

RESEARCH & RELATED Senior/Key Person Profile (Expanded)

PROFILE - Project Director/Principal Investigator				
Prefix: Dr.	First Name*: PETER	Middle Name	Last Name*: DASZAK	Suffix:
Position/Title*:	President			
Organization Name*:	EcoHealth Alliance			
Department:				
Division:				
Street1*:	460 West 34th Street, Suite 1701			
Street2:				
City*:	New York			
County:				
State*:	NY: New York			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	10001-2317			
Phone Number*:	(b) (6)		Fax Number:	212-380-4465
E-Mail*:	(b) (6)			
Credential, e.g., agency login:	(b) (6)			
Project Role*:	PD/PI	Other Project Role Category:		
Degree Type:	PHD,BS	Degree Year: 1994,1986		
Attach Biographical Sketch*:	File Name:	Biosketch_(Daszak,Peter)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Kevin	Middle Name J.	Last Name*: Olival	Suffix:
Position/Title*:	Senior Research Scientist			
Organization Name*:	EcoHealth Alliance			
Department:				
Division:				
Street1*:	460 W. 34th Street			
Street2:	Suite 1701			
City*:	New York			
County:				
State*:	NY: New York			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	10001-2317			
Phone Number*:	(b) (6)	Fax Number:		212-380-4465
E-Mail*:	(b) (6)			
Credential, e.g., agency login:	(b) (6)			
Project Role*:	Co-Investigator	Other Project Role Category:		
Degree Type:	PHD	Degree Year: 2008		
Attach Biographical Sketch*:	File Name:	Biosketch_(Olival,Kevin)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03_FINAL.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Ralph	Middle Name S	Last Name*: Baric	Suffix:
Position/Title*:	Professor			
Organization Name*:	University of North Carolina			
Department:				
Division:				
Street1*:	Department of Epidemiology			
Street2:				
City*:	Chapel Hill			
County:				
State*:	NC: North Carolina			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	275997435			
Phone Number*:	(b) (6)	Fax Number:		(919) 966-2089
E-Mail*:	(b) (6)			
Credential, e.g., agency login:	(b) (6)			
Project Role*:	Co-Investigator	Other Project Role Category:		
Degree Type:	PHD	Degree Year: 1983		
Attach Biographical Sketch*:	File Name:	Biosketch_(Baric,Ralph)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Linfa	Middle Name	Last Name*: Wang	Suffix:
Position/Title*:				
Organization Name*: Duke-NUS Medical School				
Department:				
Division:				
Street1*: 8 College Road				
Street2:				
City*: Singapore				
County:				
State*:				
Province:				
Country*: SGP: SINGAPORE				
Zip / Postal Code*: 169857				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login: (b) (6)				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: PHD			Degree Year: 1986	
Attach Biographical Sketch*:		File Name:	Biosketch_(Wang,Linfa)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Danielle	Middle Name	Last Name*: Anderson	Suffix:
Position/Title*:				
Organization Name*: Duke NUS				
Department:				
Division:				
Street1*: 8 College Road				
Street2:				
City*: Singapore				
County:				
State*:				
Province:				
Country*: SGP: SINGAPORE				
Zip / Postal Code*: 169857				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: PHD			Degree Year: 2007	
Attach Biographical Sketch*:		File Name:	Biosketch_(Anderson,_Dani)_EIDRC_RFA-AI-19-028_(PI- Daszak)_v02.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Supapom	Middle Name	Last Name*: Wacharapluesadee
Suffix:			
Position/Title*:			
Organization Name*:	Chulalongkorn University Hospital		
Department:			
Division:			
Street1*:	1873 Rama IV Road		
Street2:			
City*:	Bangkok		
County:			
State*:			
Province:			
Country*:	THA: THAILAND		
Zip / Postal Code*:	10330		
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*: Co-Investigator		Other Project Role Category:	
Degree Type: PHD		Degree Year: 2006	
Attach Biographical Sketch*:	File Name:	Biosketch_(Wacharapluesadee,Supapom)_EIDRC_RFA-AI_19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Mr.	First Name*: Tom	Middle Name	Last Name*: Hughes
Suffix:			
Position/Title*:			
Organization Name*:	Conservation Medicine Ltd.		
Department:			
Division:			
Street1*:	13H Villamas Condo		
Street2:			
City*:	Selangor		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:	47000		
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*: Co-Investigator		Other Project Role Category:	
Degree Type: Post Grad Diploma		Degree Year: 2009	
Attach Biographical Sketch*:	File Name:	Biosketch_(Hughes,Tom)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Christopher	Middle Name	Last Name*: Broder	Suffix:
Position/Title*:				
Organization Name*:	Uniformed Services University			
Department:				
Division:				
Street1*:	4301 Jones Bridge Road			
Street2:				
City*:	Bethesda			
County:				
State*:	MD: Maryland			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	20814-4799			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	c (b) (6)			
Credential, e.g., agency login:				
Project Role*: Co-Investigator		Other Project Role Category:		
Degree Type: PHD		Degree Year: 1989		
Attach Biographical Sketch*:	File Name:	Biosketch_(Broder,Chris)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf		
Attach Current & Pending Support: File Name:				

