

THE LANCET Microbe

Supplementary appendix

This appendix formed part of the original submission and has been peer reviewed. We post it as supplied by the authors.

Supplement to: Gould CV, Free RJ, Bhatnagar J, et al. Transmission of yellow fever vaccine virus through blood transfusion and organ transplantation in the USA in 2021: report of an investigation. *Lancet Microbe* 2023; published online Aug 3. [https://doi.org/10.1016/S2666-5247\(23\)00170-2](https://doi.org/10.1016/S2666-5247(23)00170-2).

Supplementary Materials

Supplemental Methods

UCSF Center for Next-Gen Precision Diagnostics Metagenomic Next-Generation Sequencing

Briefly, total nucleic acid extract from lysed samples was enriched for microbial nucleic acid and prepared into DNA (methyl-DNA reduced) and RNA (DNase treated) libraries. Barcoded libraries were sequenced by Illumina NextSeq 550 instrument with at least 5 million reads and analyzed using the SURPI+ bioinformatics pipeline for pathogen detection.^{3,4}

UCSF Generation of Gene Expression Based Classifier Models

FASTQ files from patients who had clinical CSF mNGS testing performed at UCSF were preprocessed for removal of primers and low-quality or low-complexity sequences.¹³ The resulting reads were aligned using STAR.¹² After exclusion of long non-coding RNAs, read counts were log transformed. Assignment of patient samples as autoimmune / non-infectious diseases or viral infection was performed by review of the patient electronic medical record under protocols approved by the UCSF institutional review board (IRB).

Samples were partitioned into training and test sets in an approximately 80%/20% ratio. Training set samples (n=117 samples from patients with autoimmune / non-infectious disease, 117 samples from patients with viral infection) were used to generate the final model. For selection of differentially expressed genes to include in the model, feature selection using LassoCV from Scikit-learn 0.20.4 (Python software) was performed using iterative cycles of cross-validation and gene pruning (10 cycles of 5 80%/20% cross-validation splits) to identify appropriate parameters for the final model. The final highest performing model yielded in 48 genes, 33 associated with autoimmune / non-infectious disease and 13 with viral infection. Heatmaps and

Heatmaps were generated using pheatmap version 1.0.12 in R 4.1.0 (R Foundation for Statistical Computing, Vienna, Austria). RNA gene expression levels were log-transformed and normalized prior to visualization.

Infectious Diseases Pathology Branch Immunohistochemistry (IHC)

For identification of yellow fever (YF) virus in tissue specimens, IHC was performed using monoclonal antibody against 17D YF vaccine strain. This antibody shows cross-reactivity with Zika and dengue viruses but no cross-reactivity with chikungunya or Japanese encephalitis viruses. Prepared 4µm tissue sections were incubated at ambient temperature for 30 minutes with 1:200 dilution of 17D anti-NS1 monoclonal antibody (clone 1D6) followed by sequential incubation with polymer-based indirect aminoalkane phosphatase detection system (MACH 4 Universal AP Polymer Kit, Biocare Medical, Pacheco, California). The antibody/polymer conjugate was visualized by Permanent Red Chromogen (Cell Marque, Rocklin, California). Tissue sections were counterstained in Mayer's modified hematoxylin (Poly Scientific R&D Corp., Bay Shore, New York) for microscopy examination. Uninfected mouse serum was used as a non-specific control for primary antibody incubation with sequential tissue sections from case patients. Specifically for the heart recipient, sections of dentate, hippocampus, pons, and basal ganglia were examined for YF virus RNA using primers and probes targeting the 5' noncoding region (NCR) and 3' untranslated region.

Arboviral Diseases Branch Metagenomic Next-Generation Sequencing

Briefly, RNA was treated with DNase to remove host genome, followed by cDNA synthesis (Tecan Genomics), generation of sequencing libraries, and read assembly, as previously described.⁹ Libraries were prepared for sequencing using the Ion Chef 530 sequencing kit and

sequenced on the Genestudio S5 instrument (Thermo Fisher). Specimens were sequenced on 530 chips (Thermo Fisher) resulting in an average of 8 million reads per sample. Individual sequence reads with matches to viral genes were identified using custom Python scripts that separated reads into individual FASTA files and submitted to the Basic Local Alignment Search Tool nucleotide (BLASTn) program using default parameters. Output data were formatted to include alignment quality information (alignment length, percentage of identical matches, number of mismatches, number of gap openings, E-values, the start and end of the alignment in the query, and subject and bitscores) and was filtered by reads that aligned to viral genes.

