

Novel laboratory diagnos<mark>tic tools for Emergency Animal</mark> Diseases including FMD

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Australian Centre for Disease Preparedness



Traditional serology for EADs

- Detection of antibodies to pathogens forms an integral part of the diagnostic process and is essential for surveillance studies
- Inherently difficult to perform and interpret
 - Non-specific cross-reactivity
 - Multi-serotype viruses cross-reaction
 - Timing of collection
 - Time consuming
 - Gold standard VNTs often require high biocontainment
 - Reagent production requires high biocontainment
 - Lack of standardisation
 - Lack of validation data



Traditional serology for EADs

- Most commonly used:
 - ELISA (different formats e.g. indirect, direct, sandwich, capture, competition) inactivated whole Ags vs. recombinant Ags
 - Haemagglutination inhibition (HAI)
 - PRNT and VNT
 - Immunofluorescence antibody test (IFAT)
 - Lateral flow devices (field)
 - Luminex (multiplex up to 100 analytes) emerging technology
- Multiple assays required per single sample in diagnostic setting
- Targeted sero-surveillance (100s to 1000s samples) focuses on a single target (virus and/or serotype) to remain feasible



Filling the gaps requires a unique approach

- Distinguishing cross-reactive antibodies to similar viruses
- Single test vs. multiple tests
- Higher resolution (epitope vs. whole virus/protein antigen)
- Serotyping without VNT in containment
- Syndrome-based diagnostic tool vs. disease/virus specific



Developments in human health research

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Application of a synthetic human proteome to autoantigen discovery through PhIP-Seg

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Qualitative Profiling of the Humoral Immune Response Elicited by rVSV- Δ G-EBOV-GP Using a Systems Serology Assay, Domain Programmable Arrays

Mariano Sanchez-Lockhart,^{1,2} Daniel S. Reyes,^{1,2} Jeanette C. Gonzalez,¹ Karla Y. Garcia,^{1,2} Erika C. Villa,³ Bradley P. Pfeffer, John C. Trefry, Jeffrey R. Kugelman, Margaret L. Pitt, and Gustavo F. Palacios1.5. Cell Reports 24, 1050-1059, July 24, 2018

Comprehensive serological profiling of human populations using a synthetic human virome SCIENCE

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George J. Xu, Tomasz Kula, Qikai Xu, Mamie Z. Li, Suzanne D. Vernon, Thumbi Ndung'u, Kiat Ruxrungtham, Jorge Sanchez, Christian Brander, Raymond T. Chung, Kevin C. O'Connor, Bruce Walker, H. Benjamin Larman, Stephen J. Elledge*



Autoimmune disease research

a.



Patient Info	-Log10 P value	Protein	# Peptides	Validation
: 63 y.o. female with non- mall cell lung cancer. resents with classic erebellar syndrome. CSF ositive for anti-NOVA ntibodies.	15.38	NEURO-ONCOLOGICAL VENTRAL ANTIGEN 1 (NOVA1)	1	WB+
	14.76	HYPOTHETICAL PROTEIN LOC26080	7	DB+
	14.54	TGFB-INDUCED FACTOR HOMEOBOX 2-LIKE, X-LINKED (TGIF2LX)	1	WB+
	8.00	NEBULIN (NEB)	1	NT
	6.49	DEBRANCHING ENZYME HOMOLOG 1 (DBR1)	1	WB-,DB+
	6.20	PROTOCADHERIN 1 (PCDH1)	1	WB-,DB+
	4.29	INSULIN RECEPTOR (INSR)	1	NT
: 59 y.o. female with non- mall cell lung cancer. resents with dysarthria, taxia, head titubation and nuscle lock. araneoplastic antibody anel is negative.	15.18	SOLUTE CARRIER FAMILY 25 MEMBER 43 (SLC25A43)	1	NT
	13.06	GLUTAMATE DECARBOXYLASE 2 (GAD65)	2	RIA+,WB-,IP+
	12.96	TESTIS EXPRESSED SEQUENCE 2 (TEX2)	1	DB+
	12.11	ATAXIN 7-LIKE 3 ISOFORM B (ATXN7L3)	1	NT
	11.93	ETS-RELATED TRANSCRIPTION FACTOR ELF-1 (ELF1)	1	NT
	11.91	TGFB-INDUCED FACTOR HOMEOBOX 2-LIKE, X-LINKED (TGIF2LX)	1.1	WB+
	11.34	INSULIN RECEPTOR SUBSTRATE 4 (IRS4)	1	NT
	6.98	HEPATOMA-DERIVED GROWTH FACTOR-RELATED PROTEIN 2 (HDGFRP2)	1	NT
	6.60	TUBULIN, BETA (TUBB)	1	WB-
	6.54	CANCER/TESTIS ANTIGEN 2 (CTAG2)	1	WB+
	6.30	DENN/MADD DOMAIN CONTAINING 1A (DENDD1A)	1	WBDB+
	6.09	DOUBLESEX AND MAB-3 RELATED TRANSCRIPTION FACTOR (DMRT2)	1	NT
	5.53	TUDOR AND KH DOMAIN CONTAINING ISOFORM A (TDRKH)	1	NT
: 59 y.o. female with nelanoma. Presents with taxia, dysarthria,	15.72	TRIPARTITE MOTIF-CONTAINING 67 (TRIM67)	2	WB+
	15.65	TRIPARTITE MOTIF-CONTAINING 9 (TRIM9)	3	WB+
	12.13	FIBROBLAST GROWTH FACTOR 9 (GLIA-ACTIVATING FACTOR) (FGF9)	1	WB-,DB+
	10.18	DUAL-SPECIFICITY TYROSINE-(Y)-PHOSPHORYLATION REGULATED KINASE 3 (DYRK3)	1	WB-,DB+
	6.93	CENTROSOMAL PROTEIN 152KDA (CEP152)	1	NT
	6.57	TITIN (TTN)	1	NT
orizontal gaze palsy.	6.34	NUCLEOPORIN LIKE 2 (NUPL2)	ROTEIN 152KDA (CEP152) 1 NT KE 2 (NUPL2) 1 NT	
araneoplastic antibody	5.43	HISTONE DEACETYLASE 1 (HDAC1)	1	WB-,DB+
anel is negative.	5.36	MITOCHONDRIAL RIBOSOMAL PROTEIN L39 (MRPL39)	E 1 (HDAC1) 1 WB-,DB+ SOMAL PROTEIN L39 (MRPL39) 1 WB-,DB+	
lowever CSE stained	5.35	CHROMOSOME 10 OPEN READING FRAME 82 (C10ORF82)	1	WB-,DB+
rain and cerebellar IHC	5.15	NLR FAMILY, PYRIN DOMAIN CONTAINING 5 (NLRP5)	PROTEIN L39 (MRPL39) 1 WB-,DB+ ING FRAME 82 (C100RF82) 1 WB-,DB+ INTAINING 5 (NLRP5) 1 NT	
lides.	4.83	TASPASE, THREONINE ASPARTASE, 1 (TASP1)	1	NT
	4.70	KIAA0090	1	NT
	4.55	SERINE (OR CYSTEINE) PROTEINASE INHIBITOR, CLADE A (ALPHA-1 ANTIPROTEINASE, ANTITRYPSIN), MEMBER 9 (SERPINA9)	1	NT
	4.21	PROTEIN TYROSINE PHOSPHATASE, NON-RECEPTOR TYPE 9 (PTPN9)	1	WB-,DB+



