## Personalized Nutrient Interventions in the era of Precision Medicine

David H. Haase, MD, CNS, IFM-CP

doc@maxwellclinic.com

# Acknowledgements:

- Jeff Bland, PhD
- Helen Messier, PhD, MD
- Sidney Baker, MD
- David Hagedorn, PhD
- David Cantor, PhD
- Lee Hood, MD, PhD
- Andy Braley PhD
- Richard Lord, PhD

- Stephen Hines, MD
- David Agerter, MD
- Terry Dermody, MD
- Mark Percival, ND, DC
- Gregory Kelly, ND
- Rex Cannon, PhD
- Kara Fitzgerald, ND
- Todd Lepine, MD

## Faculty Disclosure

Commercial Interest	Nature of Relevant Financial Relationship (Include all those that apply)	
	What was received	For what role
• Xymogen	Honoraria/ Shares	Consultant
BioCeuticals	Honoraria	Consultant

After participating in this presentation, learners should be better able to:

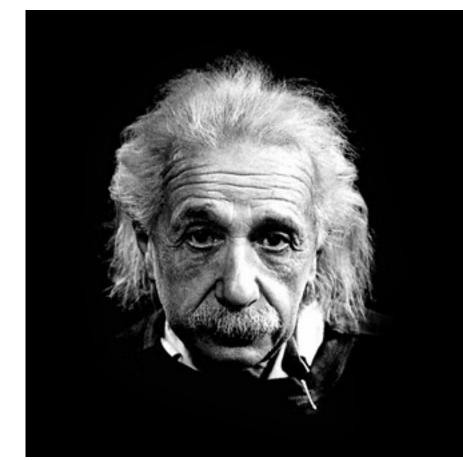
- Use precision medicine to provide insight in assessing toxicity and nutrient insufficiency
- Use data to identify mechanisms of toxic burden
- Employ nutrient interventions to reduce risk of toxicity.

After participating in this presentation, clinicians should be better able to:

 Recognize that while precision medicine as applied to nutrition has strengths, it also has some pitfalls and that as our knowledge evolves over the next years, so will its application in practice. Pheno from Greek 'phaino' = shining and Greek 'phainein' = to show

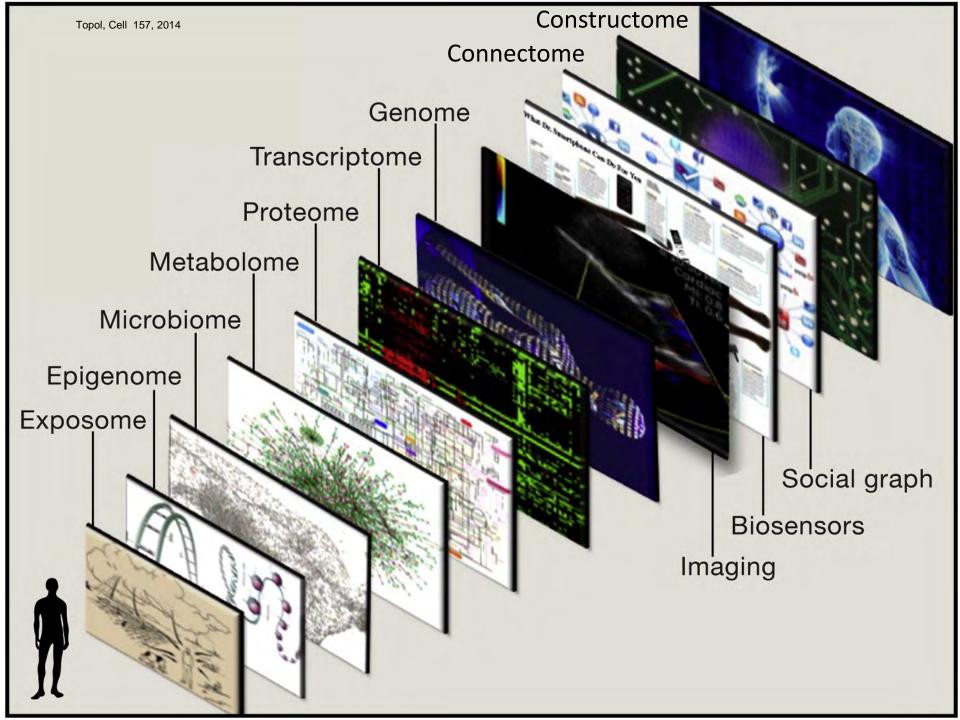
> Phenotype = How we each show up and shine

## Creating Health...



"Make everything as simple as possible, but not simpler." – Albert Einstein

That we may live as our Highest Potential Phenotype



I think that I shall never see A poem lovely as a tree.

A tree whose hungry mouth is prest Against the earth's sweet flowing breast;

A tree that looks at God all day, And lifts her leafy arms to pray;

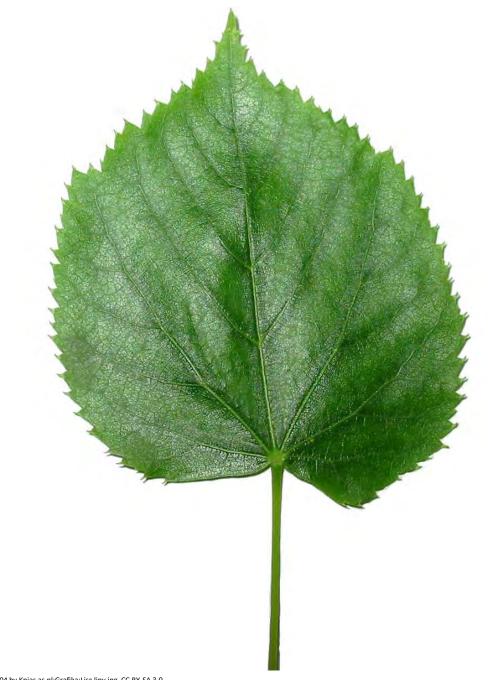
A tree that may in Summer wear A nest of robins in her hair;

Upon whose bosom snow has lain; Who intimately lives with rain.

Poems are made by fools like me, But only God can make a tree.

-Joyce Kilmer







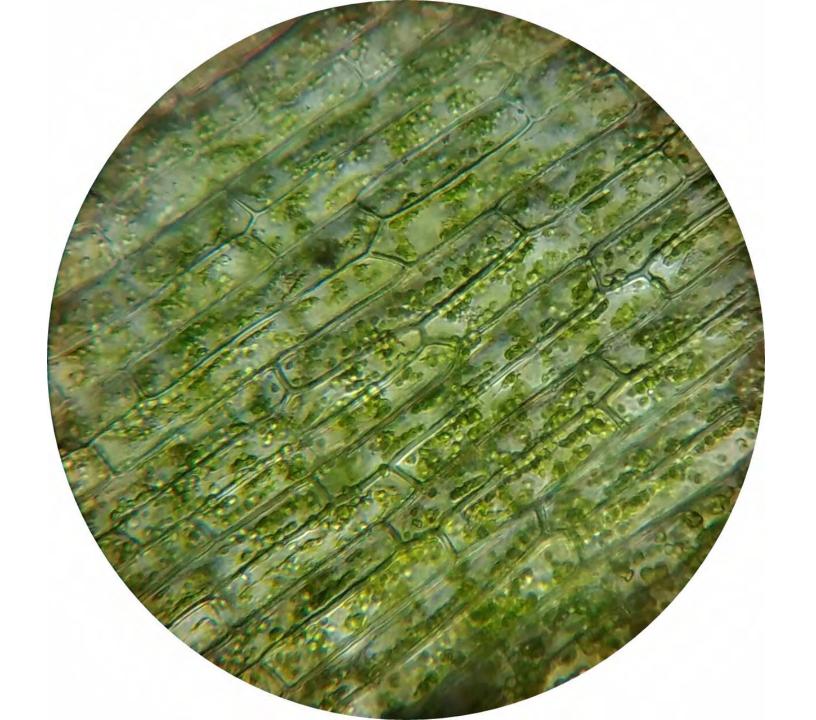












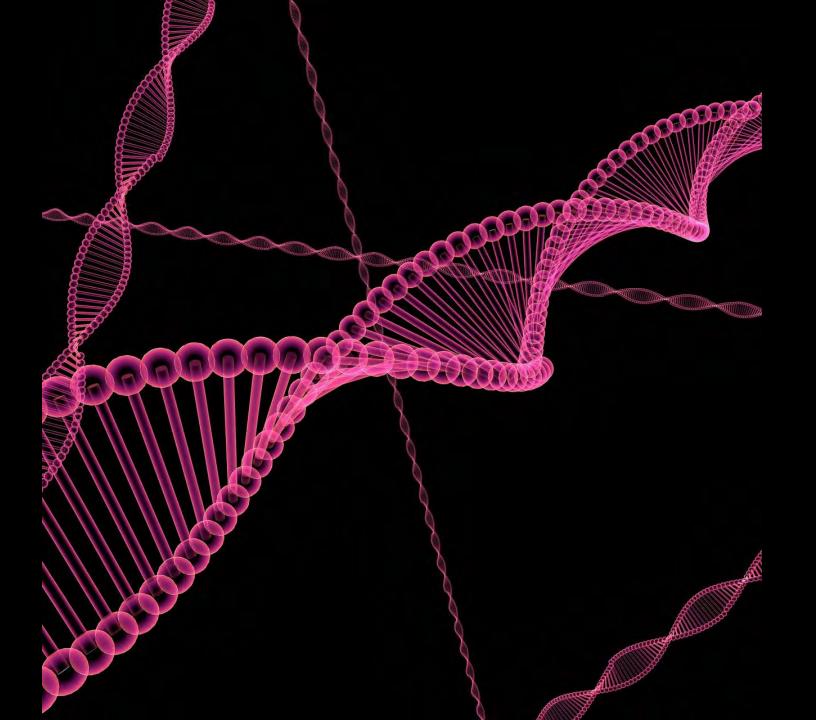


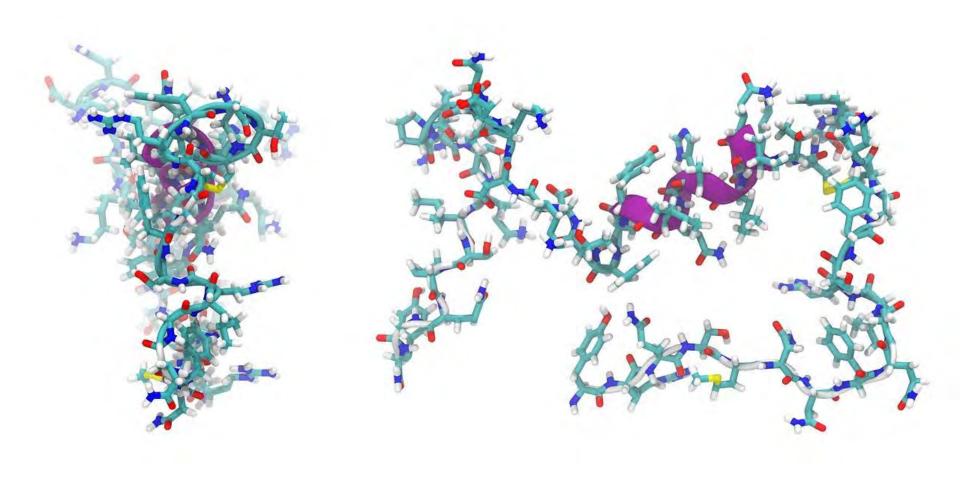














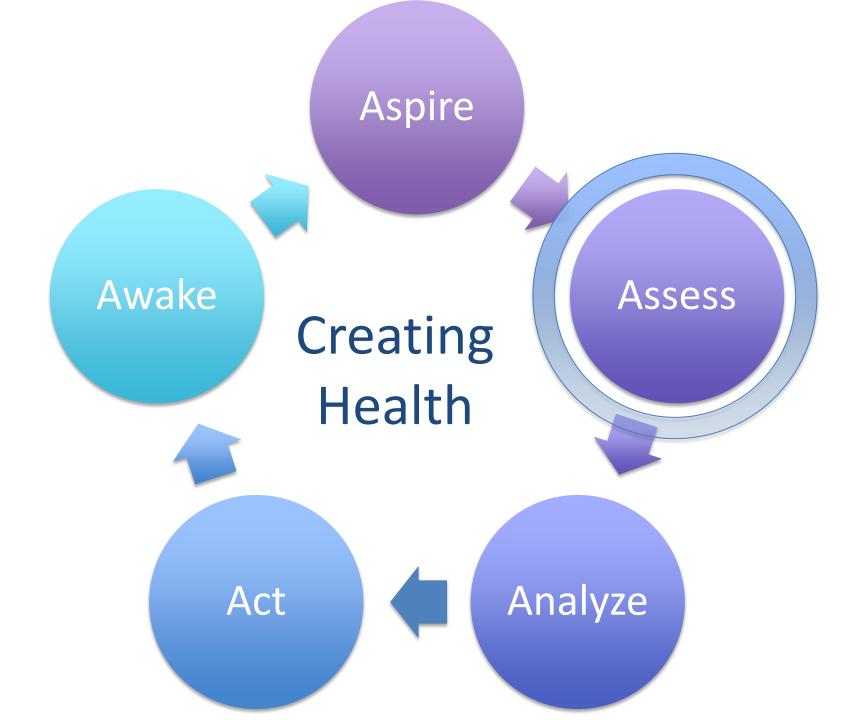












## **Digging Deeper in Assessment**

#### Genomics

- Mitomics
- CNVs
- VUS
- Microbiome

#### Connectomics

• QEEG

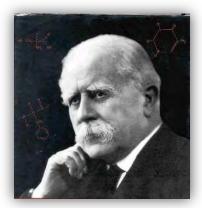
• fMRI

#### Metablolomics

- Lipomics
- Toxomics
- Microbiome

### Genetic Origins of Individual Variations in Metabolism

More than 100 years ago, Archibald Garrod already suggested a link between *chemical individuality* and *predisposition to disease*.



### INBORN ERRORS OF METABOLISM

Ву

ARCHIBALD E. GARROD, K.C.M.G.

D.M., LL.D., F.R.S., F.R.C.P. Regius Professor of Medicine in the University of Oxford Consulting Physician to St. Bartholomew's Hospital and to the Hospital for Sick Children

First Edition 1909

'.....merely extreme examples of variations of chemical behaviour which are probably everywhere present in minor degrees' and that this 'chemical individuality [confers] predisposition to and immunities from the various mishaps which are spoken of as diseases'

-Archibald Garrod

# A brief History of metabolomics

### Quantitative Analysis of Urine Vapor and Breath by Gas**wid** Metabolomics Partition Chromatography

(orthomolecular medicine/vitamins/controlled diet)

LINUS PAULING\*, ARTHUR B. ROBINSON\*, ROY TERANISHI<sup>†</sup>, AND PAUL CARY

\* Department of Chemistry, Stanford University, Stanford, California 94305; and † Western Regional Laboratory, U.S. Department of Arriculture

Contributed by Linus Pauling, July 29, 1971

- metabolomics developed by Pauling in 1970  $\bullet$
- the term metabolomics first used in 1998

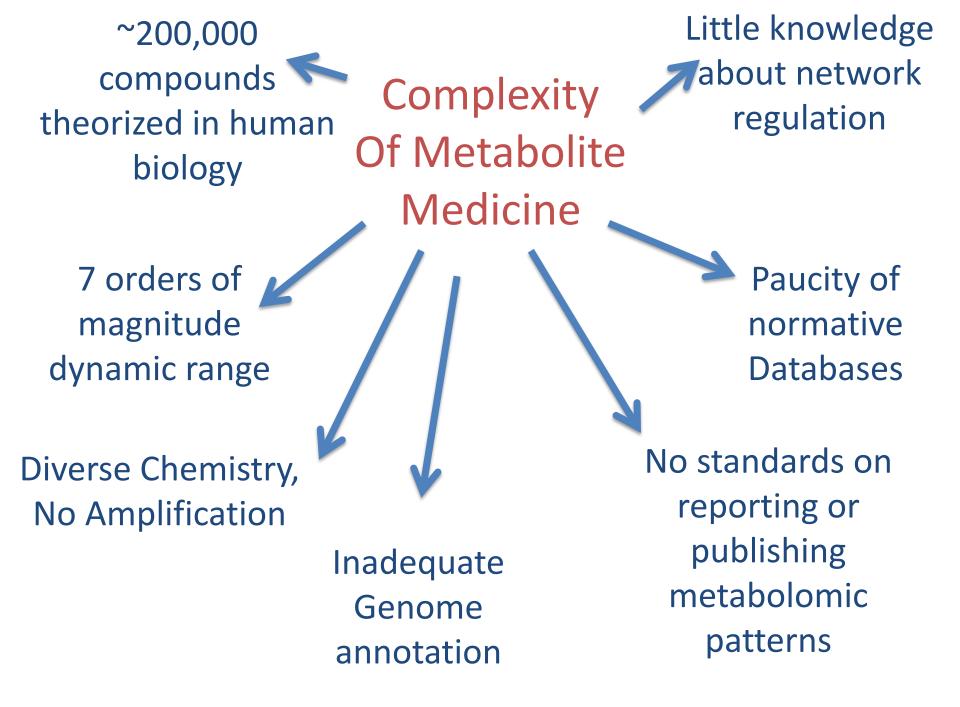
- Oliver SG et al (1998). Trends Biotechnol 16:373

- Metabolomics Society founded 2004
- January 23rd, 2007 first draft of the human metabolome "completed"

# Examples of metablolites

- Peptides
- Oligonucleotides
- Sugars
- Nucleosides
- Organic acids
- Ketones
- aldehydes

