

Blood XMRV Scientific Research Working Group

- **Mission - design and coordinate research studies to evaluate whether XMRV poses a threat to blood safety**
- **Working Group includes representatives from transfusion medicine, retrovirology, and CFS scientific communities, as well as representatives from key Federal Agencies including HHS, FDA, NCI, CDC and NHLBI**
- **Evaluation of blood safety risks includes several steps:**
 - Evaluate XMRV nucleic acid and antibody assays
 - Establish prevalence of XMRV in blood donors
 - Determine if XMRV is transfusion-transmitted
 - Determine if transfusions are associated with CFS or prostate cancer (epidemiology studies)

Blood XMRV Scientific Research Working Group

NHLBI - Simone Glynn - Chair

HHS - Jerry Holmberg - Co-chair

NIH - Harvey Alter

ABC - Celso Bianco

CDC - William Bower

BSRI - Michael Busch

ARC - Roger Dodd

FDA - Jay Epstein

FDA - Diane Gubernot

NIH - Eleanor Hanna

CDC- Michael Hendry

MVRBC - Louis Katz

AABB - Steven Kleinman

CDC - Stephan Monroe

NCI - Francis Ruscetti

ARC - Susan Stramer

BSRI - Leslie Tobler

CFIDS - Suzanne Vernon

Testing Labs - Investigators

BSRI - Graham Simmons

CDC - Bill Switzer, Walid Heneine

FDA - Indira Hewlett

FDA - Shyh-Ching Lo

NCI - John Coffin

WPI - Judy Mikovits

***Funding for currently launched studies
via NHLBI REDS-II Program***

XMRV SRWG REDS-II Panel Study Phases

■ Phase I - Analytical Panels

- Evaluate performance of XMRV NAT assays

■ Phase II - Pilot Clinical Studies

- Whole Blood versus PBMC
- Timing of sample preparation

■ Phase III - Clinical Sensitivity/Specificity Panel

- Assay performance on pedigreed clinical samples

■ Phase IV - Blood Donor Clinical Panel

- Initial estimation of XMRV nucleic acids prevalence in blood donors
- Initiation of donor seroprevalence studies

Phase I - Analytical Panels

■ Analytical performance panels

- Comparison of Limit Of Detections and accuracy of Viral Loads of current assays; standardize performance of future XMRV detection assays for blood cells and plasma
- Whole blood panel - spiked with XMRV positive cells
- Plasma panel - spiked with supernatant containing XMRV

■ 22Rv1 cells

- Human prostate cell line chronically infected with XMRV
- Contain at least 10 XMRV proviral copies each
- Metzger et al (2010) J Virol 84:1874 (PMID:20007266)

■ Virus supernatant

- Supernatant from cultured 22Rv1 cells
- Approximate Viral Load of 5×10^9 RNA copies/ml

Analytical Panel Production

Whole blood

Whole Blood (WB) unit from
pedigreed (NAT and serology)
negative donor

22Rv1 cells spiked into WB to yield
9,900 22Rv1 cells per ml of WB

Three-fold dilutions in fresh WB

0.5 ml aliquots to give 15 panels
with three replicates at each
dilution, plus 6 negative controls

Plasma

Plasma components from two
pedigreed (NAT and serology)
negative donors

22Rv1 supernatant spiked to give
approximately 250,000 RNA copies
per ml of plasma

five-fold dilutions in fresh plasma

0.5 ml aliquots to give 15 panels
with three replicates at each
dilution, plus 6 negative controls


Analytical Panel Set-up

Whole blood

9,900 cells/ml
3,300
1,100
367
122
41
13.6
4.5
1.5
0.5
0
0

Plasma

250,000 copies/ml
50,000
10,000
2,000
400
80
16
3.2
0.64
0.128
0
0

 Distributed as two blinded panels of 36 samples each

Participating Lab Assays - Whole Blood

Lab	Extraction method	Blood Volume (μl)	Input DNA (ng)	Assay #	Primer Reference	Target	Assay type	Quant/ Nested
CDC	QIAamp mini blood	400	1000	1	Urisman	gag	PCR southern	Nested
				2	Switzer	pol	PCR southern	Nested
BSRI	QIAamp mini/midi blood	100/400	100/250		Outer - Lombardi Inner - Switzer	gag	PCR	Nested
FDA (Lo)	Qiagen DNeasy blood	200	30-50	1	Outer - Lombardi Inner - Urisman	gag	PCR	Nested
			30-50	2	Outer - Lombardi Inner - Unpublished	gag	PCR	Nested
FDA (Hewlett)	QIAamp mini blood	200	500-1000		Urisman	gag	PCR	Nested
WPI	QIAamp DNA mini blood	250	100		Dong	5' UTR of gag	qPCR	Quant
NCI	Promega Wizard Genomic DNA	500	4000		Unpublished	5' UTR of gag	PCR SCA	Quant