Supplemental Table. Test results for diseases^a other than yellow fever on specimens from organ and tissue recipients

Patient	Days relative to transplant	Specimen	Pathogen	Test	Result
Right kidney recipient	31	NP swab	SARS-CoV-2, influenza A/B	PCR	Negative
	32	NP swab	SARS-CoV-2	PCR	Negative
	36	CSF	Multiple pathogens	Biofire® FilmArray® ME panel	Negative
			Human polyoma virus 2	PCR	Negative
			<i>Treponema pallidum</i>	VDRL	Negative
			<i>Histoplasma capsulatum</i>	Antibody	Negative
			<i>Cryptococcus neoformans</i>	Antigen	Negative
			Acid-fast bacilli (AFB)	Smear, culture	Negative
			Fungi	Culture, Fungitell®	Negative
		<i>Toxoplasma gondii</i>	PCR	Negative	
	Epstein Barr virus (EBV)	PCR (quantitative)	Negative		
36	Serum	Fungi	β-D-glucan	Negative	
40	CSF	Multiple pathogens	Biofire® FilmArray® ME panel	Negative	
		WNV, SLEV, EEEV, POWV, HRTV, CVV, CAL serogroup	Real-time RT-PCR	Negative	
		WNV	IgM ELISA	Negative	
		SLEV, EEEV, WEEV, CAL serogroup	IgG	Negative	
		WNV, POWV	E & NS1 polyvalent MIA	Negative	
		LCMV	PCR	Negative	
		HSV-1, HSV-2, HHV-6, VZV, CMV, EBV, Adenovirus	Real-time PCR	Negative	
	Enterovirus	RT and Real-time PCR	Negative		
	Alphavirus	RT-PCR	Negative		

	40	Serum	WNV, SLEV, EEEV, POWV, HRTV, CVV, CAL serogroup WNV SLEV, EEEV, WEEV, CAL serogroup WNV, POWV LCMV Alphavirus	Real time RT-PCR IgM ELISA IgG E & NS1 polyvalent MIA PCR, sequencing RT-PCR	Negative Negative Negative Negative Negative Negative
	41	Serum	<i>Ehrlichia chafeensis</i> , <i>E. ewingii/caris</i> , <i>E. muris-like</i> , <i>Anaplasma phagocytophilum</i> <i>Rickettsia rickettsii</i> <i>Aspergillus</i> spp HTLV	PCR IgM/IgG ELISA Galactomannan ELISA	Negative Negative Negative Negative
	42	Serum	Coxsackie B (1–6)	Antibody	Negative
	43	Serum	HBV, HCV	PCR	Negative
	43	Urine	Microsporidia	PCR	Negative
	44	Stool	Microsporidia	PCR	Negative
	49	Stool	<i>Clostridioides difficile</i>	Toxin NAAT	Negative
Heart recipient	9, 17, 23	Heart tissue	Microsporidia, human polyoma virus	IHC	Negative
	31	BAL cell block	<i>Encephalitozoon cuniculi</i> , human polyoma virus	IHC	Negative
	29	CSF	Multiple pathogens <i>C. neoformans</i>	Biofire® FilmArray® ME panel Antigen	Negative Negative

			AFB Fungi WNV CMV, EBV, human polyoma virus 2	Smear, culture Culture IgM, IgG ELISA PCR	Negative Negative Negative Negative
	36	CSF	Multiple pathogens <i>C. neoformans</i> Fungi WNV CMV, EBV Human polyoma virus 2 Autoimmune disease	Biofire® FilmArray® ME panel Antigen Culture IgM, IgG ELISA PCR PCR Autoimmune panel	Negative Negative Negative Negative Positive Negative
Liver recipient	0	Liver tissue	Microsporidia, HSV-1, HSV-2	IHC	Negative
	21	Serum	CMV, EBV	PCR	Negative
	23	Stool	<i>C. difficile</i> <i>C. difficile</i> Multiple pathogens	Toxin NAAT GDH Antigen Biofire® FilmArray® GI panel	Positive Negative Negative
	24	Serum	WNV <i>C. neoformans</i> Parvovirus B19, HHV-8, HHV-6, CMV HSV-1, HSV-2 <i>Borrelia burgdorferi</i> <i>T. pallidum</i>	IgM, IgG ELISA Antigen PCR PCR PCR, EIA Antibody cascade/EIA	Negative Negative Negative Negative Negative Negative
	24	CSF	Multiple pathogens AFB Fungi Viral	Biofire® FilmArray® ME panel Smear, culture Culture Culture	Negative Negative Negative Negative

	26	Serum	<i>T. gondii</i> <i>R. rickettsii</i> <i>T. gondii</i> <i>Babesia microti</i> Parasites <i>Plasmodium</i> spp	IgG ELISA IgM, IgG ELISA PCR (qualitative) PCR Smear (thick & thin) Antigen	Negative Negative Negative Negative Negative
	28	Serum	BK virus EEEV, WEEV WNV, SLEV, EEEV, POWV, LACV, JCV JCV, CVV, HRTV <i>A. phagocytophilum</i> , <i>E. chaffeensis</i> , <i>B. microti</i> <i>B. duncani</i> <i>B. burgdorferi</i> <i>Blastomyces dermatitidis</i> <i>C. immitis</i> Paraneoplastic syndrome	PCR (quantitative) IgM IFA, IgG IFA IgM ELISA RT-PCR IgM ELISA, IgG ELISA IgG ELISA Antibody screen Antibody immunodiffusion IgM, IgG ELISA Paraneoplastic antibody panel	Negative Negative Negative Negative Negative Negative Negative Negative
	28	Urine	<i>Histoplasma capsulatum</i>	Antigen	Negative
	29	CSF	EEEV, WEEV Multiple pathogens AFB Fungi LCMV Human polyoma virus 2 <i>C. immitis</i> , <i>H. capsulatum</i>	IgM IFA, IgG IFA Biofire® FilmArray® ME panel Smear, culture Culture IgM ELISA, IgG ELISA PCR Antigen quantitative EIA	Negative Negative Negative Negative Negative Negative
	30	NP/OP swab	SARS-CoV-2	NAT	Negative