- Amines
- Amino acids
- Lipids
- Steroids
- Alkaloids
- Drugs
- Xenobiotics



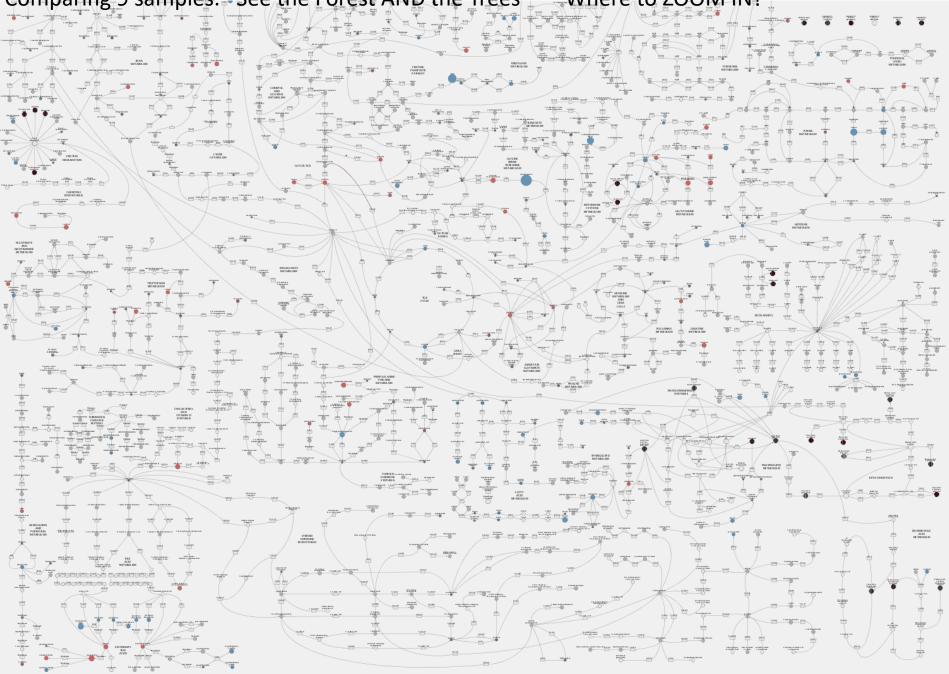
Subfathery	toohemical Name	4355	PURCHEM	HMOR	DUMBRY VS	DUMMY VS. 19.2	DUMBRY VS	DUMBY VS	DUMBRY VS	DUMBY VS. IP_6	DUMBRY VS	DUMBY VS.	DOMENT VS	10175	IOTF2	10173	ISTPR	101PS	10197	10179	
	Eyave	620817	10	HMDHDDDJ	-1.1548	0.2051	0.5282	p.966	0.5641	012954	-1.5427	<3835	3.193	-1.5548	0.2051	0.5181	p.566	0.5645	-5.5427	-2836	F
	ty-acitylgycane	Cito213	45932-	HMDR02512 HMDR02271	-1.1254	0.0622	-016001	-0.8418	-2.1017	-1.1346	1.890#	-1.32	1.5292	-1.1354	0.0622	-016002	-0.8418 1.3057	-0.1017	1.890.9	1.32	+
	sphoosing (N-Methylg/yc/w), domethylgrycine	distain.	41	HMDR00271	1,302	-0.3025	1.684	-0.4624	-0.109	0.629	0.8195	0.3879	0.0774	1,302	-0.3225	-1.819	-0.4634	-0.1057	0.8195	0.3879	+
	betavle	CB0715	60	Hendersteit	02531	-0.0236	-1.5329	-0.5457	2.4908	1.004	-3634	-1.046	-1:8548	02531	-20236	-1.5329	-0.5,057	2.4608	-3616	-0.1346	
Byone, famore and Threeshore	or The-	CINORIA	663	HMDRODUR7	1.2894	0.0058	CINI	-0.21119	-0.472	0.9025	0.3271	0.3466	1,7855	1.1994	0.1054	0.042	-0.2119	-0.432	0,3291	0.3466	
MN4sborr/II	79-goldykent/w		49149	HMDH02(81)	2,3852	-0.1859	-4.5410	13649	0.2034	-2.14M	-4.4570	-1.6389	0.8655	3.832	-2.1959	-4.5210	1,2649	010074	-14170	-5.6389	
	threating	CIRCUM	40	HMDRODOS7	2.1488	0.5135	1,1771	0.9491	0.8187	-0.1817	-5:8829	-0.151	1.0418	2.1488	0.Sitis	14771	0.9961	0.3187	-1.8829	-0.151	
	ts-postylthrep/w/e	CIIISTR	61208		-2.0859	1.51/1	-26123	12046	-1.1042	0.6228	-4.5824	1.3057	-49637	-2.0659	1501	-0.6123	1.2,055	-1.1042	4.9421	1,3053	
	all streame	GRI515	19239	HMDR04041	点出57	1.0672	-0.0217	0.316	1.9945	0.3452	-0.6527	-14671	-13673	0,2167	1.3872	-0.0213	0,716	1,6645	-0.8127		
	C-a; Hylforrose//w	Citata (O	Any last		0.419	-0.1078	-0.3091	-0.106	3:1159	-2.454	-13334	-0.9645	-0.1299	£.418-	-0.1578	-4.3634	-0.106	3,3159	-18104		-
	2210+	050345	100	HMDH005555	0.683.2	0.4982	1.2878	1.84	6.646.0	-1.7157	-1.1268	-1.1288	-016236	616832	0.4902	1.2878	2.344	0.8678	-1.1268	-1.1288	
Name and Aspartane Verapolium	b-acetybranine accertation	CILIDA?	Calcol.	HMDROC765	1.6329	0.8245	-1.1015	0.8244	-0.1585-	-0.3326	-4.5819 2.577	1,016	0.5884	1.6329	0.6245	-1.3055	0.6244	-0.3585	-4.1819 1.5P7	1816	<u>+</u> -
Carl & and Style Last Vision Con	asparagine	CECELU	462	HMDHODDER	-2.1522	1,3665	0.000	-0.1051	-2.0976	0.1798	-1.5385	0.0112	0.535	-2.1522	1.5665	02903	-0.1051	-0.0976	-1.5385	0.0113	
	N-portylacourtaine (NAN)	Citter.	6265	HMDRODEL2	13456	-1.3217	0.4237	-0.5421	-0.4679	-0.7957	0.5425	0.9195	-0.0529	1,5454	-1.3287	0.4237	-0.5421	-0.8679	0.5425	0.9185	
	gizanise	Citorius-	41	Heybelictes	-0.1564	-5.1789	1.2015	0.6782	1.6(2)	0.4535	-16425	4,3058	0.3893	-0.3564	-5.3289	1,2045	0.6782	1.6923	-16425	-2.3558	
	guiantis-	C10001-4	100	HMDR00941	-0.9029	0.8034	0.048.8	-0.2519	-1.0945	03761	-1.0099	-0:133	4.3248	-0.9029	0.00140	0.048.8	-0.2519	-5.0945	-5.0099	-0:131	
Guterupe Metabolien	N-portylgistamen-	CEDEPA	4884	HMDHDDDD388	0.6525	0.4295	-41112	-1.3407	0.6272	-2.847	0.5785	-0.1816	1.9629	0.6525	0.4295	4.03	-1.3427	0.6272	0.5745	-江14%	
	Neoitygistamnie	diligits	442.82	HMOROSOBE	0.967	-0.4477	obliet.	0.9947		-0.5481	4,1518	13935	0.34	2,867	-0.4477	0.2565	0.6947	\$1778	4,1518	12806	1
	theory is superty glutamate (NAAG)	CLIPTE	4555	Heybecook/	0.176a	-0.1013	0.662.8	0.864.9	-0.3285	1.68/15	-26.75	-0.0511	-8.1521	0.1165	41012	0.662.8	0.8623	-0.1385	-2675	-0.0511	1
	pyrightamina*	000915	204508	HMDecc677	0.9565	-0.1818	0.8358	1,2911	13166	-1.71.14	-8.7523	-0.1754	-0.1817 -1.4423	0.8565	-0.1918	0.8158	1,2901	-1,3866	-8.7523	-0.1754	_
	Nidotyk atilize	000015	A234	HMDR00027	-1.1526-	1.015	-0.6897 -0.1465	1,2911	-0.4483	1,2845	-0.7067	1.0458	-0.4428	-1.1536 6.5k38	1.5355	-0.3465	1.2911	-0.4490	-0.7067	12468	+
	1-methalteridine	CITIZIA	100.00	HMDRODOD:	6,1478	41221	-0.1449	-0.0928	-0.0023	-2.4889	-1 2048	0.2805	-0.7648	6,3434	Hang.	-0.1980	-10928		-1.3948	0.2355	1
	3 metholigicine	ditaia	A1969	HMDRODEDE	2.4642	-0.0626	-11752	-0.5202	C2548	0.5902	-0.7227	1.3747	-1.113	14848	0.0626	-1.1752	-0.5,102	D.D.Bell	-0.7227	13947	-
	N-porty1-II-Mathubititicine*		491271		1.8111	-0.4576	-0.3756	-2.16	-2.6581	0.1152	-18114	1.816	-181M	1.6111	-0.45%	-1.1716	-2.16	-0.6581	-1811		
Hutchine Metapolitan-	N-sorty) 1-methyltistics/w*				3:2318	-24883	-0.0188	0.3006	02135	-0.1279	-5.4654	1.034	-1.4828	12118	-2488	-0.0188	0.3006	02136	-14654	1.024	
	trans-Lipcarate	620785	08745	Hby by topics	-1.5421	0.4484	-43581	-1.DIM	-2.6476		0.4065	Ú.REH	0.869	-1.5421	0.4484	-4.3584	4.7314	-2.6476	0.4065	O.REM	
	OP-LINERUSE		Adjuit	S fait and	-2.017	<u>6,7625</u>	0.0675	-0.510	-0.7081	4.3034	-5.3617	soites .	-0.9687	-0.1313	0.7991	0.0675	-04187	-0.3685			
	intedasola proprioriutar		2610	HMD#03291	0.5781	1.6683	0.3075	0.5465	0.4567	-31,1532	-1.5565	-11111	-2.4523	0.5791	1.668.1	0.3025	0.5445	0.4967	-1.5565	-11971	-
	evidancie tactate	<b>CEINIA</b>	101525	HMDRODROD	-1.2657	0.9005	-1.7288	1350	1.3118	-0.7808	-26(1)	0.6606	0.2964	-4.2657	0.6005	-1.7210	1361	1.3118	-2645	0.9606	-
	3-methologidazzi eacetator Instine	Citistan CitoseJ	5820 ·	HMDR00082	1.8907	1.665	-0.1129	0.2057	0.80%	-1.7621	-2.0928 0.9908	-0.1588	0.3627	1.8907	0.887	-0.4611	0.2057	0.80%	-2.0938 0.9958	-0.1548	
	Nanceshilysare	Ch2889	A STATE	HMDRODAK2	2,3765	-1.0346	-5.0346	0.3121	0.5482	0.5855	-2.0346	2.755	1.3257	1.3765	1.636	-1.0346-1	0.3171	0.576	-2.0346	0.5799	+-
	No-acetylpane	012222	A112	HMDR00206	1.985.8	1.8151	-0.1874	-1.5463	0.3485	0.0932	-1-1048	-0.4215	-dioft.8	1.985.8	1.8151	-0.5874	-1:546.8	0.3435	-1-1048	-0.4315	
	19-6-climathylispie	C18290	ACC N	HMD#01105	\$.4157	-1.0829	-10818	-0.0546	-0.4975	-1.5419	-0.1455	-1.1886	0.7769	5.4117	-5.0829	-0.0818	-10546	-0.4575	-1345	-0.5828	
Lyuiw Metadoliami	J-ammoadioarte	citor 56	64	HIMDHODIED	1.8799	1.0%	0.0521	-5.0661	0.0848	0.2658	0.000#	-0.5545	-0.105	1.8799	1.094	-0.0527	-5.0661	0.1848	2,000#	-0.5545	
Lytime NetGoonam	giutanuté (peritahedicaté)	C20889	44	HM/D#00662	-1.1466	-5.0557	0.3082	0.9878	2,795	42,1429	0.0135	0.7752	1.8985	-1.1006	-5.0557	0.2082	0.5878	£1,795	0.00235	0.3752	
	gutary(arritine (CS)		46448	HMORESCHOL	0.3635	1.9254	0.3848	¢Shi6	0.5406	NLD-	2.9654	0.5292	-5:1054		1.8054	0.8848	0.5166	0.905	2.5454	0.5242	
	3-methylgistatylcarridine (5)		428345	HMD#GESS2	-4.7769	-0.6781	2.665	0.8073	-0.6387	0.3041	-1.8262	-41022	1.810	-0.7769	-16381	0.665	0.4073	-0.6267	-1.8242	-0.1721	-
	3-methyigistaryisenitine (2)		49915	HMDH00152	1.9977	-0.0234	0.4055	0.5706	0.4009	0.019	-1.0129		0.2557	1.9907	410214	0.4055	0.5766	0.4809	-1.0129	-1.8464	-
	prpecolate	CEORDS	ALC: NO	HMD#05003	0.5579	0.5845	0.4685	-0.0013	0.5254	-2.9558	-15166	1.80%6	-2.6996	6522.0	0.5M1	0.4685	-10011	0.5254	-18166	1.8054	-
	phenyia anne Nebostylphenyia anne	C20379-	ALAS	HMDRODSS9	15181	1.2857	-0.088	0.2964	-0.4178	-1.1129 -0.53 M	-0.107	0.3295	-0.1518	1.5181	1,2857	0.9161	0.3954	0.8345	-0.107	-1.1559 0.3195	<u>+-</u>
	Shenyipyovite	CICITATE	Call Call	HMDROENCY	1.45	-0.8857	0.9992	0.5005	-0.1328	1.3998	-13824	0.3095	-2.018	1.05	-0.8857	0.9982	0.3034	-0.1328	-1.8814	0.3688	
	cherylactate (PLA)	C#1607	1048	HMD#00774	3.6575	-0.0911	-0.1047	OSTJA	-0.0281	-12/153	-0.45 88	0.4629	24263	3.6425	-10911	-0.1047	0.0734	-0.0581	-0.45 88	0.4429	<u>+-</u>
	phenylacetate	037946	60	Herefore	0.2265	<1.738	-0.5307	-0.7687	0.4095	-0.4447	12512	32179	-0.4852	0.3265	-1.798	-0.5327	-0.7687	D 0096	1052	1203	
	phenylacety/giutamine-	C0454#	42158	HM/DetCis INA	4.000	-1.5366	1.6754	0.5154	0.2081	-8.3671	-0.2685	-0.1481	0.1859	1.000	-1.53406	1.6754	0.5\$54	0.1081	-0.2583	-0.1481	
	fprixite-	CIRCENT .	100	HMDHODDSA	1.198	0.8952	-0.2661	-0.1039	-0.4306	-0.9884	-0.1856	+6.5625	0.5489	1.1748	6.896.9	-3.2662	4.1029	-0.1306	-0.1856	+6:58229	
	Te-sortyltyrosine-		46/20	HMDHODRES .	13675	0.6552	0.8064	02585	0.1475	4.1/14	-1.4673	4.156	-1.3998	1055	0.6452	0.8064	0.2585	0.1425	-4.4673	-6.1614	
	<ul> <li>A hyperparameters in the second se</li></ul>	GB1279	A13	HMDHOD 207	1.5142	14778	-5.8223	1.165	-2.7699	-44049	-0.1116	042	1.8001	15142	14771	-5:6223	-1.146	-0.7699	-0.1316	042	
	3-(9-hydroxyphery) actable	Colo73	101	HMDe0cHSS	0.3499	-4.21%	1,36,15	1.6105	0.5629	-2.6328	-1.5456	0.9069	-1.9772	0.3499	-12196	1,36,15	1.6105	0.5629	-1.5456	0.5058	+
	phenal suffice	CE258C	And No.	HMDR60015	-1.7181 1.668.h	0.0109	0.5134	1.3145	1.847	-0.0801	0.3467	-0.1881 0.8531	-2.2003	-4.75 kg.	0.0109	0.5134	1.3145	12512	0.3467	-0.7810	1
Phony and Tyronne Metado and	provepal kulfarbe provepal kulfarbe	CD106a	ALCINE.	HMDR10585	-0.2662	1.6637	-0.0428	-1.3573	-0.0321	-0.4821	0.2304	0.8532	1.3187	-0.2652	1.6637	-0.0428	-1.3571	-1.6321 -0.1589	0.2804	0.8535	+
	saminamanderate (VVA)	CallARE	1245	Hewbelloging	1.669	0.5406	-415287	0.6169	1,2154	-4.9543	-2.4575	0.4051	-1.1617	1.469	0.5406	-15287	0.8189	1.1154	-2.4875	0.4051	1
	Jonethaeitytaine		1010	HMDROSALA	D Bick	0.4798	0.562	0.2185	0.3186	1,2654	-0.7761	-1460	-1.9081	California -	0.018	0.5607	0.3185	0.3186	-0.7761	-14883	
	3-methosphyramine suffate				0.6627	1.3651	0.01189	0.5825	-0.152	0.6557	-2.12%	1.3397	-1.9929	0.6627	1.3651	0.01189	0.3846	-0.452	-2.12%	1.5197	
	gertisate	0.00528	ALC: N	RM2805652	-1.4306	1,214	-0.1941	-0.1566	-0.28108	1.0017	-0.2619	0.4862	-5.1047	-1.4326	1,214	-0.1381	-0.1566	42818	-0.2619	D 4hit	
	3-[3-(suttoon)[pheny][prepartox acts	1.1	10.00		-0.28%3	1.9081	0.5344	(13 C	-0.1898	- 2.1521	1.815	-0.7089	-4.1373	(\$\$\$C>	1.5095	0.3344	(111	-0.1898	1.815	-0.7089	
	3-(3-hydroxyphany)propioneta	Castel0	A.	HM0800805	-24529	5,2138	-0.152	-0.2629	-2.4.333	-0.5414	-1.1365	0.1187	6,7154	-0.4509	\$2133	-0.152	-0.1670	-0.4303	-1.1365	03137	1
	3-(4-hydrosycheryljaroparate	CI1344	AIH	HMDHDDDDNH	-2.0336	-0.1855	0.6134	-2.0326	1,2758	-4.0153	0.5795	0.3245	1,3458	2.0006	-0.1855	0.6134	-2:05:36	1.1158	0.5795	0,3245	1
	3-phrey(propriorable (hydrocemamate)	025629	421	HMDRODPER .	-1.0945	1.925.0	ALC: N	-0.1127	0.505.6	4.22	DAIS	-0.444	-1.2879	-1.0945	1.925.8	MARCO.	-0.1127	0.5054	D.415	-0.466	1
	27/y/cic/re	C01829	1813	HMDHDDHDDHDB	-0.3925	-5.0658	1.1.1.1	0 4.9 89 4.4 86	1985	3.2788	-1.0514	-0.1852	-1.0614	-0.3925	-50654	1.5818	0.9973	0.8585	-5.0654	-0.1851 0.0133	+
	phenylacetylcamitine p-creati-gruculturilar*		64015	HEADELISES	1.5045	1.5017		0.9 8	- 124	-0.7615	-0.9890	1,3105	1898.D	1.5348	1.5624	-0.9961	-0.9889	-0.104	-13651	13001	1
	proved-guourprede*	030574	64040	HMDRIDHE	-0.166	0.4105	0.44	-1.4 16	-1 173	1.3002	-0.7971	2.8529	0.3467	-0.165	0.4125	0.86	-0.061	-1.0078	-0.7971	2.85.99	1
	tryptophan te-acety/blyptophan	Calcore Calcore	20654	HMDRDBDD	1.7291	04105	0.8022	0.5298	41082	-0.1654	-0.7971	-1.1546	-2.5346	1.3281	6458.0	0.8072	0.5299	-0.0933	-0.7871	-1.1546	1
	indoleractate	(112043	20424	HM DRODAT:	-2.4652	-0.8611	1.05	1.405	0.912	0.3995	-2.4648	0.2862	-2.6507	-0.4652	-0.8611	1.176	1.4006	0.512	-0.4648	0.0161	1
	indol+aoHada-	CIDOR54	(A)	HM/DRODON7	1,3228	0.1539	0.8655	0.2992	-0.9821	-1.1288	-1.165/	0.2942	-1.8428	1.5728	0.4549	0.3655	0.2992	-0.5821	-1.166.0	0.3942	
	indoleurop anabe		640	HMDRODINC2	-00657	-0.4240	114147	0.2169	0.01157	12061	0.6283	-0.1515	-8.904	-010252	-0.4547	0.3147	0.3169	0.0117	0.6183	-0.1515	
	3-Endowy) curture		A158	Hey SelopSe2	0.5251	0.6857	0.6679	0.6585	5,303	-6.9076	0.5156	-1.1264	-14734	0.5251	0.6857	0.6679	0.6186	5,400	0.5156	-0.1264	
	available and a second s	cinónica.	ALC: NO	HMDRODER	2,6846	-0.509	0.5632	-6,2287	-0.7823	0.594	10.0661	32 4802	-0.30%	上市時代	48.69	0.5622	-0.4287	-0.7923	0.665	124802	
	intrum/abr	Ga1713	4945	HMDH00725	3.41ab	0.5151	0.8275	0.3504	-0.7779	-0.8416	-0.5883	-0.547#	-1.1625	3:4186	0.5151	0.8275	0.3554	-0.7779	-0.5823	-0.5478	4