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Eric	Middle Name	Last Name*: Laing	Suffix:
Position/Title*:				
Organization Name*:	Uniformed Services University			
Department:				
Division:				
Street1*:	4301 Jones Bridge Road			
Street2:				
City*:	Bethesda			
County:				
State*:	MD: Maryland			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	20814-4799			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Co-Investigator		Other Project Role Category:		
Degree Type: PHD		Degree Year: 2016		
Attach Biographical Sketch*:	File Name:	Biosketch_(Laing,Eric)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support: File Name:				

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Gerald	Middle Name	Last Name*: Keusch	Suffix:
Position/Title*:				
Organization Name*: BU NEIDL				
Department:				
Division:				
Street1*: 620 Albany Street				
Street2:				
City*: Boston				
County:				
State*: MA: Massachusetts				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 02118-2516				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: MD			Degree Year: 1963	
Attach Biographical Sketch*:		File Name:	Biosketch_(Keusch,Gerald)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Ronald	Middle Name	Last Name*: Corley	Suffix:
Position/Title*:				
Organization Name*: BU NEIDL				
Department:				
Division:				
Street1*: 620 Albany Street				
Street2:				
City*: Boston				
County:				
State*: MA: Massachusetts				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 02118-2516				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: PHD			Degree Year: 1975	
Attach Biographical Sketch*:		File Name:	Biosketch_(Corley,Ron)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v03.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Amy	Middle Name	Last Name*: Sims	Suffix:
Position/Title*:				
Organization Name*: University of North Carolina at Chapel Hill				
Department:				
Division:				
Street1*: 2107 McGavran-Greenberg Hall				
Street2:				
City*: Chapel Hill				
County:				
State*: NC: North Carolina				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 27599-7400				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: PHD			Degree Year: 2001	
Attach Biographical Sketch*:		File Name:	Biosketch_(Sims,Amy)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Alice	Middle Name	Last Name*: Latinne	Suffix:
Position/Title*:				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 W. 34th Street				
Street2: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Other (Specify)			Other Project Role Category: Bioinformatician	
Degree Type: PHD			Degree Year: 2012	
Attach Biographical Sketch*:		File Name:	Biosketch_(Lattine,Alice)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Kendra	Middle Name	Last Name*: Phelps	Suffix:
Position/Title*:				
Organization Name*:	EcoHealth Alliance			
Department:				
Division:				
Street1*:	460 W. 34th Street			
Street2:	Suite 1701			
City*:	New York			
County:				
State*:	NY: New York			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	10001-2317			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Field Scientist		
Degree Type: PHD		Degree Year: 2016		
Attach Biographical Sketch*:	File Name:	Biosketch_(Phelps,Kendra)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Ms.	First Name*: Emma	Middle Name	Last Name*: Mendelsohn	Suffix:
Position/Title*:				
Organization Name*:	EcoHealth Alliance			
Department:				
Division:				
Street1*:	460 W. 34th Street			
Street2:	Suite 1701			
City*:	New York			
County:				
State*:	NY: New York			
Province:				
Country*:	USA: UNITED STATES			
Zip / Postal Code*:	10001-2317			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Data Scientist		
Degree Type: MEM		Degree Year: 2015		
Attach Biographical Sketch*:	File Name:	Biosketch_(Mendelsohn,Emma)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Patrick	Middle Name	Last Name*: Dawson	Suffix:
Position/Title*:				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 W. 34th Street				
Street2: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Epidemiologist		
Degree Type: PHD		Degree Year: 2019		
Attach Biographical Sketch*:	File Name:	Biosketch_(Dawson,Patrick)_EIDRC_RFA_AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Ms.	First Name*: Stephanie	Middle Name	Last Name*: Martinez	Suffix:
Position/Title*:				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 W. 34th Street				
Street2: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Epidemiologist		