Infectious disease research







Mohan et al., 2018, Nat Protoc Xu et al., 2015, Science Monaco et al., 2018, bioRxiv



Infectious disease research



Sanchez-Lockhart et al., 2018, Cell Reports



Infectious disease research



Ladner, J. T. et al. (2021). Cell Reports Mo 2(1).



PhiP-Seq vs. traditional approaches

Comparison between the T7-Pep + PhIP-Seq approach and current proteomic methods for autoantigen discovery.

Feature	Classic cDNA Phage Display	Protein Array	T7-Pep + PhIP-Seq
Proteome representation	 Incomplete Highly skewed distribution 	 Small fraction Uniform distribution 	Nearly completeUniform distribution
Fraction of clones expressing an ORF peptide in frame	As low as 6%	Up to 100%	~83%
Size of displayed peptides	Up to full-length proteins	Up to full-length proteins	36 amino acid overlapping tiles
Rounds of selection	Requires multiple selection rounds, which favor more abundant and faster growing clones	No selection	Single selection, which eliminates clone growth bias and population bottleneck
Analysis	Individual clone sequencing: • Initial abundance unknown • Requires population bottleneck	Microarray scanning: • Quantitative • Statistical analysis of antibody binding	Deep sequencing of library: • Quantify population before and after a single round of selection • Statistical analysis of enrichments
Determination of antibody polyclonality	Difficult	Not possible	Often straightforward for antigens of known crystal structure
Epitope mapping	Difficult	Not possible	Often straightforward
Effort	Labor intensive	Minimal	Minimal
Sample throughput	Low	Medium	Adaptable to 96 well format
Multiplexing capability	No	No	Yes
Cost	Low	Moderate to high	Moderate



How can we apply it to improve EAD serology?

- Foot-and-mouth disease
 - Single assay to distinguish between 6 serotypes (serotype C was last recorded in 2004 in the Amazon province, Brazil; is considered extinct)
 - Differentiating Infected from Vaccinated Animals (DIVA) in FMD-free countries when emergency vaccination is considered – SP vs NSP
- Bluetongue disease
 - Single assay to distinguish between serotypes of importance in Australia
- BVDV, BDV, CSF and other diseases caused by pestiviruses of importance
 - Single assay to distinguish between different pestiviruses
- Differential tool for CSF vs. ASF
- Species specific syndromic diagnostic tool



Typical design process and workflow

- Literature review and bioinformatics for design of Oligonucleotide Library Synthesis (OLS)
 - FMD all 7 serotypes, 6 proteins
 - A, O, Asia-1, C, SAT1, 2 and 3
 - VP1 (1D); VP2 (1B); VP3 (1C); VP4 (1A); 2B; 3ABC
- Collapse FMD sequences to 85% identity (serotype differentiation threshold at aa level)
- pepsyn tool used:
 - peptide length 36 aa
 - tile every 7 aa (thus overlap 29 aa)
 - remove duplicate peptides (100% identity, cd-hit)
 - reverse translate peptides to nucleic acid sequences
 - E. coli codon optimised
- Immunoprecipitation reaction (serum + phages + protein A/G magnetic beads)
- Perform barcoding and sequencing of enriched phages
- Determine enriched peptides to characterise reactive antibodies in serum sample





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