (5 bins)	1.3 - 2.5	0.063 - 0.625	-1 - 1
Glucose Unsaturated lipids	1.2	0.813	1.1
Lactate	1.5	0.625	-1.2
Leucine (2 bins)	1 - 2.1	0.063	-1.1 - -1.1
Lipids (2 bins)	0.7 - 0.9	0.063	-1.1 - -1.1
Lysine Arginine	0.8	0.063	-1.1
Overlap (4 bins)	0.6 - 1.5	0.063 - 1	1.3 - 7.8
Proline	1	0.063	-1.1
Propylene glycol	1.6	0.063	-1.4
Taurine Betaine Glucose TMAO	2	0.813	-1
Unknown	0.9	0.625	-5.6
VLDL LDL HDL Isocaproate	1.4	0.438	1.1

*Wilcoxon Signed Rank Test

**A positive fold change indicates median of Post-vaccine > median of Baseline

How do samples from subjects that had elevated troponins compare at baseline versus post-vaccination?



● Baseline
● Post-vaccine

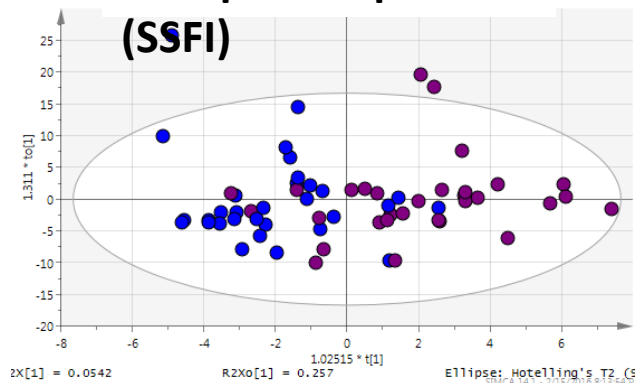
Metabolite	VIP	p-value*	Fold Change**
2-Aminobutyrate (2 bins)	0.4 - 0.5	0.003 - 0.02	-1.1 - -1.1
2-oxoisocaproate	0.4	0.034	-1.1
3-Hydroxybutyrate VLDL LDL	2.1	0.451	-1.1
3-Methyl-2-oxovalerate	0.6	0.006	-1.1
Acetate Lysine Arginine	0.9	0.017	-1.1
Alanine	2.8	<.001	-1.2
Arabinose	0.1	0.282	2.4
Asparagine (3 bins)	0.4 - 0.9	0.005 - 0.027	-1.2 - -1.1
Asparagine N,N-Dimethylglycine	0.6	0.013	-1.1
Choline O-Phosphocholine sn-Glycero-3-phosphocholine	1.8	0.008	-1.1
Citrate (2 bins)	0.7 - 0.9	<.001 - 0.002	-1.2 - -1.1
Citrate Glutamine	0.5	0.095	-1.1
Creatine Creatine Phosphate Tyrosine	1.1	0.476	-1.1
Creatinine Creatine Creatine phosphate Lysine	1.3	0.006	-1.1
Fructose Histidine Phenylalanine Serine	1.3	0.315	-1.1
Glucose (8 bins)	1.6 - 3.9	<.001 - 0.017	1 - 1.2
Glucose Glycerol	2	0.001	1.1
Glucose Unsaturated lipids	2	<.001	1.1
Glutamate Proline	0.8	0.001	-1.1
Glutamine (3 bins)	0.8 - 1.6	<.001 - 0.051	-1.1 - -1.1
Isoleucine 3-Methyl-2-isovalerate	0.6	0.012	-1.1
Isoleucine Leucine	1.3	0.629	-1
Isoleucine Valine	1.1	0.372	-1
Lactate	2.3	0.025	-1.2
Lactate Threonine	4.7	0.014	-1.2
Leucine (2 bins)	0.4 - 1	0.068 - 0.125	-1.1 - -1.1
Lipids (3 bins)	0.5 - 1.1	<.001 - 0.002	-1.2 - -1.1
Lysine (2 bins)	0.5 - 0.5	0.02 - 0.069	-1.1 - -1.1
Lysine Arginine	0.6	0.002	-1.1
Methionine Citrate	0.6	<.001	-1.2
Overlap (9 bins)	0.2 - 1.3	0.004 - 0.476	-1.2 - 3.3
Proline (2 bins)	0.7 - 1.3	<.001 - 0.006	-1.1 - -1.1
Propylene glycol	0.9	0.003	-1.2
Taurine Betaine Glucose TMAO	1.9	0.507	1
Trimethylamine	0.4	0.033	-1.1
Unknown (2 bins)	0.3 - 0.6	0.001 - 0.103	-1.1 - 4.8
Unsaturated lipids	1	0.212	-1.1
VLDL LDL	1.3	0.934	1
VLDL LDL HDL Isocaproate	1.4	0.11	-1.1
sn-Glycero-3-phosphocholine	0.9	0.094	-1.3

*Paired t-test

**A positive fold change indicates mean of Post-vaccine > mean of Baseline

How do SSFI subjects baseline & post-vaccination samples compare?