Degree Type: MPH		Degree Year: 2017		
Attach Biographical Sketch*:	File Name:	Biosketch_(Martinez,Stephanie)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v03.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Aleksei	Middle Name	Last Name*: Chmura	Suffix:
Position/Title*:				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 W. 34th Street				
Street2: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Senior Program Manager		
Degree Type: PHD		Degree Year: 2018		
Attach Biographical Sketch*:	File Name:	Biosketch_(Chmura,Aleksei)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Ms.	First Name*: Hongying	Middle Name	Last Name*: Li	Suffix:
Position/Title*:				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 W. 34th Street				
Street2: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Other (Specify)		Other Project Role Category: Epidemiologist		
Degree Type: MPH		Degree Year: 2015		
Attach Biographical Sketch*:	File Name:	Biosketch_(Li,Hongying)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Thiravat	Middle Name	Last Name*: Hemachudha	Suffix:
Position/Title*:				
Organization Name*:	Chulalongkorn University Hospital			
Department:				
Division:				
Street1*:	1873 Rama IV Road			
Street2:				
City*:	Bangkok			
County:				
State*:				
Province:				
Country*:	THA: THAILAND			
Zip / Postal Code*:	10330			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: MD			Degree Year: 1981	
Attach Biographical Sketch*:	File Name:	Biosketch_(Hemachudha,Thiravat)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v05.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Timothy	Middle Name	Last Name*: William	Suffix:
Position/Title*:	Head			
Organization Name*:	Gleneagles Hospital			
Department:	Infectious Disease Unit			
Division:				
Street1*:	Riverson at Sembulan			
Street2:				
City*:	Kota Kinabalu			
County:				
State*:				
Province:				
Country*:	MYS: MALAYSIA			
Zip / Postal Code*:				
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: FRCP			Degree Year: 2013	
Attach Biographical Sketch*:	File Name:	Biosketch_(William,Timothy)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Helen	Middle Name B	Last Name*: Lasimbang	Suffix:
Position/Title*:	CEO			
Organization Name*:	Hospital Universiti Malaysia Sabah			
Department:				
Division:				
Street1*:	Hospital Universiti Malaysia Sabah			
Street2:				
City*:	Kota Kinabalu			
County:				
State*:				
Province:				
Country*:	MYS: MALAYSIA			
Zip / Postal Code*:				
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*:	Co-Investigator	Other Project Role Category:		
Degree Type:	MBBS	Degree Year:	1991	
Attach Biographical Sketch*:	File Name:	Biosketch_(Lasimbang,Helen_Benedict)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Heng	Middle Name	Last Name*: Gee Lee	Suffix:
Position/Title*:				
Organization Name*:	Queen Elizabeth State Hospital			
Department:				
Division:				
Street1*:	13a, Jalan Penampang			
Street2:				
City*:	Kota Kinabalu			
County:				
State*:				
Province:				
Country*:	MYS: MALAYSIA			
Zip / Postal Code*:				
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*:	Other (Specify)	Other Project Role Category:	Senior Clinician	
Degree Type:	MRCP	Degree Year:	2011	
Attach Biographical Sketch*:	File Name:	Biosketch_(Lee,Heng_Gee)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Giri Shan	Middle Name	Last Name*: Rajahram
Suffix:			
Position/Title*:			
Organization Name*:	Queen Elizabeth State Hospital		
Department:			
Division:			
Street1*:	13a, Jalan Penampang		
Street2:			
City*:	Kota Kinabalu		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*:	Other (Specify)	Other Project Role Category: Infectious Disease Epidemiologist	
Degree Type: MRCP		Degree Year: 2011	
Attach Biographical Sketch*:	File Name:	Biosketch_(Rajahram,Giri_Shan)_EIDRC_RFA-AI_19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Jayaseelan	Middle Name	Last Name*: Sekaran
Suffix:			
Position/Title*:			
Organization Name*:	Lintang Clinic, Kuala Kangsar District Health Office		
Department:			
Division:			
Street1*:	31100 Sg. Siput		
Street2:			
City*:	Kuala Kangsar		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*:	Co-Investigator	Other Project Role Category:	
Degree Type:		Degree Year:	
Attach Biographical Sketch*:	File Name:	Biosketch_(Sekaran,_Jayaseelan)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Cheng Siang	Middle Name	Last Name*: Tan
Suffix:			
Position/Title*:			
Organization Name*:	Universiti Malaysia Sarawak		