Super Pathway	Sub Pathway +	Biochemical Name					Fold Change	£			
Super Fattiway	Sub Faulway -	Biochemical Name	IDEP1	IDEP2	IDEP3	IDEP4	IDEP5	IDEP6	IDEP7	IDEP8	IDEP9
Amino Acid	Alanine and Aspart	alanine	0.63	0.49	1.19	1.34	0.87	-1.74	-1.23	-1.13	-0.60
Amino Acid	Alanine and As art	N aceptalanine	1.83	0.62	-1.31	0.62	-0.36	-1.23	-1.59	1.03	0.34
Amino Acid	Alanine and As alt.	aspartate	0.03	0.33	0.96	0.35	0.41	-0.42	1.58	-3.74	-0.76
Amino Acid	Alarine and Aspart	asparagine	-2.15	2.17	0.09	-0.31	-0.04	0.18	-1.54	0.91	0.56
Amino Acid	Alanine and Aspart	N-acetylaspartate (NAA)	3.14	-1.22	0.42	-0.54	-0.87	-0.78	0.54	0.92	-0.71
Carbohydrate	Aminosugar Metab	glucuronate	0.63	0.52	-0.29	-0.45	-0.22	-1.34	-0.87	-0.49	4.28
Carbohydrate	Aminosugar Metab	N-acetylneuraminate	0.80	0.92	-1.59	-1.11	-1.50	0.54	1.68	-0.39	0.52
Carbohydrate	Aminosugar Metab	erythronate*	0.55	0.06	1.10	1.06	1.45	-1.13	-1.54	-1.60	-0.11
Cofactors and Vitamins	Ascorbate and Ald	threonate	1.07	1.36	-0.91	-1.39	-1.33	1.00	1.18	-0.24	-0.72
Cofactors and Vitamins	Ascorbate and Ald	oxalate (ethanedioate)	0.91	1.36	-1.47	-1.49	-0.96	0.88	1.27	-6.40E-3	-0.57
Cofactors and Vitamins	Ascorbate and Ald	gulonic acid*	1.09	1.20	4.60E-3	-0.35	0.30	-1.24	-2.65	-0.18	1.29
Xenobiotics	Bacterial/Fungal	tartrolate (hydroxymalonate)	1.42	1.33	-0.75	-0.42	1.13	-1.04	0.41	-0.11	-2.14
Xenobiotics	Benzoate Metaboli	hippurate	-0.30	3.15	0.12	-0.40	-0.72	-1.52	-1.00	0.66	0.84
Xenobiotics	Benzoate Metapoli	2-h dro cyhippurate (salicylurate)	-1.73	-0.89	-0.08	-0.32	-0.45	2.18	-0.64	0.76	1.51
Xenobiotics	Benzoate Metaboli	3-hydroxyhippurate	0.38	3.10	0.31	0.25	-0.09	-1.27	-2.00	-0.41	0.28
Xenobiotics	Benzoate Metaboli	4-hydroxyhippurate	-0.13	0.16	0.14	-0.50	3.15	0.32	-2.60	-0.56	0.36
Xenobiotics	Benzoate Metaboli	benzoate	-0.67	0.49	0.25	1.14	-1.17	0.02	2.68	-0.85	-1.33
Xenobiotics	Benzoate Metaboli .	catechol sulfate	-0.32	4.00	-0.23	-0.28	-0.76	-0.16	-1.70	0.06	0.86
Xenobiotics	Benzeate Metaboli.	C-methylc ite hor sulfate	-0.36	4.17	0.19	0.26	-0.54	-0.18	-1.74	-0.73	0.47
Xenobiotics	Benzoate Metaboli	3-methyl catechol sulfate (1)	0.06	3.05	-0.58	-0.81	-0.71	-0.46	-0.27	-0.89	1.74
Xenobiotics	Benzoate Metaboli	4-methylcatechol sulfate	1.85	1.93	-0.11	-0.21	-0.87	-1.76	-0.97	0.05	0.38
Xenobiotics	Benzoate Metaboli	4-ethylphenylsulfate	1.85	0.67	-1.18	-1.13	-1.02	-0.86	0.11	1.71	0.15
Xenobiotics	enzoate Metaboli	4-vinylphenol sulfate	-0.86	0.60	0.57	0.35	0.30	1.34	0.83	-3.21	-0.91
Xenobiotics	Binzoale letaboli	4-sulfcoxy-nethylbenzoate	1.41	-0.70	-1.22	-1.33	-1.20	1.09	1.50	0.25	0.26
Cofactors and Vitamin	Bictip Metabalism		-0.35	-0.35	-0.35	-0.35	-0.35	0.00E0	-0.35	-0.35	-0.35
Lipid	Carnitine Metabolism	deoxycarnitine	-1.42	-0.90	1.20	1.95	1.32	-1.04	-0.58	-0.04	-0.18
Lipid	Carnitine Metabolism	carnitine	-0.18	0.29	1.38	1.84	0.44	0.15	-2.22	-1.18	-0.66
Xenobiotics	Chemical	1,2-propanediol	3.84	-0.77	0.13	-0.44	-0.38	-0.72	-0.57	-0.80	1.32
Xenobiotics	Chemical	2-pyrrolidinone	-0.22	-0.53	-1.22	0.38	0.76	4.30	-0.94	-0.36	0.40
Xenobiotics	Chemical	sulfate*	2.37	-0.52	-0.42	1.10	0.87	-1.73	0.06	-0.22	-1.19
Xenobiotics	Chemical	O-sulfo-L-tyrosine	2.98	-0.82	-0.19	0.68	-0.56	0.13	-0.95	0.93	-1.46
Xenobiotics	Chemical	2-aminophenol sulfate	-3.11	0.14	1.08	0.85	0.61	1.18	-0.48	-0.06	-1.10
Xenobiotics	Chemical	2-ethylhexanoate	0.20	0.31	0.04	0.48	-0.84	3.37	0.01	-0.79	-1.99
Xenobiotics	chemical	2_hydroxyisobutyrate	0.65	2.94	-0.92	-0.43	-0.33	-0.92	-0.83	1.37	-0.62
Xenobiotics	Chemical	-(3 hydro cypropyl)mercapturic	0.23	-0.62	1.10	-0.62	-0.62	-0.62	-0.62	-0.62	4.37
Xenobiotics	Chemical	dimethyl sulfone	-0.35	0.05	-0.32	-0.62	-0.33	0.10	10.08	-0.83	-0.47
Xenobiotics	Chemical	EDTA	0.41	1.59	0.20	1.86	0.31	-0.37	-1.03	-1.35	-1.47
Xenobiotics	Chemical	glycolate (hydroxyacetate)	1.98	-0.80	0.29	1.06	-1.00	-2.10	0.85	-0.45	0.14
Xenobiotics	Chemical	iminodiacetate (IDA)	-0.29	-1.18	1.39	1.15	1.04	-0.91	1.11	-1.13	-1.09
Xenobiolics	Che nic I	plieny carni in 😤	-1.98	3.09	0.38	0.37	-0.66	-0.95	-0.38	0.24	0.49
Xenobiotics	Chemical C	-neth/phrecoate	2.79	0.23	0.53	0.48	0.48	-1.67	-1.23	-0.94	-0.22
Xenobiotics	Chemical	4-hydroxychlorothalonil	1.08	0.24	0.70	0.80	0.73	-3.47	-1.10	-0.55	- 0.34
Xenobiotics	Chemical	1,2,3-benzenetriol sulfate (2)	-0.70	1.37	0.58	0.14	-0.25	-0.42	-3.05	0.04	1.66
Xenobiotics	Chemical	3-hydroxypyridine sulfate	-0.82	2.23	-0.34	-0.38	-0.04	-0.57	-0.51	-1.05	2.45
Amino Acid	Creative Metabolism	Cheat me	1.45	-1.32	-0.58	-0.86	0.88	2.19	-0.32	0.03	-1.06
Amino Acid	Creatine Metabolism	creatinne	0.38	-0.41	1.50	1.47	1.10	-1.73	-1.32	-0.38	-0.59
Amino Acid	Creatine Metabolism	guanidinoacetate	-1.45	0.07	1.04	1.06	-3.28	-0.06	0.44	0.55	0.48
Peptide	Dipeptide	aspartylleucine	-0.38	1.03	-0.70	-0.23	0.70	-3.15	0.33	-0.10	1.80
Peptide	Dipeptide	cyclo(gly~pro)	0.56	1.21	0.77	0.73	0.77	-2.20	-1.86	-0.60	0.02
Peptide	Dipeptide	cyclo(leu~pro)	1.33	1.04	-0.13	-0.92	-0.99	-0.86	-0.14	-1.09	2.25
Pentide	Dinentide	ovclo(I_nhe_D_nro)*	0.66	2.14	-0.73	-0.51	-0.73	-0.73	-0.73	-0.73	2.10

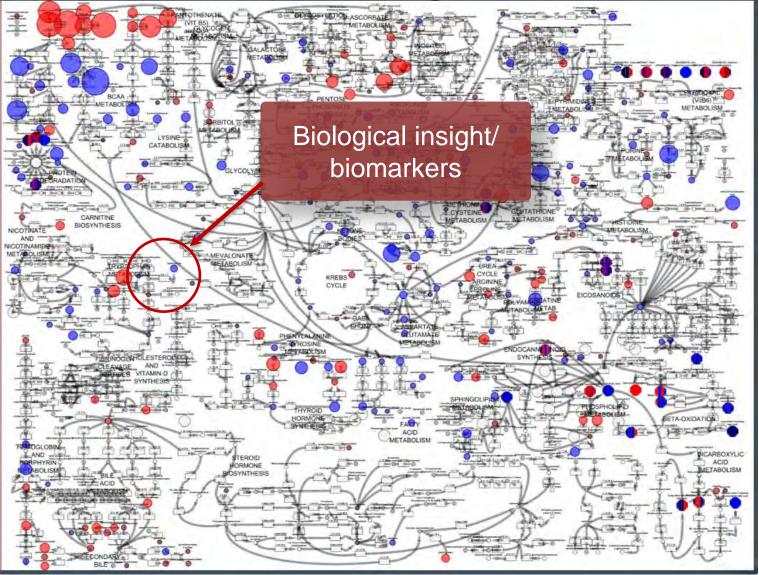
# Identifying Hubs of Interest

Pathway	IDEPI	IDEPZ	IDEP3	IDEP4	IDEP5	IDEP6	IDEP7	IDEP8	IDEP9
Tocopherol Metabolism	3.2	1	1	1	1	1.1	1	1	2.4
Tryptophan Metabolism	2.6	1	2.6	2.7	1	1.5	1.4	1	1.5
Pentose Metabolism	2.4	2	10.9	1	1	1	1	1	1
Leucine, Isoleucine and Valine Metab	2.2	1.1	1	1.6	1	0.6	1.6	1.4	0.9
Purine Metabolism, (Hypo)Xanthine/I	1.1	1	7.2	1	1	1	1	1.4	4.2
Sphingolipid Metabolism	1.1	1	1	1	4.5	3.5	1.3	1	1
Long Chain Fatty Acid	1	1	1	1	6.3	1	1	5.4	1
Polyunsaturated Fatty Acid (n3 and n6)	1	1	1	1	1.9	0.6	1	2.9	2.7
Benzoate Metabolism	1	3.3	1	1	1.1	0.7	2	0.7	1
Polypeptide	1	4.8	1	1	1	1	1	1	1.3
Medium Chain Fatty Acid	1	4	1	1	1	1.1	1	2	1
Urea cycle: Arginine and Proline Meta	1	0.6	1	1	1	1	3.7	1	1.5
Dipeptide	0.9	2.6	1.6	1	1	1.2	1.7	1	1.1
Xanthine Metabolism	0.9	4.8	1	1	1	3.4	1	1	1
Lysolipid	0.6	1.1	0.6	1	0.3	1.6	0.8	1.7	1.1
Secondary Bile Acid Metabolism	0.5	0.6	6.2	3.3	1	0.6	1.7	0.6	0.5
Fatty Acid Metabolism(Acyl Carnitine)	0.5	1.7	3.1	1	5.8	2.4	1	1.2	1

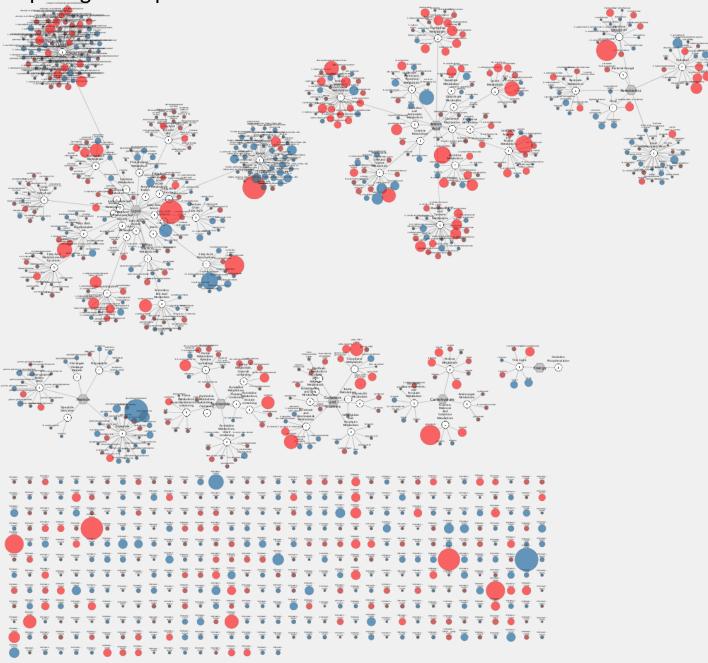
Comparing 9 samples. - See the Forest AND the Trees<sup>™</sup> Where to ZOOM IN?