Group 3 samples (SSFI)



● Baseline
● Post-vaccine

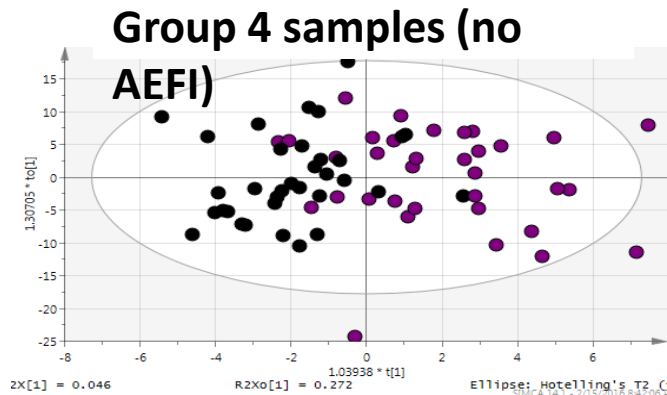
Significant metabolites identified by group-differentiating bins

Metabolite	VIP	p-value*	Fold Change**
3-Hydroxybutyrate VLDL LDL	2.3	0.916	-1
Alanine	1.8	0.009	-1.1
Arabinose	0.5	0.003	10.7
Asparagine N,N-Dimethylglycine	0.7	0.069	-1.1
Choline O-Phosphocholine sn-Glycero-3-phosphocholine	1.6	0.13	-1.1
Creatine Creatine Phosphate Tyrosine	2.2	0.082	1.2
Creatinine Creatine Creatine phosphate Lysine	1.5	0.11	-1.1
Fructose Histidine Phenylalanine Serine	1.7	0.208	1.1
Glucose (8 bins)	1.6 - 2.6	0.014 - 0.762	1 - 1
Glucose Glycerol	2.3	0.058	1
Glucose Unsaturated lipids	1.2	0.576	-1
Glycerol Isoleucine	2.3	0.004	1.1
Histidine	1.2	0.178	-1.1
Lactate	2.1	0.294	-1.1
Lactate Threonine	6.1	0.02	-1.1
Methionine Citrate	0.6	0.006	-1.1
N-Acetylamino acids Proline	2.4	0.018	1.1
Overlap (10 bins)	0.6 - 1.7	0.003 - 0.178	-1.2 - 4
Oxypurinol	0.3	0.205	-2.1
Proline	1	0.007	1.1
Taurine Betaine Glucose TMAO	2.5	0.147	-1
Threonine (2 bins)	1.1 - 1.2	0.065 - 0.121	1.1 - 1.2
Unknown	0.1	0.221	-2
Unsaturated lipids	1.1	0.754	1
VLDL LDL	1.5	0.605	-1
VLDL LDL HDL Isocaproate	1.3	0.814	1
Valine	1.3	0.009	1.1
sn-Glycero-3-phosphocholine	1.1	0.125	1.3

*Paired t-test

**A positive fold change indicates mean of Post-vaccine > mean of Baseline

How do No AEFI subjects baseline & post-vaccination samples compare?



Significant metabolites identified by group-differentiating bins

Metabolite	VIP	p-value*	Fold Change**
3-Hydroxybutyrate VLDL LDL	1.8	0.754	-1
3-Hydroxyisobutyrate Valine Isobutyrate	1.2	0.063	1.1
Acetate Lysine Arginine	3.1	0.006	1.2
Choline O-Phosphocholine sn-Glycero-3-phosphocholine	1.2	0.758	-1
Creatine Creatine Phosphate Tyrosine	1.2	0.91	-1
Formate	0.4	0.209	2.4
Glucose (4 bins)	1.3 - 2.1	0.589 - 0.993	1 - 1
Glucose Glycerol	1.5	0.624	1
Glucose Unsaturated lipids	1.3	0.847	1
Glutamate Proline	0.7	0.055	1
Glycerol Isoleucine	2.3	0.041	1.1
Isoleucine Leucine	2.4	0.006	1.1
Isoleucine Valine	1.7	0.035	1.1
Lactate	3.4	0.031	-1.2
Lactate Threonine	6.4	0.05	-1.1
Leucine (2 bins)	0.9 - 2	0.008 - 0.042	1.1 - 1.1
Methionine Citrate	0.5	0.082	-1.1
N-Acetylamino acids Proline	2.5	0.065	1.1
Overlap (2 bins)	0.6 - 1	0.098 - 0.269	-1.2 - 1.1
Oxypurinol	0.5	0.357	2.3
Phenylalanine	0.6	0.061	1.1
Proline	0.9	0.068	1.1
Taurine Betaine Glucose TMAO	1.8	0.665	1
Threonine	1	0.436	-1.1
Unknown	0.2	0.471	-2.7
VLDL LDL HDL Isocaproate	1.1	0.941	-1
Valine	1	0.234	1.1
sn-Glycero-3-phosphocholine	1	0.183	-1.2

*Paired t-test

**A positive fold change indicates mean of Post-vaccine > mean of Baseline

Metabolites common and unique between Group 1 (+MyoC) and Group 2 (+Trop-Sx).