Participating Lab Assays - Plasma

Lab	Extraction method	Volume plasma (µl)	Assay #	Primer Reference	Target	Assay type	Quant/Nested
CDC	Ultracentrifuge /QIAamp viral RNA mini	500	1	Unpublished	pro	qRT-PCR	Quant
			2	Urisman	gag	RT-PCR southern	Nested
FDA (Lo)	Ultracentrifuge /TRIzol	250	1	Outer - Lombardi Inner - Urisman	gag	RT-PCR	Nested
			2	Outer - Lombardi Inner - Unpublished	gag	RT-PCR	Nested
FDA (Hewlett)	Qiagen Viral RNA mini	140	1	Urisman et al	gag	RT-PCR	Nested
WPI	QIAamp viral RNA mini	140	1	Lombardi et al	pro	qRT-PCR	Quant
NCI	Ultracentrifuge including internal standard Guanidinium Isothiocyanate	~ 200-500ul plasma	1	Unpublished	5' UTR of gag	RT-PCR SCA	Quant

Analytical Panel Results - Whole Blood

Cells per ml of blood	Fraction of positive replicates					NCI
	CDC	BSRI	FDA (Lo)	FDA (Hewlett)	WPI	
0	0/6	0/6	1/6*	0/6	1/6	0/6
0.5	2/3	0/3	1/3	0/3	1/3	2/3
1.5	3/3	0/3	2/3	0/3	1/3	1/3
4.5	3/3	1/3	2/3	1/3	2/3	2/3
13.6	3/3	3/3	3/3	3/3	3/3	3/3
41	3/3	3/3	3/3	3/3	3/3	3/3
122	3/3	3/3	3/3	3/3	3/3	3/3
367	3/3	3/3	3/3	3/3	3/3	3/3
1100	3/3	3/3	3/3	3/3	3/3	3/3
3300	3/3	3/3	3/3	3/3	3/3	3/3
9900	3/3	3/3	3/3	3/3	3/3	3/3

* False positive result identified as non-specific band of human genomic origin by sequencing subsequent to decoding of results

Analytical Panel Results - Whole Blood

Cells per ml	CDC	BSRI	FDA (Lo)	FDA (Hewlett)	WPI	NCI	Proviral copies per ml
0				*			0
0.5							≥5
1.5							≥15
4.5							≥45
13.6							≥136
41							≥410
122							≥1220
367							≥3670
1100							≥11000
3300							≥33000
9900							≥99000

	0/3 or 0/6
	1/6
	1/3
	2/3
	3/3

* False positive result identified as non-specific band of human genomic origin by sequencing subsequent to decoding of results

Analytical Panel Results - Plasma

RNA copies per ml	CDC	FDA (Lo)	FDA (Hewlett)	WPI	NCI
0					
0.128					
0.64					
3.2					
16					
80					
400					
2,000					
10,000					
50,000					
250,000					

	0/3 or 0/6
	1/3
	2/3
	3/3

Conclusions and Limitations

- **XMRV NAT detection assays were sensitive**
 - All WB assays detected at least 136 proviral copies/ml and four out of six [CDC, FDA(Lo), WPI and NCI] assays demonstrated even greater limits of detection
 - Four out of five plasma RNA assays performed similarly, with limits of detection of at least 80 RNA copies/ml
- **Limitations**
 - The study is too small to conduct meaningful statistical comparisons or additional analysis (such as probit to derive confidence intervals around limits of detection)
 - WB panel lacked sufficient dilutions to reach endpoints
 - XMRV isolate with which 22Rv1 cells are infected may not adequately represent the diversity of XMRV clinical isolates
 - Further work on analytical panel development will need to be performed

Phase II - Pilot Studies

■ Whole Blood versus PBMC versus plasma

- Original Lombardi et al. study performed on isolated PBMC and plasma
- Large scale studies for prevalence facilitated by using WB or plasma
- Donor-recipient and other repositories are mainly comprised of frozen WB and/or plasma

■ Timing of Processing

- Processing and freezing of donor samples slotted to be included in the blood donor clinical panel (phase IV) vary from 2-4 days due to requirements for completion of ID testing. Available donor repositories include frozen WB and plasma samples processed 1-3 days post-phlebotomy.
- Studies with other cell-associated viruses (HERVs, HTLV, herpesviruses and anelloviruses), demonstrate that levels of viral nucleic acid in plasma and whole blood vary with time from collection to processing and frozen storage.