Department:			
Division:			
Street1*:	Jalan Datuk Mohammad Musa		
Street2:			
City*:	Kota Samarahan		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*: Co-Investigator		Other Project Role Category:	
Degree Type: PHD		Degree Year: 2012	
Attach Biographical Sketch*:	File Name:	Biosketch_(Tan,Cheng_Siang)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Anwarali Khan	Middle Name	Last Name*: Faisal Ali
Suffix:			
Position/Title*:			
Organization Name*:	Universiti Malaysia Sarawak		
Department:			
Division:			
Street1*:	Jalan Datuk Mohammad Musa		
Street2:			
City*:	Kota Samarahan		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*: Other (Specify)		Other Project Role Category: Zoologist and Biotechnician	
Degree Type: PHD		Degree Year: 2013	
Attach Biographical Sketch*:	File Name:	Biosketch_(Anwarali_Khan,Faisal)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Nadia Diyana	Middle Name	Last Name*: Hamzah
Suffix:			
Position/Title*:			
Organization Name*:	Bario Clinic, Rural Area Service Ministry of Health Malaysia		
Department:			
Division:			
Street1*:	Dataran Tinggi Kelabit Baram		
Street2:			
City*:	Bario		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*:	Other (Specify)	Other Project Role Category: Medical Officer and Clinician	
Degree Type: MD		Degree Year: 2015	
Attach Biographical Sketch*:	File Name:	Biosketch_(Hamzah,_Nadia)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person			
Prefix: Dr.	First Name*: Ahmed	Middle Name	Last Name*: Kamruddin
Suffix:			
Position/Title*:			
Organization Name*:	Universiti Malaysia Sabah		
Department:			
Division:			
Street1*:	Jalan UMS		
Street2:			
City*:	Kota Kinabalu		
County:			
State*:			
Province:			
Country*:	MYS: MALAYSIA		
Zip / Postal Code*:			
Phone Number*:	(b) (6)	Fax Number:	
E-Mail*:	(b) (6)		
Credential, e.g., agency login:			
Project Role*:	Co-Investigator	Other Project Role Category:	
Degree Type: PHD		Degree Year: 1992	
Attach Biographical Sketch*:	File Name:	Biosketch_(Kamruddin,Ahmed)_EIDRC_RFA-AI-19-2018_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:	File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Tsin Wen	Middle Name	Last Name*: Yeo	Suffix:
Position/Title*:				
Organization Name*:	Lee Kong Chian School of Medicine			
Department:				
Division:				
Street1*:	59 Nanyang Dr			
Street2:				
City*:	Singapore			
County:				
State*:				
Province:				
Country*:	SGP: SINGAPORE			
Zip / Postal Code*:	636921			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Consultant		Other Project Role Category:		
Degree Type: PHD		Degree Year: 2008		
Attach Biographical Sketch*:	File Name:	Biosketch_(Yeo,Tsin_Wen)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Andrew	Middle Name	Last Name*: Hickey	Suffix:
Position/Title*:				
Organization Name*:	Thailand MOPH-CDC			
Department:				
Division:				
Street1*:	Tivanon Road			
Street2:				
City*:	Nonthaburi			
County:				
State*:				
Province:				
Country*:	THA: THAILAND			
Zip / Postal Code*:	11000			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Consultant		Other Project Role Category:		
Degree Type: PHD		Degree Year: 2010		
Attach Biographical Sketch*:	File Name:	Biosketch_(Hickey,Andrew)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Hume	Middle Name	Last Name*: Field	Suffix:
Position/Title*:				
Organization Name*: Jeppesen Field Consulting				
Department:				
Division:				
Street1*: 19 Counihan Street				
Street2:				
City*: Brisbane				
County:				
State*:				
Province:				
Country*: AUS: AUSTRALIA				
Zip / Postal Code*: 4160				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Consultant			Other Project Role Category:	
Degree Type: PHD			Degree Year: 2005	
Attach Biographical Sketch*:		File Name:	Biosketch_(Field,Hume)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Carloz	Middle Name	Last Name*: Zambrana-Torrelío	Suffix:
Position/Title*: Associate Vice President				
Organization Name*: EcoHealth Alliance				
Department:				
Division:				
Street1*: 460 West 34th Street				
Street2*: Suite 1701				
City*: New York				
County:				
State*: NY: New York				
Province:				
Country*: USA: UNITED STATES				
Zip / Postal Code*: 10001-2317				
Phone Number*: (b) (6)		Fax Number:		
E-Mail*: (b) (6)				
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: PHD			Degree Year: 2017	
Attach Biographical Sketch*:		File Name:	Biosketch_(Zambrana-T,Carlos)_EIDRC_RFA-AI-19-028_(PI-Daszak).pdf	
Attach Current & Pending Support:		File Name:		