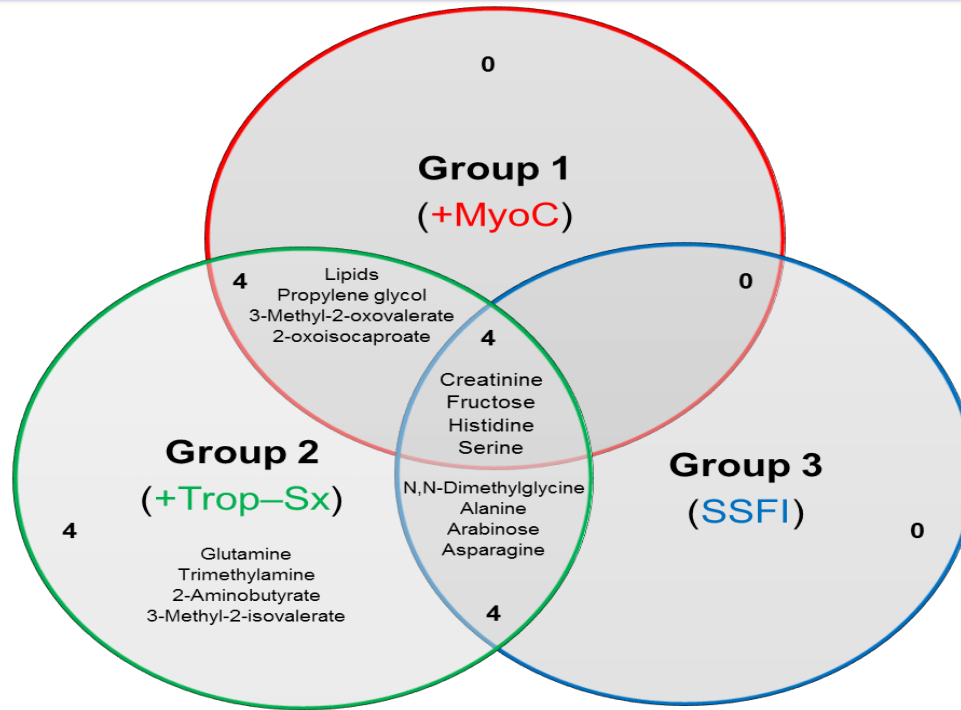
Common Library-matched Metabolites

2-oxoisocaproate	3-Methyl-2-oxovalerate
Acetate	Arginine
Betaine	Creatine
Creatine Phosphate	Creatinine
Fructose	Glucose
HDL	Histidine
Isocaproate	Lactate
LDL	Leucine
Lipids	Lysine
Phenylalanine	Proline
Propylene glycol	Serine
Taurine	TMAO
Tyrosine	Unsaturated lipids
VLDL	

Unique Group 2 Metabolites

2-Aminobutyrate	3-Hydroxybutyrate
Alanine	Arabinose
Asparagine	Choline
Citrate	Glutamate
Glutamine	Glycerol
Isoleucine	Methionine
N,N-Dimethylglycine	Threonine
Trimethylamine	Valine
O-Phosphocholinesn-Glycero-3phosphocholine	
3-Methyl-2-isovalerate	

Venn diagram of common and unique metabolites for all AEFI Groups



Summary

- We describe for the first time metabolic profiling of pre- and post-vaccination to include subjects with known AEFI
- We did not identify any unique metabolic signatures pre-vaccination that was able to predict which individuals developed an AEFI
- Broad spectrum metabolomics differentiated pre- and post-vaccination samples for those individuals with serious AEFIs
- A few metabolites unique to the three clinical groups with AEFI. (creatinine, fructose, histidine and serine)

Current Conclusions



- Individuals may have differential responses to smallpox vaccination that can be detected by metabolic profiling.
- Baseline and post-vaccination metabolic profiles from subjects who experienced AEFI with subclinical (elevated troponins) or clinically verified myocarditis were more clearly differentiated in the multivariate analysis compared to subjects who experienced no AEFI or only systemic symptoms (SSFI).
- Additional metabolomics analysis in the field of vaccinology is warranted.

Contributions



DHA-IHB Personnel:

Mrs. Nora Rachels

Mrs. Gervon Collins

Mrs. Christina Spooner

Dr. Limone Collins

Dr. Renata Engler



Womack Army Medical
Center Personnel:

Dr. Y. Sammy Choi



NIH Eastern Regional Comprehensive
Metabolomics Resource Core (RCMRC)
at RTI International contributors:

Delisha Stewart, PhD

Andrew Novokhatny, MS

Wimal Pathmasiri, PhD

Jason Burgess, PhD

Susan McRitchie, MS

Susan Sumner, PhD

Questions