Phase II – Pilot Study Setup

■ XMRV-positive samples

- WPI has collected blood from four CFS patients previously identified as XMRV positive in the Lombardi et al. study (by PCR, serology and culture)
- Samples separated into tubes and were processed immediately, or left at 4°C for 2 or 4 days
- Each sample was processed into PBMC, WB and plasma.

■ Analysis

- Panels were distributed by WPI to CDC and NCI for testing; WPI retained one panel for testing. One set of the panel was distributed to BSRI to keep and use for follow-up work as needed.

Phase III - Clinical Sensitivity and Specificity

- **The ability of participant assays to effectively detect clinical XMRV-positive and -negatives will be examined**
 - To attempt to overcome the issues of clinical variation and specificity, larger numbers of pedigreed clinical XMRV-positive and -negative samples are being assembled into coded cell and plasma panels to be distributed to all labs
- **Positives**
 - 25 clinical samples will be collected by WPI. All will be from patients reported in the Lombardi et al. study to be positive for XMRV by PCR, serology and virus culture. Method and timing of processing will be determined based on pilot study data
- **Negatives**
 - PCR detection assays have the potential to amplify non-specific human derived genomic sequences
 - Thus, a larger group of pedigreed negative donors is required in order to introduce generic variability (10 donors, with 3 replicates per donor = 30 negative donor samples in each panel)
 - The donors will be pedigreed negative by PCR at WPI, FDA (Dr. Lo) and CDC labs, and for serology at WPI, CDC and NCI (Dr. Ruscetti) labs

Phase IV - Clinical Panel for Donor Prevalence

Source and coding of donor specimens:

- BSI/CTS processed residual blood in “pilot tubes” (vacutainer tubes used for routine ID screening) from 396 donations given by apheresis and double-RBC donors in the Reno/Tahoe area in Dec 2009 into replicate frozen WB and plasma aliquots.
- Aliquots were anonymized as sequentially coded samples after capturing donor gender, age and zip code of residence

Phase IV - Clinical Panel for Donor Prevalence

- **Blinded panels consisting of approximately 300 blood donor samples, 25 confirmed XMRV-positive clinical samples and about 30 pedigreed-negative samples from 10 independent donors will be created for WB and plasma**
- **Blinded panels will be distributed to at least four of the participating laboratories for testing.**
- **Test results will be analyzed:**
 - Correlation between whole blood and plasma testing will be determined for each lab and between labs.
 - Preliminary XMRV prevalence in blood donors (proportion positive for XMRV DNA or RNA) will be estimated based on compiled results from each lab.

NHLBI specimen repositories* for potential future studies of XMRV prevalence in donors over time and rates of transfusion transmission

Study Name	Time Frame	Population	Specimen Type	Number of Specimens	Major Agents Studied
TTVS	1974 - 79	Donor - Recip	Serum	5,655 donat'ns 1533 recip'ts	HCV, HBV
REDS: RADAR	1999 - 2003	Donor - Recip	Plasma; Frozen Whole Blood	13,201 donat'ns 3,574 recip'ts	Parvovirus B19
TRIPS	2001 - ongoing	Donor - Recip	Plasma; Frozen Whole Blood	~6,000 donat'ns [†] ~1,000 recip'ts [†]	HHV-8, CMV, EBV, Parvo B19
NIH Clinical Center	1968 - 97	Donor - Recip	Serum	29,055 donat'ns 3,429 recip'ts	HCV, HGV/GBV-C, TTV, SENV
VATS	1995 - 99	Donor - Recip	Plasma; Frozen Whole Blood	3,864 donat'ns 531 recip'ts	HIV, CMV, HBV, HCV, HGV, HTLV
FACTS	1985-91	Recip	Serum	11,494 recip'ts	HIV, HTLV, HCV, HHV-8, <i>T.cruzi</i>
TSS	1984-85	Donations	Serum	201,212 donat'ns	HIV, HTLV
REDS GSR	1991-94	Donations	Serum	508,151 donat'ns	HBV, CMV, HHV-8
REDS GLPR	1994-95	Donations	Plasma; Frozen Whole Blood	147,915 donat'ns	HBV, CMV, HHV-8

*: ISBT International Forum: "Biobanks of blood from donors and recipients of blood products". Vox Sang, 94(2):142-260, 2008: USA: Kleinman S, Bianco C, Stramer SL, Dodd RY, Busch MP. pp 258-260. † Numbers updated as of June 2010.