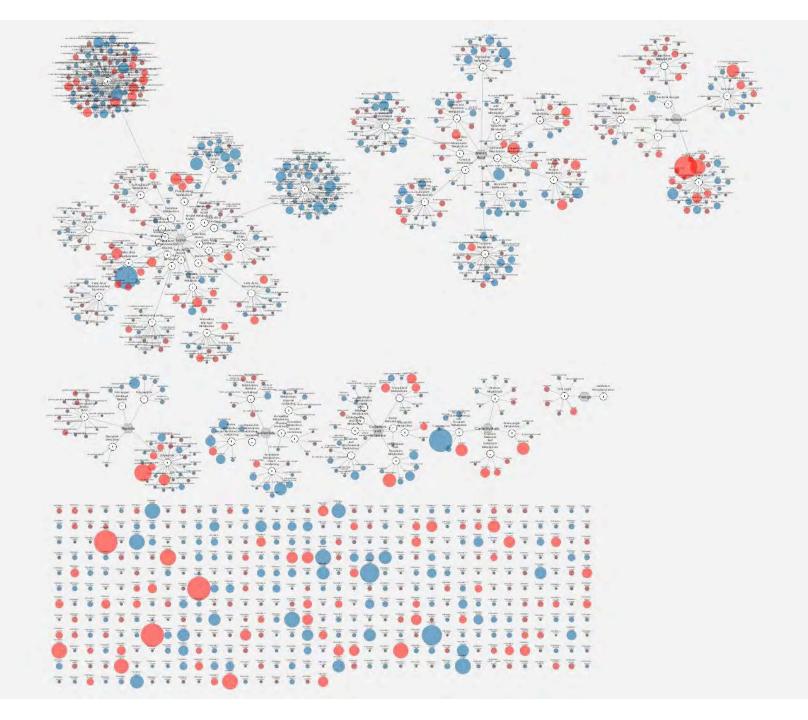


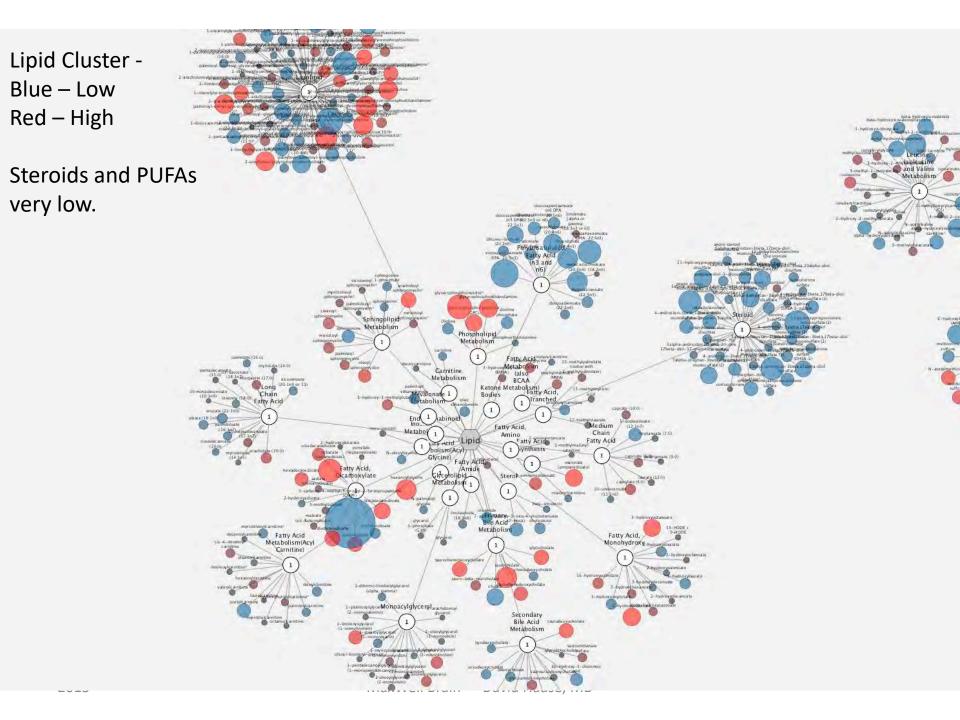
#### **Visualizing Data**

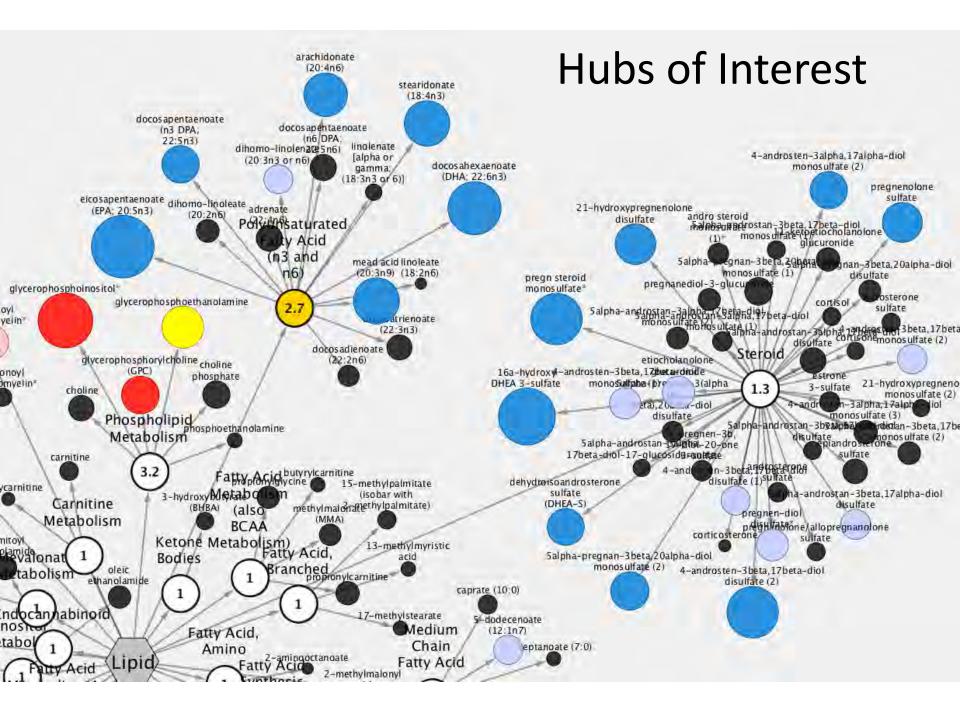


Cluster Analylis - Comparing 9 samples. See the Forest AND the Trees™

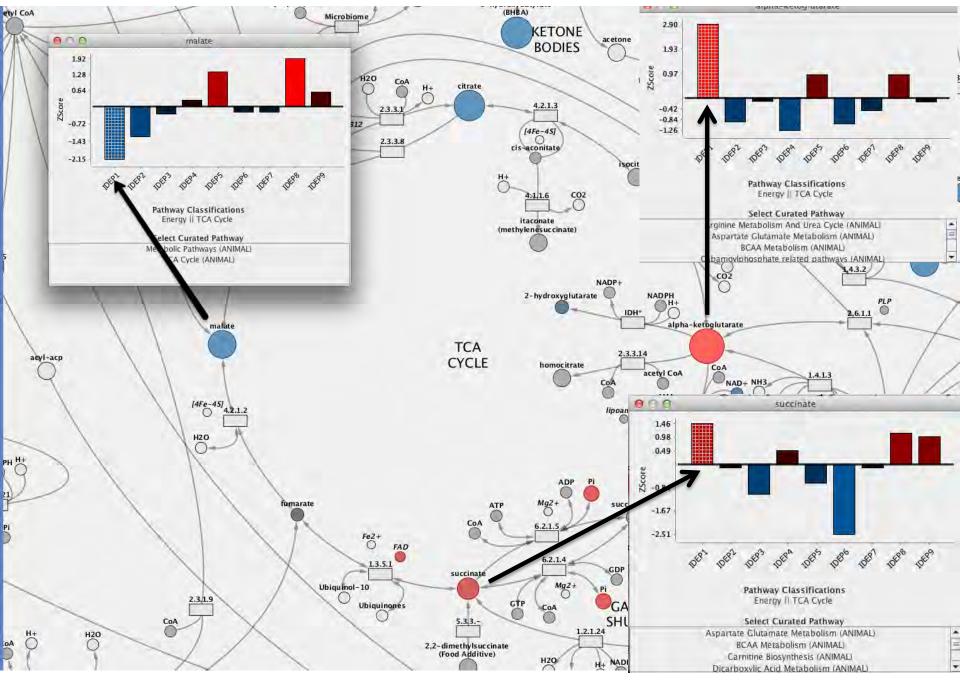


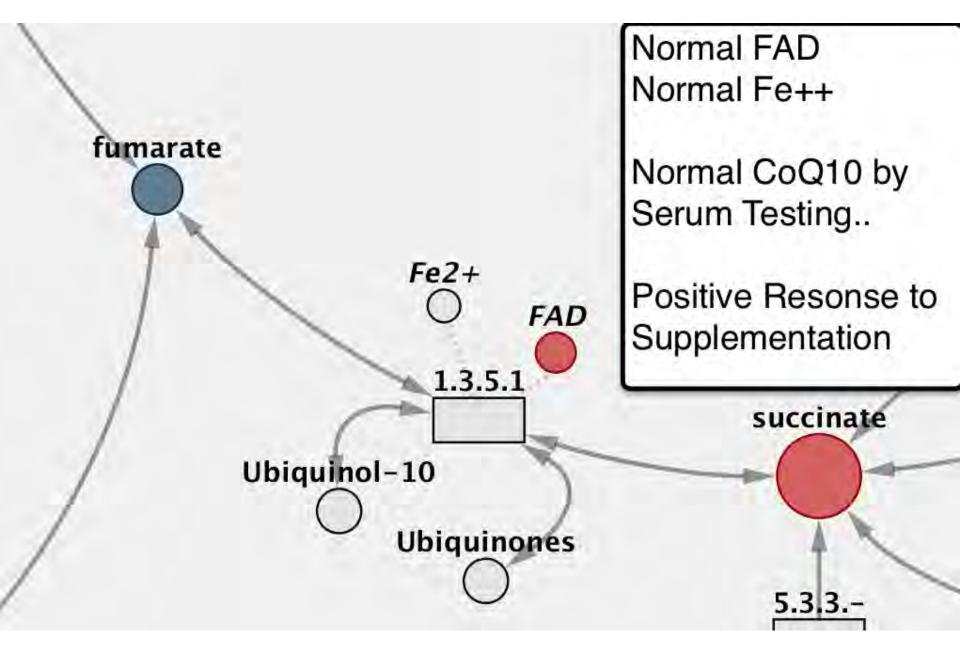


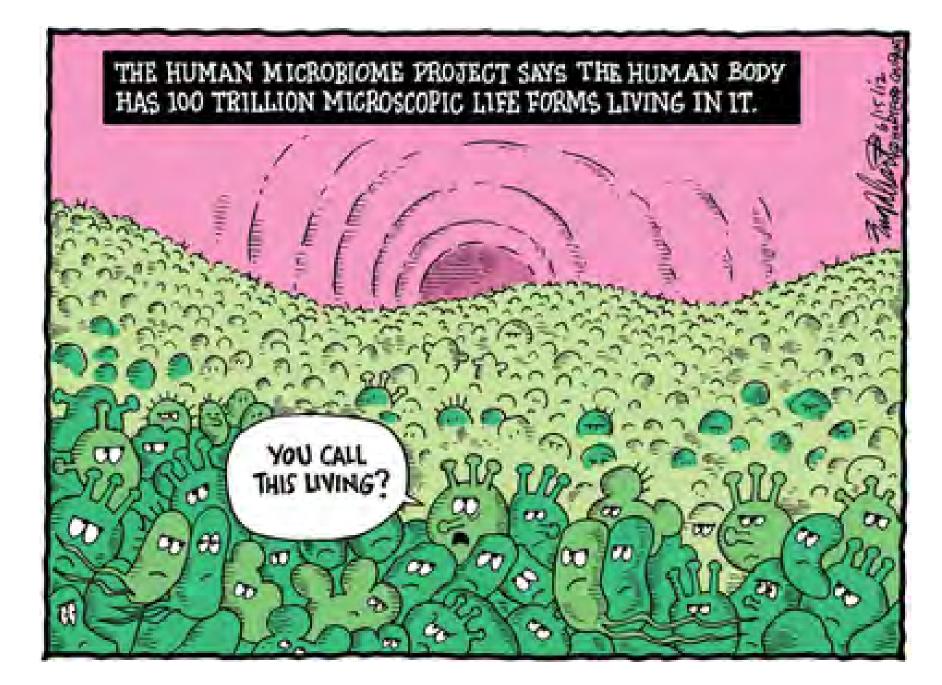




#### TCA cycle organic acid analysis, with cofactors. Where is the Defect?





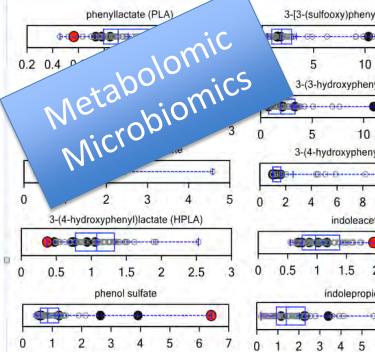


## Comprehensive Coverage of the Microbiome Metabolism

ursodeoxycholate cadaverine deoxycholate Short chain FA: putrescine Metabolomic Microbiomics glycodeoxycholate valerate riboflavin spermidine *ketodeoxycholate* Isovalerate pyridoxine spermine glycolithocholate sulfate *Methylpropionate* folate polyamine taurolithocholate Lipids: vitamins metabolism Lyso-PC, lyso-PE taurolithocholate sulfate lithocholate Monacylglycerol diketolithocholate cholesterol ketolithocholate lipid hvocholate metabolism glycocholenate sulfate +-hydroxyphenylacetate bile acid taurocholenate sulfate\* 3-hydroxyphenylacetate metabolism glycoursodeoxycholate 3,4-dihydroxyphenylacetate tauroursodeoxycholate phenylacetylglutamine phenylacetylglycine 2-(4-hydroxyphenyl)propionate hippurate *3-(3-hydroxyphenyl)propionate* xenobiotic 2-hydroxyhippurate aromatic metabolism <sup>3-hydroxyhippurate</sup> 3-(4-hydroxyphenyl)propionate amino acid 4-hydroxyhippurate 3-phenylpropionate metabolism phenol sulfate 3-hydroxybenzoate 4-hydroxybenzoate 4-hydroxycinnamate lactate indolelactate 3,4-dihydroxybenzoate formate, choline energy indoleacetate 2,4,6-trihydroxybenzoate succinate metabolism metabolism indole-3-carboxylic acid p-hydroxybenzaldehyde glucose methyl-4-hydroxybenzoate n-acetyltryptophan trimethylamine-n-oxide urea 3-indoxyl sulfate 3-(2-hydroxyphenyl)propionate betaine creatine indolepropionate vitexin *dimethylglycine* creatinine skatol daidzein ketoisovalerate indoleacetylglutamine genistein

exclusively or mainly contributed by bacteria metabolism contributed by both mammalian cells and bacteria

#### Gut Bacteria Metabolism



phenyl]propanoic acid	
•••••••••••••••••	Aromatic Amin p-cresol sulfate o-cresol sulfate
10 15 20	3-indoxyl sulfat
yphenyl)propionate	3-(4-hydroxyph 3-(3-hydroxyph
	3-(4-hydroxypheny 4-hydroxypheny
10 15 20 yphenyl)propionate	5-hydroxyindole 3-ethylphenylsu 4-ethylphenysu 4-vinylphenolsu
8 10 12 14 16 bleacetate	indolelactate indoleacetate Indolebutyrate indolepropional indoleacetylglu methyl indole-3 phenylacetylglu
5 2 2.5 3 3.5	phenylactetyigit phenyllactate phenol sulfate
epropionate	

6 7 8 9 10

no Metabolism nenyl)lactate nenyl)propionate Vitamins nenyl)propionate Riboflavin vlacetate eacetate ulfate ulfate ulfate gut bacteria metabolism te tamine 3-acetate utamine Energy Metabolism Lactate succinate alucose

urea creatine Creatinine Lipid Metabolism: Secondary Bile Acids: cholate Isovalerate glycohyocholate Methylpropionate taurodeoxycholate glycodeoxycholate glycolithocholate monacylglycerol glycolithocholate sulfate cholesterol glycohyodeoxycholate hyocholate

valerate

Lyso-PC

lyso-PE

**Choline Metabolism** 

dimethylglycine

betaine

glycocholenate sulfate glycoursodeoxycholate taurocholenate sulfate tauroursodeoxycholate taurolithocholate 3-sulfate Xenobiotic Metabolism: hippurate

2-hydroxyhippurate 3-hydroxyhippurate 4-hydroxyhippurate naringenin

	ID 1	ID 2	ID 3	ID 4	ID 5	ID 6
Biochemical Name	FASTED POPULATION					
phenyllactate (PLA)	0.85	-0.88	-0.42	-0.68	1.1	-1.74
phenylacetate	1.06	0.18	1.67	-0.21	0.35	1.14
4-hydroxyphenylpyruvate	0.62	-0.25	-1.18	0.8	-0.07	-1.41
3-(4-hydroxyphenyl)lactate	-0.99	-2.1	-0.31	-0.88	-0.01	-2.74
phenol sulfate	3.61	2.7	0.93	-0.89	-0.64	4.76
3-[3-(sulfooxy)phenyl]propanoic acid	1.87	1.66	-0.1	0.1	-0.08	2.16
3-(3-hydroxyphenyl)propionate	1.8	0.29	0.72	0.3	-0.62	2,18
3-(4-hydroxyphenyl)propionate	0.61		0.49			1.48
indoleacetate	0.01	-1.07	-0.82	0.37	-0.41	1.73
indolepropionate	0.69	2.42	0.71	1.19	-0.13	2.34

Figure 4. Figure of gut microbial produced biochemicals, heat map of Z-scores where dark red and green are Zscores are significant (p<0.05) and light red and light green are Z-scores trending towards significant (0.05<p<0.1), along with box plots of associated biochemicals as described in Figure 1.

#### Dried Blood Spot Fatty Acid Profiles

Levels of Lipids w-3 w-6 MUFA Saturated FA Trans-FA



Fatty Acid Group	Total	Percentile Rank	Reference Range
Omega-3 Fatty Acids	6.56%	63 rd	2.92-13.29%
Omega 3 Index	6.22%	58 th	2.90-12.90%
Alpha-Linolenic (18:3n3)	0.68%		
Eicosapentaenoic (EPA, 20:5n3)	0.75%		
Docosapentaenoic-n3 (22:5n3)	1.57%		
Docosahexaenoic (DHA, 22:6n3)	3.56%		
Omega-6 Fatty Acids	38.20%	52 nd	26.35-45.15%
Linoleic (18:2n6)	24.41%		
Gamma-Linolenic (18:3n6)	0.28%		
Eicosadienoic (20:2n6)	0.31%		
Dihomo-y-linolenic (20:3n6)	1.66%		
Arachidonic (AA, 20:4n6)	9.72%		
Docosatetraenoic (22:4n6)	1.45%		
Docosapentaenoic-n6 (22:5n6)	0.37%		
cis-Monounsaturated Fatty Acids	21.27%	51st	15.65-32.26%
Palmitoleic (16:1n7)	0.47%		
Oleic (18:1n9)	19.28%		
Eicosenoic (20:1n9)	0.32%		
Nervonic (24:1n9)	1.20%		
Saturated Fatty Acids	33.43%	47 th	29.52-37.74%
Myristic (14:0)	0.40%		
Palmitic (16:0)	19.52%		
Stearic (18:0)	11.72%		
Arachidic (20:0)	0.22%		
Behenic (22:0)	0.70%		
Lignoceric (24:0)	0.87%		
Trans Fatty Acids	0.58%	5 th	0.35-2.69%
Trans Palmitoleic (16:1n7t)	0.10%		
Trans Oleic (18:1t)	0.32%		
Trans Linoleic (18:2n6t)	0.16%		
Trans Fat Index	0.48%	5 th	0.30-2.42%
Ratios			
AA:EPA	13.0:1	56 th	1.4 - 52.6
Omega-6:Omega-3	5.8:1	39 th	2.3 - 14.5