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Pasin	Middle Name	Last Name*: Hemachudha	Suffix:
Position/Title*:				
Organization Name*:	Chulalongkorn University Hospital			
Department:				
Division:				
Street1*:	1873 Rama IV Road			
Street2:				
City*:	Bangkok			
County:				
State*:				
Province:				
Country*:	THA: THAILAND			
Zip / Postal Code*:	10330			
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Other (Specify)			Other Project Role Category: Immunologist and Clinician	
Degree Type: MD		Degree Year: 2017		
Attach Biographical Sketch*:	File Name:	Biosketch_(Hemachudha,Pasin)_FINAL_USETHISONE.pdf		
Attach Current & Pending Support:	File Name:			

PROFILE - Senior/Key Person				
Prefix: Dr.	First Name*: Ingrid Ting Pao	Middle Name	Last Name*: Lin	Suffix:
Position/Title*:	Clinical Specialist			
Organization Name*:	Hospital Miri			
Department:	Medicine			
Division:				
Street1*:	Jalan Cahaya			
Street2:				
City*:	Sarawak			
County:				
State*:				
Province:				
Country*:	MYS: MALAYSIA			
Zip / Postal Code*:				
Phone Number*:	(b) (6)	Fax Number:		
E-Mail*:	(b) (6)			
Credential, e.g., agency login:				
Project Role*: Co-Investigator			Other Project Role Category:	
Degree Type: MD		Degree Year: 2009		
Attach Biographical Sketch*:	File Name:	Biosketch_(Lin,_Ingrid_Ting_Pao)_EIDRC_RFA-AI-19-028_(PI-Daszak)_v02.pdf		
Attach Current & Pending Support:	File Name:			

BIOGRAPHICAL SKETCH

NAME: Daszak, Peter

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: President & Chief Scientist

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE	COMPLETION DATE	FIELD OF STUDY
Bangor University, UK	B.S. (hons)	07/1986	Zoology
University of East London, UK	Ph.D.	03/1993	Infectious Diseases

A. Personal Statement

I have 20+ year's NIH-funded research experience on emerging viral zoonoses, and the scientific skills to manage this proposed work that involves a large international collaboration on human and wildlife surveillance, and translational research. I am President and Chief Scientist of EcoHealth Alliance, a US-based 501 (c) 3 institution that conducts research on emerging zoonoses. My research background is focused on understanding the process of zoonotic disease emergence, particularly viral zoonoses. This includes identifying the bat origin of SARS-CoV and SADS-CoV, analyzing the causes of West Nile, Nipah and Hendra virus emergence and spread, publishing the first unbiased analysis of global emerging disease hotspots, and analyzing patterns of viral spillover into human populations in EID hotspots. I have been the PI on 5 multidisciplinary R01s, all with international collaborating organizations, including most on the current proposal. All of these used modeling, epidemiology, laboratory and field science to test hypotheses on the emergence of wildlife-origin viral zoonoses, including SARS-CoV, Nipah and Hendra virus, Avian influenza and bat-origin viruses. I have also led large contracts from USAID (institutional lead on \$75 million PREDICT-1 and \$138 million PREDICT-2; Chief-of-Party on \$3 million IDEEAL), successfully managing teams of virologists, field biologists, mathematical modelers, veterinarians, epidemiologists, laboratorians and anthropologists.

1. Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, **Daszak P**, Eaton BT, Zhang S & Wang L-F (2005). Bats are natural reservoirs of SARS-like coronaviruses. **Science** 310: 676-679.
2. Jones KE, Patel NG, Levy MA, Storeygard A, Balk D, Gittleman JL, and **Daszak P*** (2008). Global trends in emerging infectious diseases. **Nature** 451:990-993
3. Olival KJ*, Hosseini PR, Zambrana-Torrel C, Ross N, Bogich TL, **Daszak P*** (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546, 646–650.
4. Carroll D, **Daszak P***, Wolfe ND, Gao GF, Morel C, Morzaria S, Pablos-Méndez A, Tomori O, Mazet JAK (2018). The global virome project. **Science** 359: 872-874.

B. Positions and Honors**Positions and Employment**

1993 -98 Senior Faculty Research Scientist, Kingston University UK
 1998 Guest Researcher, Centers for Disease Control and Prevention (CDC)
 1999 -01 Faculty Research Scientist, University of Georgia
 2001 - Adjunct Faculty, Columbia University
 2001 - 09 Executive Director, Consortium for Conservation Medicine, EcoHealth Alliance, New York
 2009 - President & Chief Scientist, EcoHealth Alliance New York

Other Experience and Professional Membership

- 2003 - 7 NIH: ad hoc member, ZRG1 IDM-G 90 (2003-5) ZRG1 IRAP-Q (2005-7)
- 2004 - Editorial Board, *Conserv. Biol.*
- 2005 NIAID: Steering Committee, workshop on virus-host shifts & emergence of new pathogens
- 2010 - Editor-in-Chief, *EcoHealth*; Member of IOM Forum on Microbial Threats; External Advisory Board, DHS and Kansas State Univ. Ctr. of Excellence for Emerg. & Zoonotic Animal Diseases (CEEZAD)
- 2011 Steering Committee, NIAID Workshop on Arboviruses
- 2014 - Member NRC Advisory Committee to advise the US Global Change Research Program (USGCRP)
- 2015 - Member of Supervisory Board, One Health Platform; Editorial Board *One Health*
- 2016 - Member, WHO Expert group on Public Health Emergency Disease Prioritization
- 2016 - Member, Core Steering Committee & Co-Chair, Science & Technol WG, Global Virome Project
- 2017 External Review Committee, CSIRO Health & Biosecurity Business Unit
- 2017 - Chair, Forum on Microbial Threats, National Academies of Science, Engineering & Medicine

Honors

- 1999 Meritorious service award, CDC
- 2000 CSIRO silver medal for collaborative research
- 2002 Honored by the naming of a new species of centipede, *Cryptops daszaki* (*J Nat Hist* 36: 76-106)
- 2003 6th Annual Lecturer, Medicine & Humanities, Texas A&M
- 2007 Finalist, Director's Pioneer Award
- 2008 Presidential Lecturer, University of Montana
- 2012 Elected member of the Cosmos Club, Washington DC
- 2013 Honored by the naming of a new parasite species, *Isospora daszaki* (*Parasit Res* 111:1463-1466)
- 2013 Hsu-Li Distinguished Lectureship in International Epidemiology, Univ. Iowa
- 2015 Robert Leader Endowed Lecture in Food Safety, Michigan State Univ.
- 2018 - Member, National Academy of Medicine (NAM), USA.

C. Contribution to Science

1. Research on the bat origins of emerging viruses. Numerous high impact emerging viruses appear to have bat reservoirs (e.g. SARS-CoV, EBOV, NiV, HeV, MERS-CoV, SADS-CoV). As PI on five R01s on bat-origin viruses, my work has helped demonstrate the bat origin of SARS- and SADS-CoV, analyze the drivers of bat viral emergence and risk factors for spillover. Collaborating with virologists in China, we have isolated and characterized SARSr-CoVs from bats that use the same human host cell receptor (ACE-2) as SARS-CoV. This work provides critical reagents and resources that have helped advance understanding of virus-host binding and may contribute to vaccine development. My other work identified factors leading to the emergence of NiV from *Pteropus* bats in Malaysia and Bangladesh; a likely bat origin for MERS-CoV; and proof that bats harbor a significantly higher proportion of zoonoses than all other mammalian groups.