Left kidney recipient	43	Stool	Multiple pathogens	Biofire® FilmArray® GI panel	Negative
		Serum	Amoebae	Serology	Negative
	44	CSF	Multiple pathogens	Biofire® FilmArray® ME panel	Negative
			AFB	Smear, culture	Negative
			Fungi	Culture	Negative
44	Serum	<i>C. neoformans</i>	Antigen	Negative	
		<i>Treponema pallidum</i>	VDRL	Negative	
Right cornea recipient	45	CSF	WNV	IgM ELISA	Negative
			Human polyoma virus 2	PCR	Negative
			Multiple pathogens	16S ribosomal RNA ^b	Negative
			CMV	PCR (quantitative)	Negative
45	Stool/urine	Microsporidia	PCR	Antigen	Negative
46	Plasma	EBV, HHV-6	PCR	PCR	Negative
Right cornea recipient	43	Urine	Microsporidia	PCR	Negative
Right cornea recipient	45	CSF	Multiple pathogens	Biofire® FilmArray® ME panel	Negative
			Human polyoma virus 2, EBV	PCR	Negative
			<i>C. neoformans</i>	Antigen	Negative
			<i>Treponema pallidum</i>	VDRL	Negative
			AFB	Smear, culture	Negative
			Fungi	Fungitell®, culture	Negative
			WNV, SLEV, EEEV, POWV, HRTV, CVV, CAL serogroup virus	Real time RT-PCR	Negative
			IgG	IgG index	Normal
			NMDA	Antibody	Negative
			Immunoglobulins	Oligoclonal banding	Negative

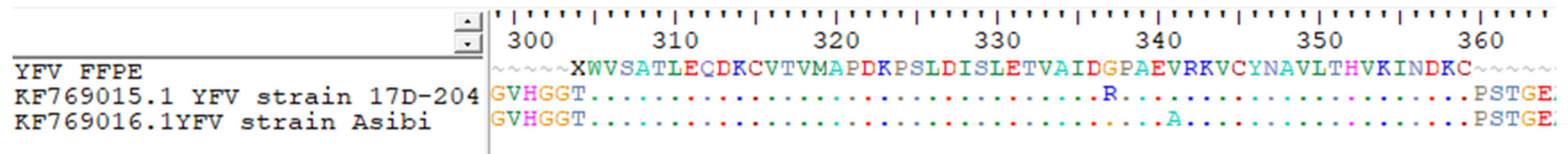
			Paraneoplastic syndrome Autoimmune disease	Paraneoplastic antibody panel Autoimmune panel	Negative Negative
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Abbreviations: IHC, immunohistochemistry; Ig, immunoglobulin; ELISA, enzyme-linked immunosorbent assay; TESA, *Trypanosoma cruzi* excreted-secreted antigens; EIA, enzyme immunoassay; NP, nasopharyngeal; PCR, polymerase chain reaction; ME, meningoencephalitis; VDRL, venereal disease research laboratory; WNV, West Nile virus; SLEV, St. Louis encephalitis virus; EEEV, eastern equine encephalitis virus; POWV, Powassan virus; HRTV, Heartland virus; CVV, Cache Valley virus; CAL, California; WEEV, western equine encephalitis virus; E, envelope; NS, non-structural; MIA, microsphere immunoassay; LCMV, lymphocytic choriomeningitis virus; HSV, herpes simplex virus; HHV, human herpesvirus; VZV, varicella zoster virus; RT-PCR, reverse transcription-polymerase chain reaction; HTLV, human T-lymphotropic virus; HBV, hepatitis B virus; HCV, hepatitis C virus; NAT, nucleic acid test; GDH, glutamate dehydrogenase; GI, gastrointestinal; LACV, La Crosse virus; JCV, Jamestown Canyon virus; IFA, immunofluorescence assay; RNA, ribonucleic acid; NMDA, N-methyl-D-aspartate

a Not including routine bacterial cultures or HIV testing

b Performed at University of Washington

Supplemental Figure. Amino acid alignment of metagenomic next-generation sequencing results of RNA from brain autopsy tissue demonstrating reversion mutation in the envelope protein



A single yellow fever virus read was recovered from formalin-fixed, paraffin-embedded (FFPE) brain autopsy tissue of the heart transplant recipient covering part of the envelope (E) protein sequence. The translated sequencing read (YFV FFPE) is compared to yellow fever 17D-204 and Asibi strains of yellow fever virus. The FFPE-recovered sequence shows a mutation reverting E amino acid 52 to a glycine (Asibi strain) from an arginine (17D-204 vaccine strain). Dots in the alignment represent amino acids shared with the YFV FFPE sequence.