#### Lipomics

Patterns of Carnitine Metabolism

Levels of Lipids Saturated PUFA w-3 w-6 w-9 MUFA

> SCFA MCFA Trans-

VLCFA

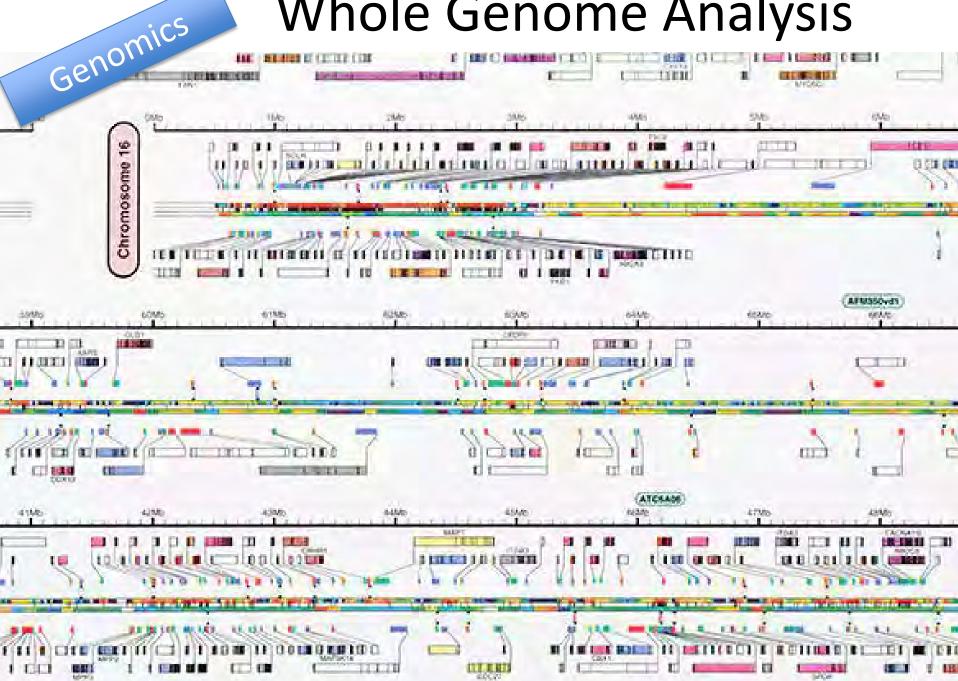
Odd Chain

Renegades

Omega ox'd

-100	-50	0	50	) 1	00		% Status		Result	Low	High
	1				1	16 DMA	58.62	н	1.81	1.34	1.78
						18:0 DMA	-11.20		2.83	2.55	3.26
						18:1 DMA	50.00	н	1.07	0.74	1.07
	l				$\triangleright$	C10:0 Capric	250.00	н	0.0080	0.002	0.004
					i	C14:0 Myristic	-76.85	L	0.18	0.21	0.31
					1	C14:1w5 Myristoleic	-50.00	L	0.0010	0.001	0.003
1	l				1	C15:0 Pentadecanoic	-87.21	L	0.07	0.09	0.13
						C16:0 Palmitic	-102.79	L	17.41	18.54	20.69
					 	C16:1w7 Palmitoleic	-49.06	L	0.09	0.09	0.20
					 	C16:1w9 Hexadecanoic	-45.83	L	0.05	0.05	0.07
I	I				 	C17:0 Heptadecanoic	-60.00	L	0.28	0.29	0.38
Ì					1	C17:1 Heptadecaenoic	-25.00		0.02	0.02	0.03
1						C18:0 Stearic	-68.47	L	14.19	14.57	16.63
					1	C18:1w5 Octadecanoic	-95.45	L	0.00	0.06	0.19
1						C18:1w7 Vaccenic	53.35	н	0.84	0.62	0.83
					i 	C18:1w9 Oleic	34.25	Н	11.87	10.47	12.14
i					LA	C18:2w6 Linoleic	9.03		9.46	7.73	10.65
$\triangleleft$						C18:2w6 Conj Rumenic	-110.00	L	0.02	0.04	0.07
1					ALA	C18:3w3 Alpha Linolenic	-31.25	L	0.09	0.07	0.14
i	İ				GLA	C18:3w6 Gamma Linolenic	92.11	Н	0.05	0.02	0.04
1					1	C20:0 Arachidic	-71.28	L	0.34	0.36	0.46
1					1	C20:2w6 Eicosadienoic	13.33		0.25	0.19	0.28
l					DOLA	C20:3w6 Dihomo-y Lino.	37.02	Н	1.49	0.99	1.56
					l	C20:3w9 Mead	5.00		0.04	0.03	0.04
					AA	C20:4w6 Arachidonic	-6.68		11.87	10.77	13.31
					EPA	C20:5w3 Eicosapenta.	69.46	н	1.19	0.17	1.03
						C22:0 Behenic	-83.42	L	1.38	1.51	1.90
i						C22:1w9 Erucic	0.00		0.05	0.04	0.06
						C22:2w6 Docosadienoic	-46.67	L	0.05	0.05	0.08
1	1				1	C22:4w8 Adrenic	-3.71		2.42	1.88	3.04
					$\triangleright$	C22:5w3 Docosapenta.	131.01	Н	2.75	1.46	2.17
1					 	C22:5w6 Osbond	-56.01	L	0.34	0.36	0.74
	1				DHA	C22:6w3 Docosahexa.	65.33	н	5.02	2.70	4.71
					1	C23:0 Tricosanoic	-90.00	L	0.23	0.26	0.33
<u> </u>						C24:0 Lignoceric	-41.86	L	4.68	4.61	5.53
					$\triangleright$	C24:1w9 Nervonic	167.05	Н	5.48	3.23	4.27
						C24:2w6 Tetracosadienoic	84.02	Н	0.76	0.43	0.67
						C25:0 Pentacosanoic	-46.77	L	0.10	0.09	0.13
i					i 	C26:0 Hexacosanoic	-1.95		0.26	0.22	0.30
1	Î				1	C26:1 Lumequic	31.82	Н	0.26	0.17	0.27
I	1				1	C26:2 Hexacosadienoic	17.31		0.14	0.07	0.17
					1	C28:0 Octacosanoic	-50.00	L	0.0030	0.003	0.005
						C30:0 Triacontanoic	50.00	Н	0.0010	0.000	0.001
						Phytanic	0.00		0.0020	0.001	0.003
						Pristanic	950.00	Н	0.0010	0.000	0.000
$\triangleleft$						Sum C16:1 Trans FAs	-108.06	L	0.02	0.04	0.07
						Sum C18:1 Trans FAs	-95.83	L	0.21	0.47	1.03
					i	Sum C18:2 Trans FAs	-84.00	L	0.06	0.07	0.12

# Whole Genome Analysis



Humans have approximately 10 trillion cells If you were to line all of the DNA found in every cell of a human body it would stretch from the earth to the sun 100 times!



# SNV's

- 6 Billion Nucleotides we sequence ~85%
- SNV's occur one in every 300 nucleotides
- Approximately 20 million in the human genome
- 8000 unique to each person
- If in a exon or regulatory region of a gene can affect the gene function
- Most are Variants of Unknown Significance
- SNPs are SNVs that have >1% prevalence

# Whole Genome Analysis

#### Variant Statistics

	SNVs	Deletions	Insertions
Total Number	3,507,174	271,870	276,245
Number in Genes	1,346,666	116,847	118,650
Number in Exons	47,010	2,898	3,137
Number in Coding Regions	19,759	235	275
Number in UTR	27,251	2,663	2,862
Splice Site Region	2,483	193	216
Stop Gained	79	0	0
Stop Lost	31	0	0
Frameshift	0	111	152
Non-synonymous	10,470	4	7
Synonymous	9,278	0	0

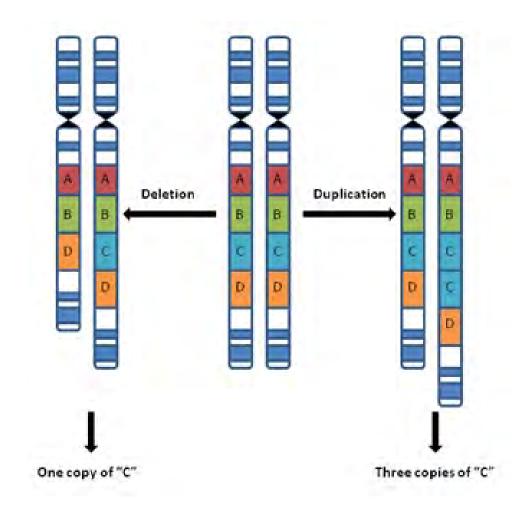
# **Copy Number Variation**

- Accounts for more variation than SNP's
- Deletions, inversions, insertions, and duplications

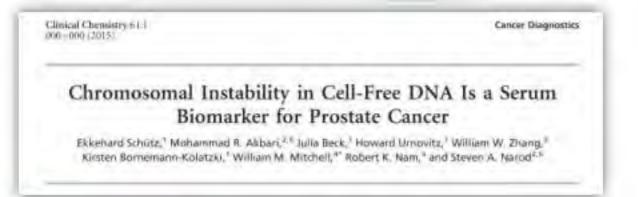
Genomics

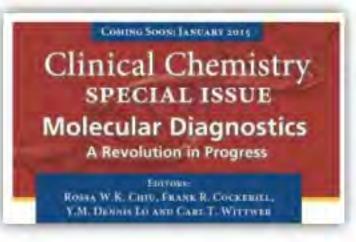
- 0.4% of the genomes of unrelated people differ with respect to copy number variation
- May be inherited or arise during development
- Variable number of tandem repeats
  - Found throughout genome and show variations in length even between related individuals

### **Copy Number Variation**



# Chromosomal Instability score from CNV Genomics as a Cancer Marker

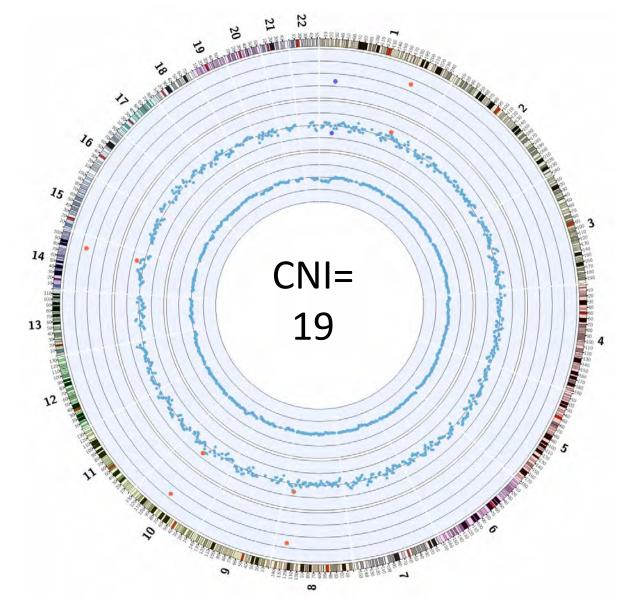




Second Opinion<sup>™</sup> Validation Study published in high impact January 2015 Special Issue "Molecular Diagnostics: A Revolution in Progress"

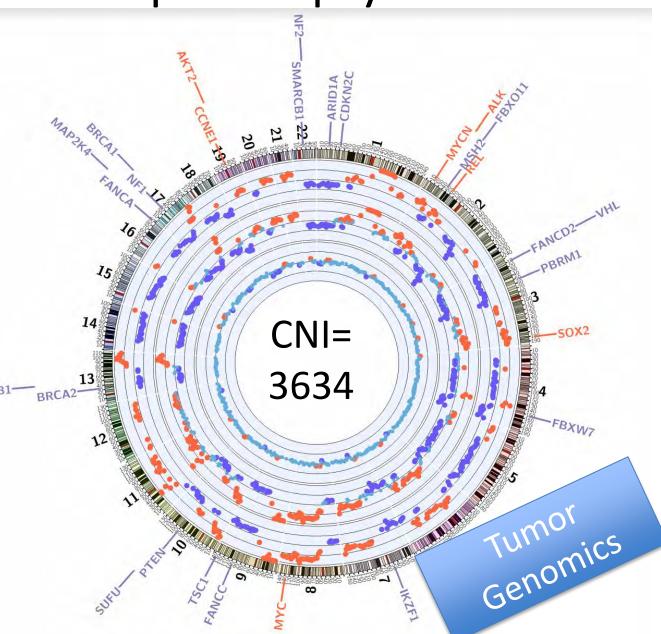
# Tumor Load Liquid Biopsy via Copy Number Instability (CNI)

- Circos Plot
  - Red = gain
  - Blue= loss
- Inner circle-PBMC CNI
- Middle Circle Cell Free DNA CNI (unadjusted)
- Outer Circle CNI remaining after adjustment for PBMC



#### Tumor Load Liquid Biopsy via CNI

- CNI = Copy Number Instability
  - Widely
     Meta static
     Triple
     Negative
     Breast
     Cancer

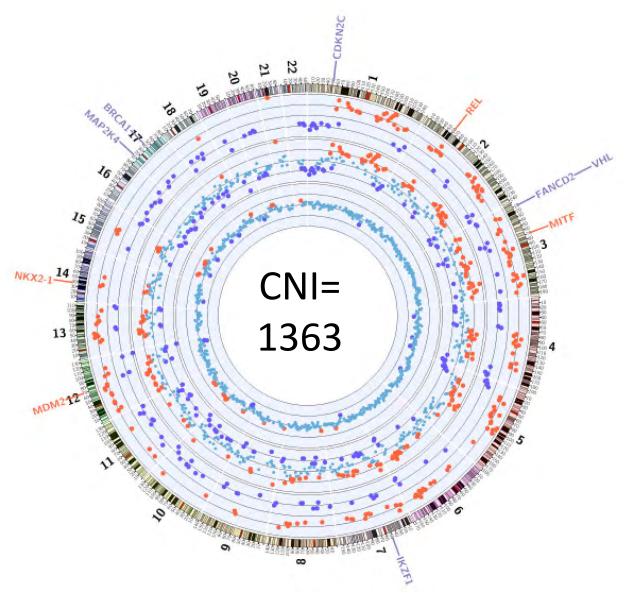


Examples of the role and the effect of deficiency of specific micronutrients on genomic stability

Micronutrients	Role in genomic stability	Consequence of deficiency
Vitamin C, vitamin E	Prevention of oxidation to DNA and lipid oxidation (157,158)	Increased baseline level of DNA strand breaks, chromosome breaks and oxidative DNA lesions and lipid peroxide adducts on DNA (157,158)
Folate and vitamins B2, B6 and B12	Maintenance methylation of DNA; synthesis of dTMP from dUMP and efficient recycling of folate (24)	Uracil misincorporation in DNA, increased chromosome breaks and DNA hypomethylation (24)
Niacin	Required as substrate for poly(ADP-ribose) polymerase (PARP) which is involved in cleavage and rejoining of DNA and telomere length maintenance (61,159)	Increased level of unrepaired nicks in DNA, increased chromosome breaks and rearrangements, and sensitivity to mutagens (61,159)
Zinc	Required as a cofactor for Cu/Zn superoxide dismutase, endonuclease IV, function of p53, Fapy glycosylase and in Zn finger proteins such as PARP (27,28)	Increased DNA oxidation, DNA breaks and elevated chromosome damage rate (27,28)
Iron	Required as component of ribonucleotide reductase and mitochondrial cytochromes (160)	Reduced DNA repair capacity and increased propensity for oxidative damage to mitochondrial DNA (160)
Magnesium	Required as cofactor for a variety of DNA polymerases, in nucleotide excision repair, base excision repair and mismatch repair. Essential for microtubule polymerization and chromosome segregation (50)	Reduced fidelity of DNA replication. Reduced DNA repair capacity. Chromosome segregation errors (50)
Manganese	Required as a component of mitochondrial Mn superoxide dismutase (152,161)	Increase susceptibility to superoxide damage to mitochondrial DNA and reduced resistance to radiation-
Fenech, G	Genome Integr. 2010; 1: 11	induced damage to nuclear DNA (152,161)

### Tumor Load Liquid Biopsy via CNI

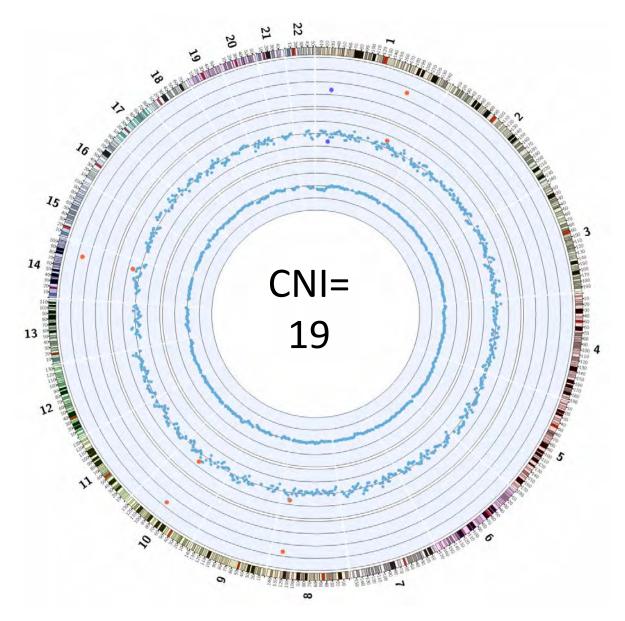
- Colon
   Cancer –
   Stage 2
   before
   resection,
   Chemo,
   Nutrition Rx.
- BRCA1 loss
- Curcumin,
- 3-6 Beta Glucan,
- w-3 oils,
- WGE- whole glucan extract



#### Tumor Load Liquid Biopsy via CNI

- Colon

   Cancer –
   Stage 2 after
   resection,
   chemo,
   Nutrition Rx.
- CNI down from 1363 to 19.



# **Clinical Presentation:**

- 55 yo male CEO –
- Fatigue, Exercise Intolerance, Brain Fog, Joint Pain, Irritability, Insomnia, Hyperlipidemia
- PastDx: Hashi, Arthritis, Asthma
- FHx: M-Lung Cancer; F Dementia
- Organic whole-food, gluten & dairy-free diet, Meditates, 10 hrs in Bed (!!!), Exercises as best as possible, Low Caffeine, Stable relationships, Has hobbies and positive mindset.
- Elevated Liver Enzymes- but why?

#### 23&Me derivitive "Detox" Report

GSTP1 I105V	rs1695	AA	-/-
GSTP1 A114V	rs1138272	СС	-/-
SOD2 A16V	rs4880	GG	+/+
NAT1 R187Q	rs4986782	GG	-1-
NAT1 R64W	rs1805158	СС	-/-
NAT2 I114T	rs1801280	СТ	+/-
NAT2 R197Q	rs1799930	GG	-1-
NAT2 G286E	rs1799931	GG	-/-
NAT2 R64Q	rs1801279	GG	-/-
NAT2 K268P	rs1208	AG	+/-



#### And no GSTM data

# **Copy Number Variations**

Gain/Loss	CytoBand	Location	Size (bp)	# Probes	Ratio	Genes
LOSS	1q44	chr1:248756215- 248790932	34,717	6	0.58	OR2T10, OR2T11
LOSS	3q26.1	chr3:162514534- 162619141	104,607	13	0.61	
LOSS	4q13.2	chr4:69360187-69512319	152,132	31	0.78	TMPRSS11E, UGT2B17, UGT2B15
LOSS	5p15.33	chr5:702100-820424	118,324	14	0.59	ZDHHC11
LOSS	5p15.2	chr5:12677352-12735332	57,980	6	0.53	
LOSS	6p21.32	chr6:32485374-32551409	66,035	15	0.65	HLA-DRB5, HLA-DRB6, HLA- DRB1
GAIN	8p23.1	chr8:6639145-6949625	310,480	35	1.43	XKR5, DEFB1, DEFA6, DEFA4, DEFA10P, DEFA1, DEFA1B, DEFA3, DEFA5
LOSS	8p11.22	chr8:39233204-39371728	138,524	26	0.74	ADAM5P, ADAM3A
LOSS	9p23	chr9:12031727-12163289	131,562	14	0.53	
GAIN	11q13.2	chr11:67479305-67750341	271,036	20	1.23	LOC645332
LOSS	12p13.31	chr12:9637084-9713425	76,341	9	0.44	
LOSS	15q11.1 - q11.2	chr15:20549990-22589756	2,039,766	82	0.75	GOLGA6L6, GOLGA8C, BCL8, POTEB, NF1P1, LOC646214, CXADRP2, LOC727924, OR4M2 OR4N4, OR4N3P
GAIN	16p11.2 - p11.1	chr16:34468000-34756866	288,866	39	1.83	LOC283914, LOC146481
GAIN		cnr21:10/51620-10916406	164,786	17	1.32	IFIE
	p11.1		2.6 - 27 - 6.8	1		
LOSS	22q11.23	chr22:24347959-24395353	47,394	17	0.36	LOC391322, GSTT1, GSTTP2

- Copy Number Variation Analysis revealed LOSS of GSTT1
- Targeted SNP testing revealed NULL GSTM

#### Markedly Elevated Aflatoxin IgG+IgA

TEST		RE	SULT	
Array 11 Chemical Immune Reactivity Screen	IN RANGE (Normal)	EQUIVOCAL*	OUT OF RANGE	REFERENCE (ELISA Index)
Aflatoxins IgG+IgA			2.69	0.4-1.8
Aflatoxins IgM	1.14			0.1-1.9
Formaldehyde and Glutaraldehyde IgG+IgA	0.72			0.3-1.4
Formaldehyde and Glutaraldehyde IgM	0.91			0.1-1.8
Isocyanate IgG+IgA	0.70			0.1-1.1
Isocyanate IgM	0.85			0.1-1.2
Trimellitic and Phthalic Anhydrides IgG+IgA	0.63			0.1-1.3
Trimellitic and Phthalic Anhydrides IgM	0.92			0.1-2.0
Benzene Ring Compounds IgG+IgA	0.65			0.2-1.3
Benzene Ring Compounds IgM	0.80			0.1-1.6
BPA Binding Protein IgG+IgA	0.87			0.2-1.8
BPA Binding Protein IgM	1.04			0.1-1.8
Bisphenol A IgG+IgA	0.66			0.1-1.8
Bisphenol A IgM	0.88			0.1-2
Tetrabromobisphenol A IgG+IgA	0.74			
Tetrabromobisphenol A IgM	0.65			0.1-20 JNOtOXO
Tetrachloroethylene IgG+IgA	0.79			noton
Tetrachloroethylene IgM	1.90	5	<u> </u>	

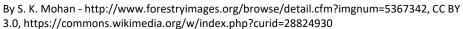
# Aspergillus







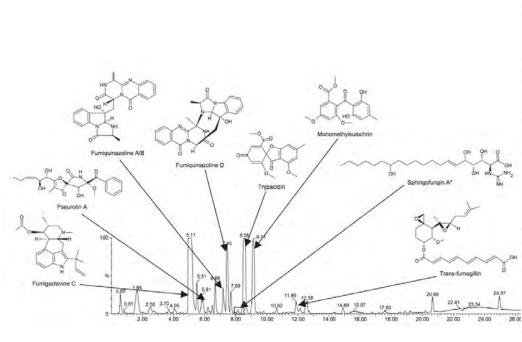






#### Metabolomics of Aspergillus fumigatus

Spinulosin Spinulosin hydrate Spinulosin quinol-hydrat Dihydrospinulosin quino Phyllostine Orsellinic acid Orcinol m-cresol 3,4-dihydroxytoluquinone 4-hydroxy-3-methoxytoluquinone 3-hydroxytoluguinone 3,6-dihydroxytoluquinone 3-hydroxy-4-methoxy-Toluquinone 1,6-epoxide 4-carboxy-5,5'-dihydroxy-3,3'-dimethyldiphenyl Fumiquinone A Fumiquinone B Trypacidin Bisdechlorogeodin Monomethylsulochrin Sulochrin-2'-methylether Asperfumin Asperfumoid Emodin Physcion 2-chloroemodin 2-chloro-1,3,8-trihydroxy-6-methylanthrone 2-chloro-1,3,8-trihydroxy-6-hydroxymethylanthrone YWA1 1,3,6,8-THN Flaviolin Scytalone 1,3,8-THN 2-HJ Vermelone 1,8-DHN Sphingofungin A-D Sphingofungins E-F? Fumifungin Pseurotin A-E 8-O-demethylpseurotin A Synerazol RK-95113 Azaspirene? FD-839 Pseurotin F2 Ergosterol Ergosterolperoxide Ergosterolpalmitat 24-methylenophenol Ergosta-4,6,8(14),22-tetraen-3-one Ergosta-4,22-diene-3β-ol 5α,8α-Epidioxy-ergosta-6,22-diene-3B-ol Helvolic acid Helvolinic acid 7-desacetoxyhelvolic acid



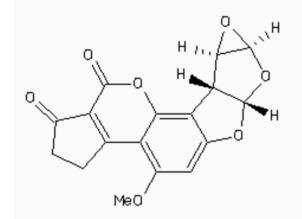
Metabolic signatures are possible to elucidate via metabolomics this guides diagnostic as well as treatment decisions.

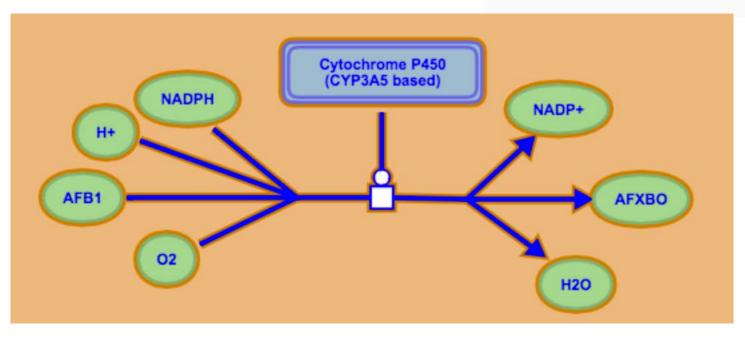
5-Demethoxyfumagillol Fumagiringillin FR-111142 Sch528647 RK-95113 **Ovalicin?** β-trans-bergamotene Hexahydropolyprenyls A-E Phthioic acid Teichoic acid bis(2-hydroxy-3-tert. butyl-5-Methylphenyl)methane (= GERI-BP002-A)Fusigen Ferrichrome Gliotoxin Gliotoxin E Gliotoxin G S-methylgliotoxin bisdethiobis(methylthio)-Gliotoxin Agroclavine Elymoclavin Chanoclavine I Festuclavin Fumigaclavine A-C Brevianamide F Fumitremorgin A-C Verruculogen 15-acetoxyverruculogen Demethoxyfumitremorgin C 12,13-dihydroxyfumitremorgin C (= TR-3) 12,13-dihydrofumitremorgin C **TR-2** Cyclotryprostatin A-D Dehydrotryprostatin Tryprostatin A & B Spirotryprostatin A & B 'Compound 6' Alanyl-leucyl and alanyl-isoleucyl, prolyl-phenylalanyl, prolyl-glycyl, prolyl-prolyl, prolyl-valyl, 4hydroxyprolyl-leucyl, 4-hydroxyprolyl-phenylalanyl, and prolyl-leucyl diketopirazines Pyripyropene A-R GERI-BP001-A Fumiquinazoline A-G Tryptoquivaline? Nortryptoquivaline? Tryptoquivaline E-N?

Restrictocin Mitogillin Asp F1

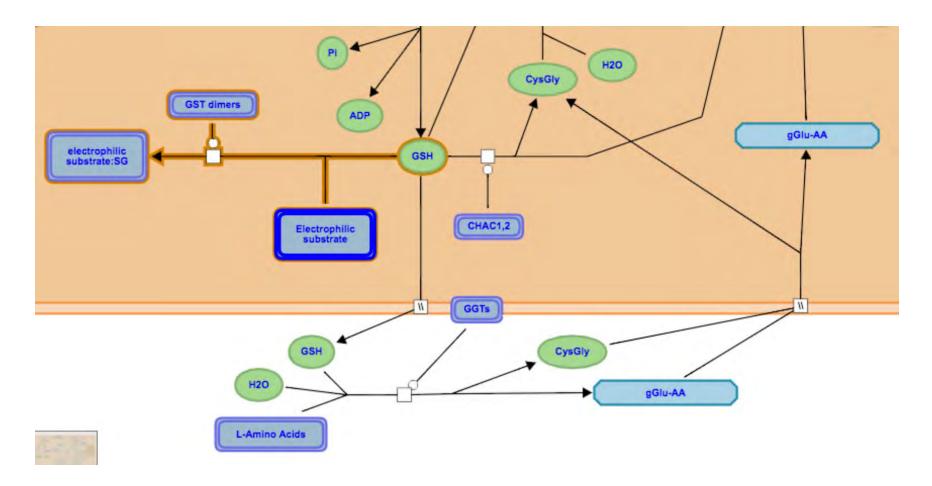
#### Aflatoxin B1 (2,3-Epoxyaflatoxin B1)

Conversion is by CYP-1A2 and CYP-3A4 and CYP-2A13



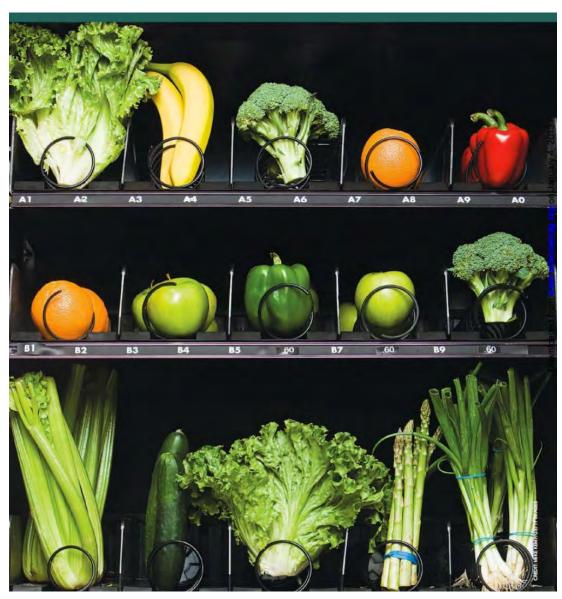


# Glutathione Congugates to Electrophilic Substrates via GSTT1



http://www.reactome.org/PathwayBrowser/#/R-HSA-156580&SEL=R-ALL-176070&PATH=R-HSA-1430728,R-HSA-211859&DTAB=MT

#### More "Good Stuff"



### Sulforaphane

Upregulates NRF-2 and PGC-alpha. This in turn...

- increases
  - Superoxide dismutase
  - Catalase
  - glutathione Stransferase
  - expression of heme oxygenase-1
- reduces
  - reactive oxygen species
  - lipid peroxidation
  - COX-2 expression

Fernandez, Mol Cell Biochem, DOI 10.1007/s11010-014-2292-z

Article

Effects of airborne Aspergillus on serum aflatoxin BI and liver enzymes in workers handling wheat flour Human and Experimental Toxicology 1–7 © The Author(s) 2015 Reprints and permission: sagepub.co.uk/journalsPermissions.nav DOI: 10.1177/0960327115573596 het.sagepub.com ©SAGE

A Saad-Hussein<sup>1</sup>, MM Taha<sup>1</sup>, NN Fadl<sup>2</sup>, A-H Awad<sup>3</sup>, H Mahdy-Abdallah<sup>1</sup>, G Moubarz<sup>1,4</sup>, H Aziz<sup>1</sup> and KA El-Shamy<sup>2</sup>

**Table 2.** Comparison of the AFB<sub>1</sub>-Alb levels and the liver enzymes between the milling workers, the bakers, and their controls.

	Contro	ls (100)	Milling wo	rkers (100)	Baker	ANOVA	
	Mean	SD	Mean	SD	Mean	SD	p Value
AFB1-Alb (ng/g) Liver enzymes	0.04 <sup>a,b</sup>	0.008	0.06 <sup>c</sup>	0.003	0.10	0.01	p < 0.0001
AST (U/L) ALT (U/L)	16.2 <sup>a,b</sup> 18.2 <sup>a,b</sup>	10.9 7.56	26.5 37.5	8.70 10.66	26.0 37.6	8.33   . 4	p < 0.05 p < 0.0001
ALP (IU/L)	77.4 <sup>b</sup>	24.50	76.7 <sup>c</sup>	25.71	90.0	32.11	p = .05

LSD: least significant difference; AFB<sub>1</sub>: aflatoxin B<sub>1</sub>; Alb: albumin; ANOVA: analysis of variance; AST: aspartate aminotransferase; ALT: alanine aminotransferase; ALP: alkaline phosphatase.

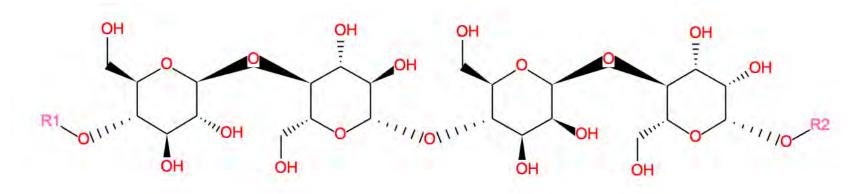
<sup>a</sup>According to LSD, significant difference between the controls and the milling workers.

<sup>b</sup>According to LSD, significant difference the controls and the bakers.

<sup>c</sup>According to LSD, significant difference between the milling workers and the bakers.



### Glucomannan



- In rats fed high fat diet KGM beneficially reduced
  - malondialdehyde levels of the colon and liver
  - DNA damage in blood lymphocytes
- Upregulated gene expressions of
  - colonic mucosa glutathione peroxidase and catalase
  - hepatic superoxide dismutase and catalase

Wu & Chen, dx.doi.org/10.1021/jf202060p |J. Agric. Food Chem. 2011, 59, 9194–9200

### Effect of Glucomannan on Mycotoxins

- Effect of glucomannan on haematological, coagulation and biochemical parameters in male rabbits fed aflatoxin-contaminated ration. –
  - » A. Eisa and A Metwally World Mycotoxin Journal 2011
  - Human studies of this would be unethical
  - 3 groups
    - Normal Chow
    - Chow spiked with naturally occuring levels of aflatoxin
    - Spiked chow with 1kg/ton glucomannan

## Effect of glucomannan on Mycotoxins

- Results..
  - Aflatoxin B1 (AFB1) spiked chow caused microcytic anemia, leukopenia, long PT and aPTT, elevated ALT, GGT, Total Bilirubin, BUN, Creatinine, total lipids and cholesterol. Decreased Protein, Albumin, glucose, calcium, phosphorous, and iron.
- Supplementation with glucomannan resulted in the return of the above parameters to normal control values.

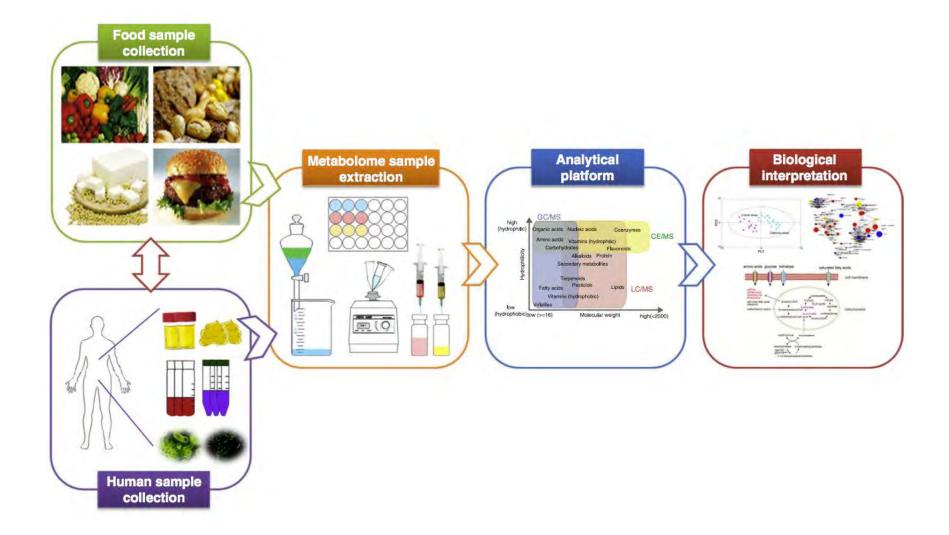
### Glucomannan and Aflatoxin B1 and T-2 Toxin

- 0.1% Glucomannan in feed was able to adsorb
  - 75-90% of Aflatoxin (Aspergillus)
  - 30-35% of T2 Toxin (fusarium)
- The longer time Glucomannan was present in the gut, the more Mold Toxins were adsorbed.





Murthy, et. al. "Evaluation of glucomannan for its adsorbing ability of Aflatoxin B1 and T-2 Toxin in the gastrointestinal tract of boiler chickens" Mycotoxin research, Volume: 18 Issue: Supplement 1, 2002 March.



### "Susan"

Since 2008, I have had chronic fatigue, Pain and brain fog, neuropathy and weakness. I have been to a large amount of specialist who do not communicate with each other and only prescribe more

led for all of these years with SUGOL. T poglicemia. I & last my wil live December as I felt my as so poor and there privonani 20 sc

### "Susan" - Outside MD Note

#### History of Present Illness:

History of Present Illness provided by patient.

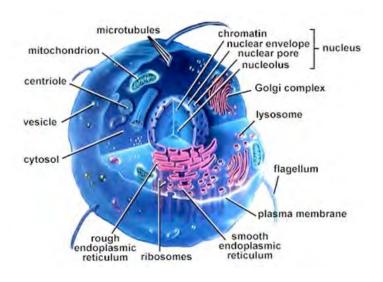
Abdominal pain over the past 9 years, 5 hospitalizations in 2015. GI consultant felt that this is going to be a recurrent situation over the rest of her life. Attributed to damage from cancer treatment. After meditation, prayer and reflection she went to work on diet and was advised to see psychologist to deal with PTSD and work on diet and yoga. She is eating very healthily. Daily wakes with feeling of being "hung-over: - dizziness, light-headedness, fatigue, dread, nausea with occasional vomiting, dehydration feeling, Persistent constipation - she has now increased her matural laxative) - 8 per day reliably results in daily BM. Dr. Economic suggested getting another opinion - EGD with gastritis and colonoscopy with internal hemorrhoids. Using CPAP nightly with good benefit. Tired of quality of life. Feels that Savella is helping with fibromyalgia pain. Brain function better with Savella compared to Cymbalta. Botox shots for migraines from Dr and the seem to help

Tramadol helps with pain without causing sedation or disorientation.

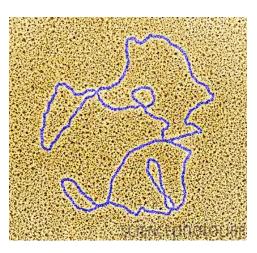
### • Tx: Tylenol, Tramadol, Miralax

DEDAILS	-		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1			
3590H1	CK	213	+ U/1	< 170		****************
250117	(TTA - TA					
3591H1	CKMB	37	+ 0/1	< 25	0	****************

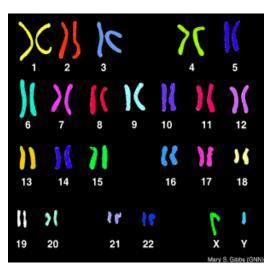
## Mito Genetics – The Basics

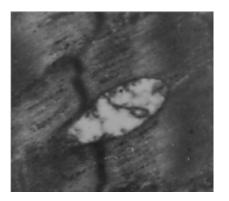


#### Mitochondrial DNA



#### Nuclear DNA





37 genes 16,000 base pairs

- Maternal inheritance
- 13 proteins for
   OxPhosphorylation
- 22 transfer RNAs
- 2 ribosomal RNAs

1,013 genes

- Autosomal recessive
- Autosomal dominant
- X-linked



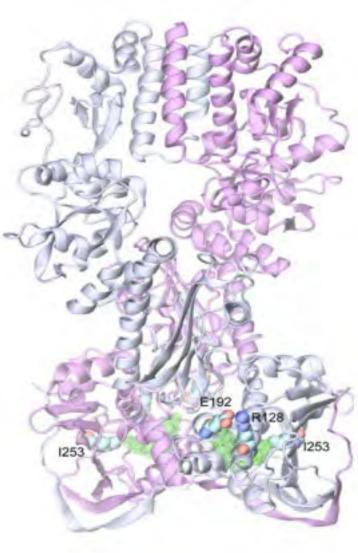
Hurt, tired and queasy: Specific variants in the ATPase domain of the *TRAP1* mitochondrial chaperone are associated with common, chronic "functional" symptomatology including pain, fatigue and gastrointestinal dysmotility



Richard G. Boles<sup>a,\*</sup>, Holly A. Hornung<sup>a</sup>, Alastair E. Moody<sup>a</sup>, Thomas B. Ortiz<sup>a</sup>, Stacey A. Wong<sup>a</sup>, Julie M. Eggington<sup>a</sup>, Christine M. Stanley<sup>a</sup>, Mu Gao<sup>b</sup>, Hongyi Zhou<sup>b</sup>, Stephen McLaughlin<sup>a</sup>, Amir S. Zare<sup>a</sup>, Katherine M. Sheldon<sup>a</sup>, Jeffrey Skolnick<sup>b</sup>, Kevin J. McKernan<sup>a</sup>

### TRAP1-Related Disease (T1ReD)

- TRAP1 encodes a 701-amino acid homodimer protein which is a mitochondrial chaperone involved in antioxidant defense.
- An ATPase domain (amino acids 108-260) hydrolyze the energy-rich triphosphate bond of ATP to convert into mechanical work of folding proteins.



Boles RG1, Hornung HA1, Moody AE, et al. Hurt, tired and queasy: Specific variants in the ATPase domain of the TRAP1 mitochondrial chaperone are associated with common, chronic "functional" symptomatology including pain, fatigue and gastrointestinal dysmotility. Mitochondrion. 2015 Jul;23:64-70. doi: 10.1016/j.mito.2015.05.002.

### TRAP1-Related Disease (T1ReD)

- Chronic pain, Fatigue and GI dysmotility.
- Tachycardia/palpitations and dizziness may also be common.
- In these patients, chronic pain and fatigue improved greatly on aggressive antioxidant therapy.

Boles RG1, Hornung HA1, Moody AE, et al. Hurt, tired and queasy: Specific variants in the ATPase domain of the TRAP1 mitochondrial chaperone are associated with common, chronic "functional" symptomatology including pain, fatigue and gastrointestinal dysmotility. Mitochondrion. 2015 Jul;23:64-70. doi: 10.1016/j.mito.2015.05.002.

# *TRAP1* variants greatly increase the prevalence of functional disease

<i>TRAP1</i> variants	Pain syndromes	Chronic fatigue	Gastro- intestinal dysmotility	Triad of pain, fatigue & GI	Total number of patients
All conserved in ATPase domain	17 (65%) 4.9 (2.2-11) P = 0.001	16 (62%) 3.3 (1.5-7.3) P = 0.004	14 (54%) 3.1 (1.4-6.8) P = 0.005	12 (46%) 6.4 (2.9-14) P < 0.0001	26
Conserved elsewhere in protein	3 (7%) 0.19 (0.06-0.61) P = 0.005	10 (22%)	11 (24%)	2 (4%)	45
p.lle253Val	11 <mark>(69%)</mark> 5.7 (2.0-17) P = 0.001	10 <mark>(63%)</mark> 3.4 (1.2-9.4) P = 0.02	9 <mark>(56%)</mark> 3.4 (1.2-9.2) P = 0.02	8 (50%) 7.5 (2.8-20) P = 0.0001	16
Conserved in ATPase excluding p.lle253Val	7 (64%) 4.6 (1.3-1.6) P = 0.02	7 (64%) 3.6 (1.0-1.2) P = 0.04	6 (55%) <i>P</i> = 0.06	5 (45%) 6.2 (1.9-21) P = 0.003	11
Salt bridges: p.Arg128His, p.Glu192Lys	5 <mark>(71%)</mark> 6.5 (1.3-34) P = 0.03	5 <mark>(71%)</mark> P = 0.053	5 (71%) 6.6 (1.3-34) P = 0.02	5 (71%) 18 (3.6-100) P = 0.0005	7
None	224 (28%)	266 (33%)	222 (27%)	95 (12%)	<b>808</b> 86

### "Susan" TRAP-1 Hetero

#### TRAP1 - TNF RECEPTOR-ASSOCIATED PROTEIN 1, NM 016292.2 (OMIM® ID: 606219) ACMG score 3 Variant 1 (chr16.hg19.g.3740911G>A) c.164C>T p.Ala55Val Heterozygous One variant of uncertain significance was identified in this gene. This gene is associated with Interpretation autosomal recessive and autosomal dominant disease. Clinical correlation is indicated. Associated disease TRAP1-Related Disease (T1ReD) Autosomal Dominant or Autosomal Disease inheritance Recessive Associated literature PMID 10652318 HSP90 proteins are highly conserved molecular chaperones that have key roles in signal transduction, protein folding, protein degradation, and morphologic evolution. HSP90 proteins Gene product/protein function normally associate with other cochaperones and play important roles in folding newly synthesized proteins or stabilizing and refolding denatured proteins after stress. TRAP1 is a mitochondrial HSP90 protein. Variant of uncertain significance Prevalence: Rare (0.00% in 1000G; 0.01% in ESP6500 (max subpopulation freq: 0.01%); 0.00% in ExAC (max subpopulation freq: 0.01%)); Evolutionary Variant 1 Classification Conservation: Low; Algorithms of protein function: SIFT: equivocal, Mutationassessor: benign, Polyphen2: benign, MutationTaster: deleterious

### DNA Oxidation Marker: 8-OH DG and Elevated CK in "Susan"

3590H1	CK	213	+ U/1	< 170	 *********
3591H1	CKMB		+ 0/1	< 25	*********

#### Oxidative Damage and Antioxidant Markers

(Vitamin C and other antioxidants)

28. p-Hydroxyphenyllactate

29. 8-Hydroxy-2-deoxyguanosine

(Units for 8-hydroxy-2-deoxyguanosine are ng/mg creatinine)



- Context: Organic, "Ideal" diet.
- Tx:
  - Sulphoraphane Glucosinolate, Resveratrol, Curcumin, - All High dose
  - NAC 1200 BID, ALA- 600 mg BID, CoQ10 50mg BID



### 8-OHDG Follow-up "Susan"

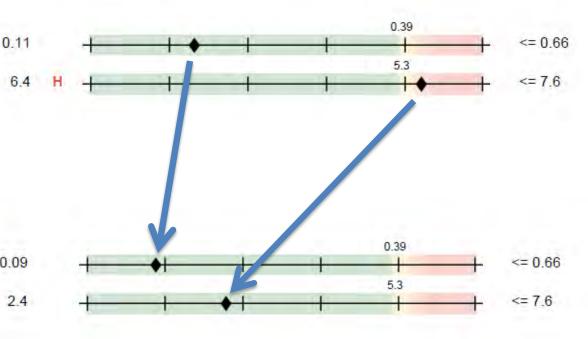
#### Oxidative Damage and Antioxidant Markers (Vitamin C and other antioxidants)

- 28. p-Hydroxyphenyllactate
- 29. 8-Hydroxy-2-deoxyguanosine
- (Units for 8-hydroxy-2-deoxyguanosine are ng/mg creatinine)

#### Oxidative Damage and Antioxidant Markers (Vitamin C and other antioxidants)

- 28. p-Hydroxyphenyllactate 0.09
- 29. 8-Hydroxy-2-deoxyguanosine

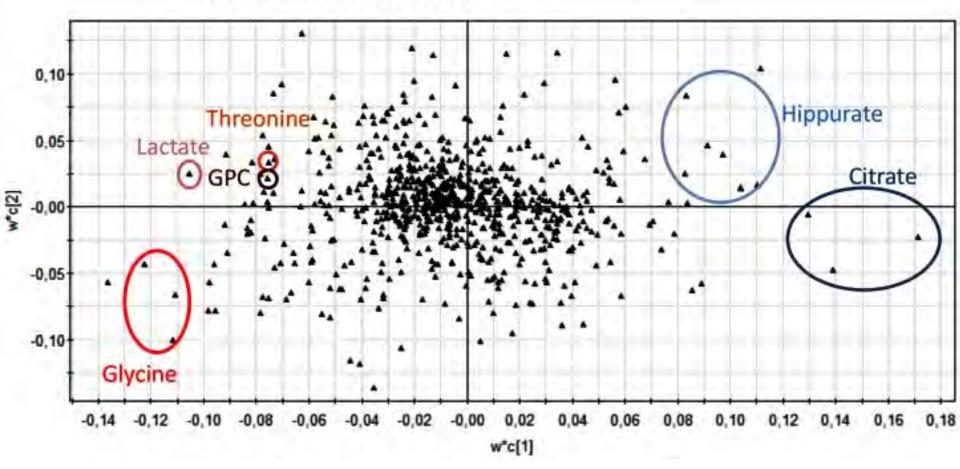
(Units for 8-hydroxy-2-deoxyguanosine are ng/mg creatinine)



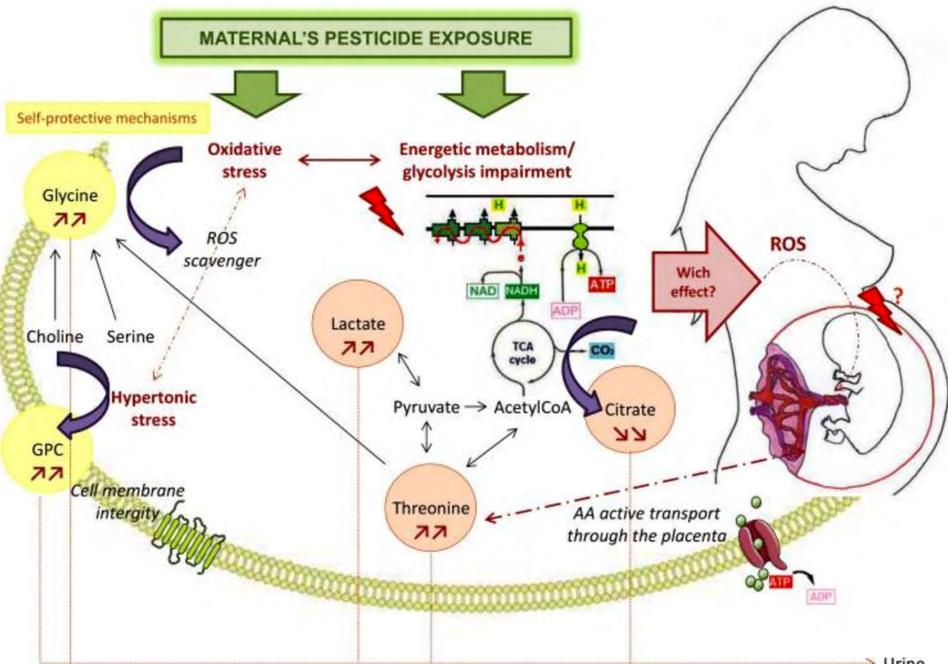
 Subsequent to this... 50 gm IV vitamin C twice a week has been very helpful.

## Metabolomics Tools for Describing Complex Pesticide Exposure in Pregnant Women in Brittany (France)

Cereal\_Group\_PW11\_OSC-PAR8.M1 (PLS-DA),PAR w\*c[Comp.1]w\*c[Comp.2] Colored accordinf to model terms



Bonvallote, Metabolomics role for assessing complex Pesticide Exposure, PLoS One. 2013; 8(5): e64433.



Bonvallote, Metabolomics role for assessing complex Pesticide Exposure, PLoS One. 2013; 8(5): e64433.

Urine

#### Integrated <sup>1</sup>H NMR-based metabolomics analysis of earthworm responses to sub-lethal Pb exposure

Ting Chen <sup>A</sup> , Yan Liu <sup>A</sup> , Ming-Hui Li <sup>A</sup> , Hua-Dong Xu <sup>A</sup> , Ji-Yang Sheng <sup>A</sup> , Li Zhang <sup>A B</sup> and Jun-Song Wang A B

<sup>A</sup> Centre for Molecular Metabolism, School of Environmental and Biological Engineering, Nanjing University of Science and Technology, Nanjing 210094, China.

<sup>B</sup> Corresponding authors. Email: wang.junsong@gmail.com; njust\_zhangli@163.com

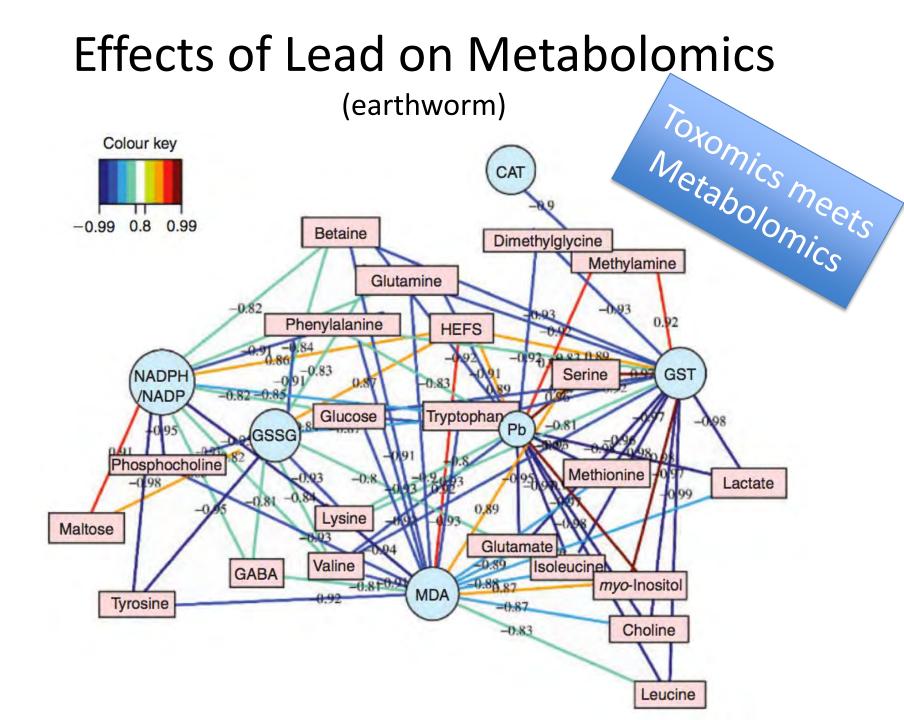
*Environmental Chemistry* - http://dx.doi.org/10.1071/EN15192 Submitted: 16 September 2015 Accepted: 5 February 2016 Published online: 23 March 2016

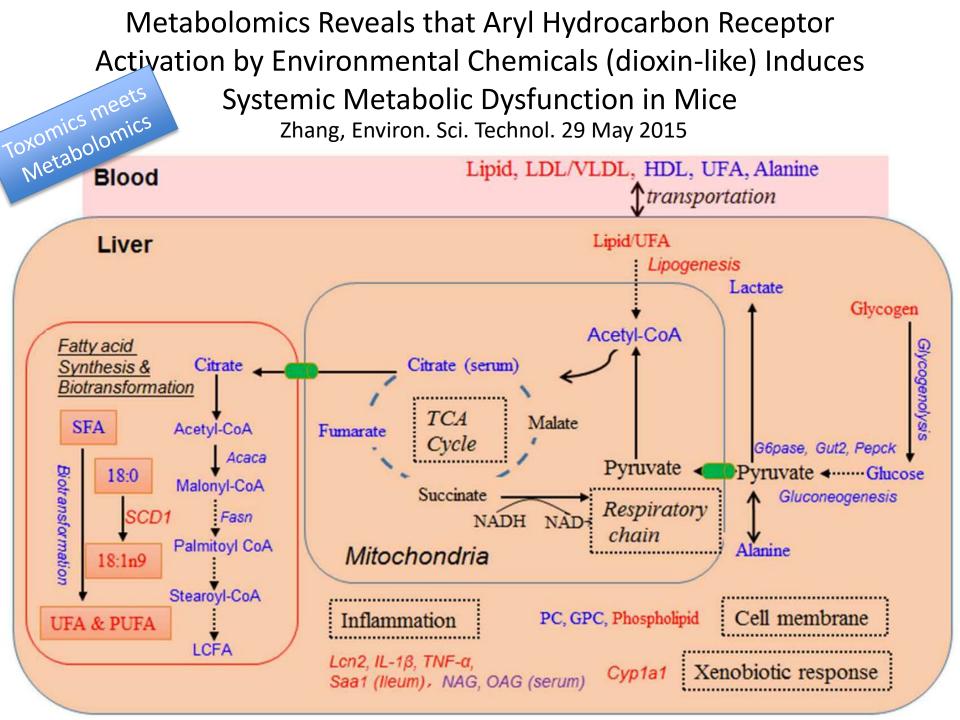
... "Pb exposure in earthworms caused widespread metabolic changes, which were associated with oxidative stress, neurotransmitter imbalance, disruption of osmotic equilibrium and interference in energy metabolism and nucleic acid metabolism."

#### Table 1. Metabolites identified from the aqueous earthworm tissue extracts, their fold change values (control v. low, control v. medium and control v. high) and associated P values

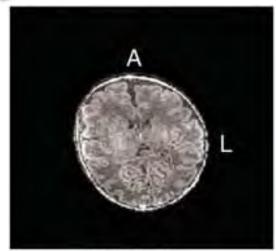
HEFS, 2-hexyl-5-ethyl-3-furansulfonate; GABA, 4-aminobutyrate. Multiplicity: s, singlet; d, doublet; t, triplet; q, quartet; m, multiplet. Colour coded according to log<sub>2</sub>(fold change value), red for decrease and blue for increase in Pb-exposed groups.\*, *P* < 0.05; \*\*, *P* < 0.01; \*\*\*, *P* < 0.001

Metabolites	Assignments	Chemical shift (ppm)	Contro	l v. low	Control	v. medium	Control v. high		
			Fold	Р	Fold	Р	Fold	Р	
				-1	-0.5	0 0.5	1		
HEFS	3	0.85 (t), 2.60 (m), 2.83 (t)	0.92		0.80	*	0.57	**	
Leucine	δ-CH <sub>3</sub> , δ-CH <sub>3</sub>	0.95 (d), 0.96 (d)	1.05		1.11	*	1.99	***	
Isoleucine	δ-CH <sub>3</sub> , γ-CH <sub>3</sub>	0.94 (t), 1.00 (d)	1.09	*	1.16	*	1.76	***	
Valine	$\gamma$ -CH <sub>3</sub> , $\gamma$ -CH <sub>3</sub>	0.98 (d), 1.04 (d)	1.06		1.21	**	1.64	***	
Lactate	CH <sub>3</sub>	1.43 (d)	1.04		1.06		1.25	**	
Lysine	CH <sub>2</sub>	1.71 (m)	1.06		1.16	*	1.24	**	
GABA	CH <sub>2</sub>	1.91 (m)	0.94		1.12	*	1.18	*	
Glutamate	CH <sub>2</sub>	2.05 (m)	1.07		1.09	*	1.26	**	
Glutamine	CH <sub>2</sub>	2.14 (m)	1.05		1.06		1.13	*	
Methionine	CH <sub>2</sub>	2.13 (m)	1.08	*	1.16	*	1.69	**	
Choline	CH <sub>3</sub>	3.20 (s)	1.09	*	1.24	*	2.91	***	
Phosphocholine	CH <sub>3</sub>	3.21 (s)	1.08	*	1.16	*	1.22	**	
Betaine	CH <sub>2</sub> , CH <sub>3</sub>	3.25 (s), 3.89 (s)	1.07		1.27	**	1.90	***	
Dimethylglycine	CH <sub>2</sub>	3.71 (s)	1.05		0.99		1.13	*	
Serine	CH <sub>2</sub>	3.95 (m)	0.93		0.89	*	0.75	**	
myo-Inositol	СН	3.54 (dd), 3.63 (t), 4.07 (t)	0.84	*	0.74	**	0.47	***	
Glucose		3.45-3.50 (m), 4.65 (d)	1.10	*	1.29	*	1.73	***	
Maltose	CH	5.41 (d)	0.91	*	0.88	*	0.89	*	
Tyrosine	-CH=	6.90 (m), 7.20 (m)	1.05	*	1.18	**	1.21	**	
Phenylalanine	CH=CH	7.33 (d), 7.38 (m), 7.43 (m)	1.12	*	1.20	**	1.33	**	
Tryptophan	Ar–H	7.53 (d), 7.73 (d)	1.06		1.15	*	1.35	**	
Inosine	O-CH-N, N-CH-N	6.90 (m), 7.20 (m)	1.09	*	1.07		1.18	*	

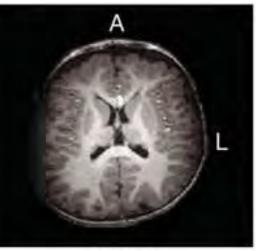




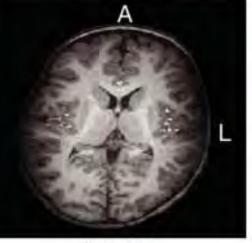




2 weeks



1 year



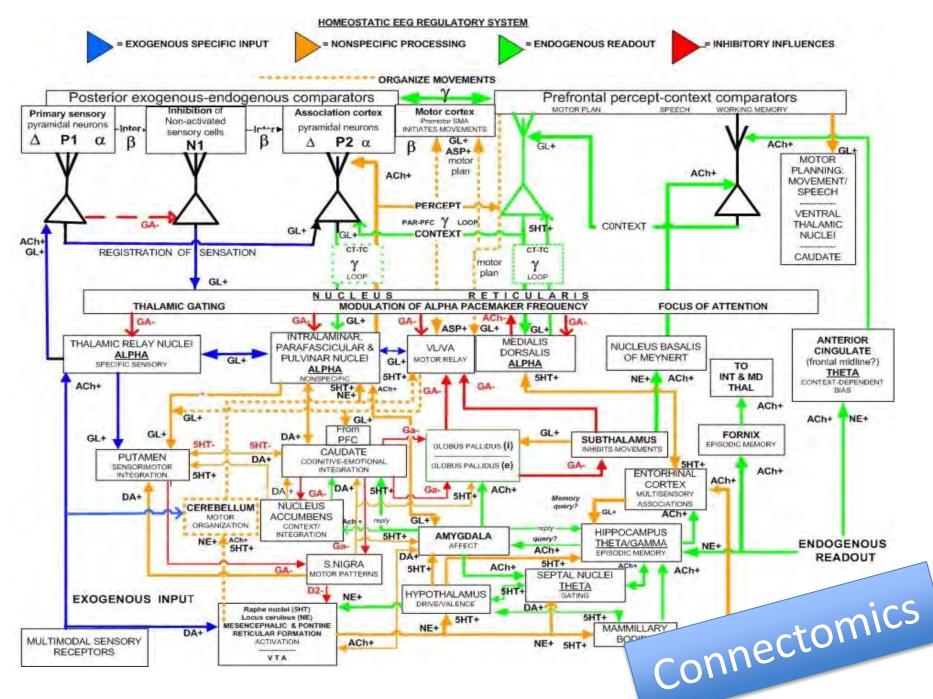




2 weeks



Adult



John, ER, Progress in Brain Research 150 (2005)

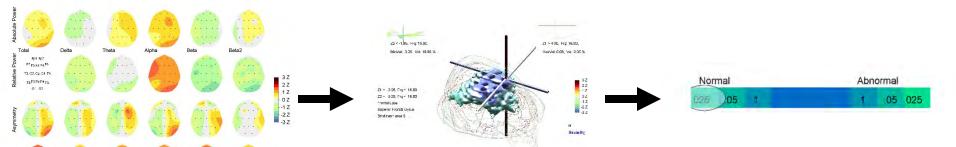


Age: 43.7591DOT: 07/22/2015

QEEG Z Spectra Maps

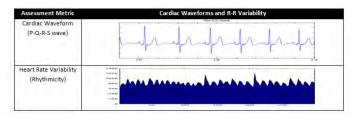
ID: F





This patient's discriminant scores lie within (p <= 0.025) of the normal limits expected for an individual of this age.

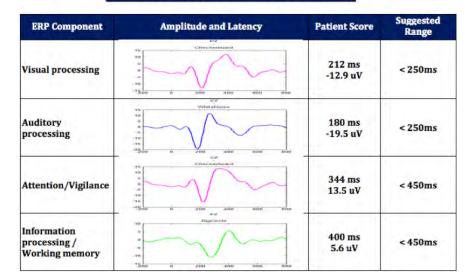
### Heart Rate Variability



			HRV	Frequency Spectrum
Neuro-Cardiac Stability	Patient Score	Normal Range	1	HRV Frequency
Heart Rate (bpm)	73	55-80	450	
QTc interval	426.7	male < 440 ms female < 460 ms	400 - 350 -	
QRS duration	0.092	0.06 - 0.12 sec	300 -	
utonomic Balance	Patient Score	Normal Range	200-	
tonomic Balance	Patient Score	Normal Range	150	
utonomic Balance	and the second s			
Autonomic Balance (SDNN (ms))	70.25	75-150	100	4.
	70.25 3394.9	75-150 >2000	100	h.
(SDNN (ms))	A.0.00			0 15 0.2 0.25 0.3
(SDNN (ms)) Total Power	3394.9	>2000	so the	0.15 0.2 0.25 0.3

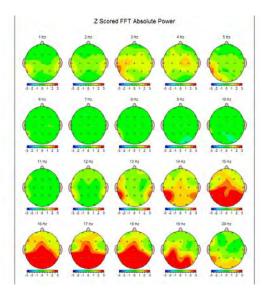
### **Event Related Potentials**

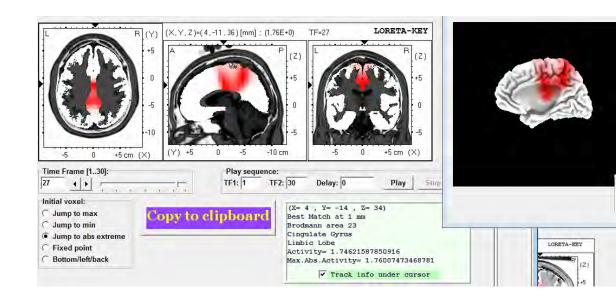
#### BRAIN PROCESSING SPEED



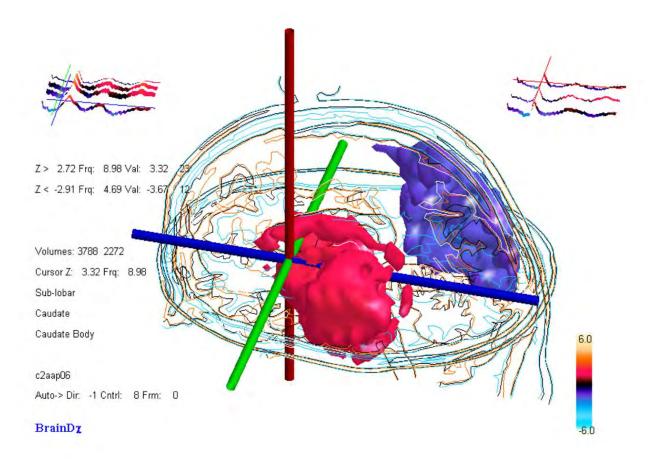
### **Brain Surface Maps**

### LORETA Brain Imaging





### Volumetric 3-D LORETA



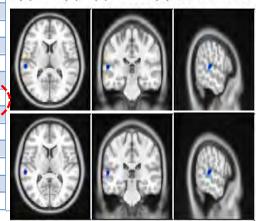
This tool can be expanded for use as a real time monitoring device for any intervention that may influence brain function

# Three dimensional axial imagery allows high level of specificity in locating brain abnormalities

	BRAIN FUNCTION: Standard Deviations - Normative database comparison																		
	Severity Eyes Closed																		
	Pre-Frontal Frontal						Central Temporal					Parieta	ıl		Occipital				
	Fp1	Fp2	F7	F3	FZ	F4	F8	C3	CZ	C4	T7	T8	P7	P3	PZ	P4	P8	01	02
2Hz	-0.2	-0.1	-0.1	-0.3	-0.4	-0.3	-0.3	-0.5	-0.5	-0.5	-0.5	-0.7	-0.7	-0.6	-0.5	-0.7	-0.9	-0.9	-0.9
3Hz	-0.2	-0.1	-0.0	-0.3	-0.3	-0.3	-0.2	-0.3	-0.4	-0.4	-0.4	-0.6	-0.6	-0.5	-0.5	-0.6	-0.8	-0.8	-0.8
4Hz	-0.7	-0.5	-0.3	-0.9	-0.8	-0.7	-0.6	-0.7	-0.6	-0.7	-0.6	-0.8	-0.9	-0.7	-0.7	-0.8	-1.0	-1.0	-1.0
5Hz	-1.0	-1.0	-0.5	-1.1	-1.1	-1.1	-1.0	-0.8	-0.6	-0.8	-0.7	-1.0	-1.0	-0.9	-0.8	-0.9	-1.1	-1.1	-1.1
6Hz	-0.9	-0.9	-0.7	-1.1	-1.2	-1.1	-1.0	-1.1	-1.1	-1.0	-0.7	-1.0	-1.0	-1.1	-0.9	-1.0	-1.1	-1.3	-1.3
7Hz	-0.6	-0.7	-0.3	-0.9	-0.9	-0.9	-0.6	-0.7	-0.7	-0.7	-0.3	-0.7	-0.8	-0.8	-0.7	-0.7	-0.9	-1.0	-1.0
8Hz	0.1	0.2	0.2	0.0	0.1	0.1	0.4	-0.0	0.0	-0.2	0.6	-0.1	-0.5	-0.5	-0.5	-0.6	-0.8	-0.8	-0.8
9Hz	0.1	0.2	0.4	0.2	0.1	0.1	0.3	-0.0	-0.1	-0.2	1.0	0.1	-0.6	-0.8	-0.8	-0.8	-0.7	-1.0	-0.8
10Hz	0.0	0.1	0.2	0.1	0.1	0.1	0.0	-0.0	0.0	-0.1	0.7	-0.0	-0.2	-0.3	-0.3	-0.4	-0.4	-0.7	-0.6
11Hz	1.1	1.0	1.2	1.1	1.0	0.9	0.7	0.8	1.1	0.7	1.3	0.4	0.8	0.8	0.9	0.5	0.6	0.0	0.0
12Hz	0.7	0.7	0.8	0.8	0.7	0.6	0.5	0.7	0.8	0.5	1.0	0.1	0.6	0.2	-0.1	-0.0	0.0	-0.5	-0.6
13Hz	0.3	0.4	0.3	0.2	0.2	0.3	0.1	0.5	0.5	0.3	0.5	-0.3	0.3	0.3	-0.2	-0.3	-0.5	-0.6	-1.0
14Hz	0.3	0.3	0.4	0.3	0.3	0.2	-0.0	0.6	0.7	0.4	0.4	-0.4	-0.1	0.3	0.2	-0.0	-0.5	-0.6	-0.8
15Hz	0.0	0.0	0.2	0.0	-0.1	-0.2	-0.4	0.3	0.3	0.1	0.2	-0.7	-0.2	0.1	0.1	-0.1	-0.6	-0.7	-0.8
16Hz	-0.0	0.0	0.0	-0.1	-0.2	-0.2	-0.3	0.1	0.1	0.1	0.0	-0.7	-0.4	-0.0	-0.1	-0.3	-0.6	-0.7	-0.9
17Hz	-0.6	-0.5	-0.4	-0.6	-0.6	-0.7	-0.8	-0.0	-0.1	-0.1	-0.3	-0.9	-0.7	-0.2	-0.3	-0.4	-0.8	-1.0	-1.2
18Hz	-0.7	-0.6	-0.7	-0.9	-0.9	-1.0	-1.1	-0.2	-0.3	-0.5	-0.6	-1.1	-1.1	-0.5	-0.5	-0.6	-1.1	-1.3	-1.3
19Hz	-0.8	-0.7	-1.0	-1.2	-1.1	-1.1	-1.1	-0.5	-0.5	-0.7	-0.9	-1.2	-1.4	-0.9	-0.7	-0.9	-1.5	-1.6	-1.5
20Hz	-0.7	-0.6	-0.7	-1.1	-1.1	-1.1	-1.0	-0.6	-0.8	-1.0	-0.9	-1.3	-1.5	-0.9	-0.8	-1.0	-1.5	-1.6	-1.5
21Hz	-0.8	-0.7	-0.7	-0.8	-0.9	-0.9	-1.0	-0.5	-0.6	-0.9	-0.8	-1.2	-1.4	-0.8	-0.6	-0.8	-1.3	-1.5	-1.4
22Hz	-0.7	-0.6	-0.6	-0.8	-0.8	-0.8	-0.8	-0.6	-0.7	-0.7	-0.7	-1.0	-1,1	-0.5	-0.4	-0.5	-1.3	-1.4	-1.4
23Hz	-0.5	-0.4	-0.5	-0.6	-0.7	-0.8	-0.8	-0.6	-0.6	-1.0	-0.8	-11	-1.5	-0.7	-0.6	-1.1	-1.9	-1.8	-1.7~,
24Hz	-0.5	-0.4	-0.7	-0.8 -0.7	-1.0	-1.0	-0.8	-0.8	-0.9	-1.2	-0.8	1.0	-2.0	-1.1 -1.2	-1.1	-1.4	-2.2	-2.1	-1.6
25Hz	-0.7	-0.7	-0.9		-0.9	-1.0	-0.8	-0.9	-0.8	-1.2	-1.0	-0.9	- <u>2.0</u>		-1.2	-1.6	-2.4	-1.9	-1.5 -1.6
26Hz	-0.8	-0.7	-0.9	-0.9	-1.1	-1.1	-0.8	-1.2	-1.1	-1.3	-1.1	-0.9	-2.3	-1.5	-1.3	- <u>1.8</u>	-2.4	-2.0	
27Hz 28Hz	-0.6	-0.6	-0.6 -0.6	-0.8 -0.8	-1.0 -0.8	-1.0	-0.7	-1.3	-1.1 -0.9	-1.3 -1.3	-1.0	-0.8 -0.8	-2.0	-1.4	-1.4	-2.0	-2.4	-2.0	-1.6
	-0.6	-0.6				-0.9	-0.6	-1.3			-1.0		- <u>1.8</u>	- <u>1.5</u>	<mark>-1.6</mark>	-2.0	-2.4	-2.2	- <u>1.6</u>
29Hz	-0.6	-0.6	-0.5 -0.5	-0.7	-0.8	-0.9	-0.6	-1.2	-0.8	-1.2	-1.1	-0.8	-2.1	-1.5	-1.4	-1.8 -1.8	-2.1 -2.1	-2.2 -2.0	-1.5
30Hz	-0.6	-0.5	-0.5	-0.6	-0.7	-0.7	-0.4	-1.2	-0.5	-1.0	-1.1	-0.8	-2.3	-1.7	- <mark>1.5</mark>	-1.8	-2.1	-2.0	-1.5

Brodmann Areas 22, 40, 42 are nearly 2 standard deviations low power from normal.

Areas govern: performing creative tasks, integer calculation; working/episodic memory, visuo-motor attention, auditory, gesture imitation, language, motor, pain, object and face perception, touch, balance (L) axial (R) (L) coronal (R) (P) sagittal (A)



## Other Substance Effect

- Lithium Generalized Slowing
- Lead –
- omics meets Acute - looks like diffuse encephalopathy
  - Chronic Inconclusive
- Mercury
  - Nonspecific diffuse slowing reflecting clinical state
- Manganese
  - EEG slowing and fast activity
- Organophosphates
  - Slow wave enhancement, paroxysmal discharges

## Mold and the Brain

- Measures of toxic mold exposure predicted QEEG measures and neuropsych test performance
  - Impairments similar to mild Traumatic Brain Injury

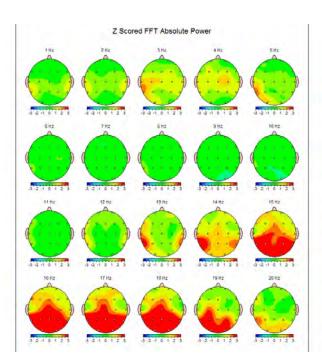
Dxomics meets

- Multiple Cognitive task impairment
- QEEG=
  - Narrowed frequency bands
  - Increased Alpha and Theta frontally
  - Hypoactivation of the cortex
    - Due to Brainstem or Reticular Activating System Dysfunction?

Crago, Gray, et. al. Archives of Environmental Health: An International Journal Volume 58, Issue 8, 2003 pp 452-463

## Severe MDD, Elevated Lead

02-2011 Severe, Chronic Depression. Past Tx: Prozac, Zoloft, Celexa, Wellbutrin, Paxil, Effexor, Geodon, Cymbalta, Seroquel, Xanax, Klonopin, Adderall, Nuvigil, Provigil, ECT x3.

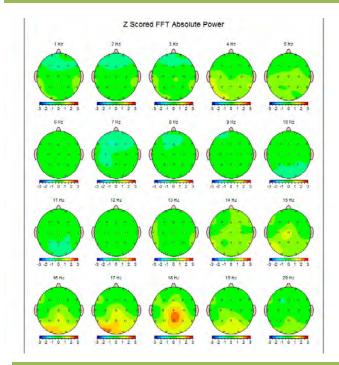


Of note, pt was infertile, and thought herself unfit to be a mother.

Found to have elevated lead on challenge testing.

Underwent QEEG guided Neurofeedback using Z-score 3D training settings. Gut Repair, DMSA Chelation →

#### 7-2011 Marked improvement on EEG and symptoms.



2-2012 "No Depression" Starting career. Changing Family Dynamics



## 2015- My Patient and her SECOND child. ©

## Functional Medicine Changes Lives

### **Digging Deeper in Assessment**

#### Genomics

- Mitomics
- CNVs
- VUS
- Microbiome

### Connectomics

• QEEG

#### Metablolomics

- Lipomics
- Toxomics
- Microbiome

#### Deep Data meets Big Data

# Leaves, Trees and Forrests..

By Krzysztof P. Jasiutowicz - first upload pl.wikipedia 11:26, 10 jul (lipiec) 2004 by Kpjas as pl:Grafika:Lisc lipy.jpg, CC BY-SA 3.0, https://commons.wikimedia.org/w/index.php?curid=166598