- a. Ge X-Y, Li J-L, Yang X-L, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W, Peng C, Zhang Y-J, Luo C-M, Tan B, Wang N, Zhu Y, Cramer G, Zhang S-Y, Wang L-F, **Daszak P***, Shi Z-L* (2013). Isolation and characterization of a bat SARS-like Coronavirus that uses the ACE2 receptor. **Nature** 503: 535-538.
- b. Memish ZA, Mishra N, Olival KJ, Fagbo SF, Kapoor V, Epstein JH, Al Hakeem R, Durosinioun A, Al Asmari M, Islam A, Kapoor A, Briese T, **Daszak P**, Al Rabeeah A, Lipkin WI. (2013). Middle East respiratory syndrome coronavirus in bats, Saudi Arabia. **EID** 19(11): 1819-1823.
- c. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chen J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Fuo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang X-L-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, **Daszak P***, Wang L-F*, Shi Z-L*, Tong Y-G*,

Ma J-Y* (2018). Fatal Swine Acute Diarrhea Syndrome caused by an HKU2-related Coronavirus of Bat Origin. **Nature** 556: 255-258.

d. Nikolay B, Salje H, Hossain MJ, Khan AKMD, Sazzad HMS, Rahman M, **Daszak P**, Ströher U, Pulliam JRC, Kilpatrick AM, Nichol ST, Klena JD, Sultana S, Afroj S, Luby SP, Cauchemez S & Gurley ES. (2019). Transmission of Nipah Virus - 14 Years of Investigations in Bangladesh. **New England Journal of Medicine** 380:1804-1814

2. Analyzing the process of disease emergence. Emerging infectious diseases are a significant threat to global health. However, their emergence is sporadic, and involves a complex process that is hard to predict. In the early 2000s I started to use analytical approaches to identify predictable patterns in the process of disease emergence. By collating a database of all known prior EID events, identifying their point origins, and correcting for reporting biases, I published the first ever predictive 'hotspots' maps of where future disease emergence is most likely. I have continued this line of research, publishing spatial analyses of the drivers of disease spread, and outlining strategies to predict pandemic emergence.

a. Kilpatrick AM, Chmura AA, Gibbons DW, Fleischer RC, Marra PP & **Daszak P** (2006). Predicting the global spread of H5N1 avian influenza. **PNAS** 103: 19368-19373.

b. Morse SS, Mazet JAK, Woolhouse M, Parrish CR, Carroll D, Karesh WB, Zambrana-Torrel C, Lipkin WI, **Daszak P*** (2012). Prediction and prevention of the next pandemic zoonosis. **Lancet** 380:1956-1965.

c. **Daszak P***, Zambrana-Torrel C, Bogich TL, Fernandez M, Epstein JH, Murray KA, Hamilton H (2013). Interdisciplinary approaches to understanding disease emergence: The past, present and future drivers of Nipah virus emergence. **PNAS** 110: 3681-3688

d. Allen T, Murray KA, Zambrana-Torrel C, Morse SS, Rondinini C, Di Marco M, Breit N, Olival KJ, **Daszak P*** (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8: 1124

3. Studies of wildlife disease ecology to understand emerging zoonoses. The majority of EIDs are zoonotic, with the majority of these originating in wildlife. I reviewed this field in a paper in *Science* in 2000 and in a more recent paper in *Nature* on the links among biodiversity and health. During the last two decades, I have led collaborative research programs on how the ecology of specific wildlife-origin zoonoses can help explain patterns of risk to people. This includes my role as PI on 4 R01s, as institutional lead for USAID-EPT-PREDICT, and Chief of Party for USAID-IDEAL. This work includes estimations of the diversity of yet-to-be discovered viruses which forms the rationale for the Global Virome Project.

a. **Daszak P***, Cunningham AA, Hyatt AD (2000). Emerging infectious diseases of wildlife - threats to biodiversity and human health. **Science** 287: 443-449

b. Keesing F, Belden LK, **Daszak P**, Dobson A, Harvell CD, Holt RD, Hudson P, Jolles A, Jones KE, Mitchell CE, Myers SS, Bogich T & Ostfeld RS. (2010). Impacts of biodiversity on the emergence and transmission of infectious diseases. **Nature** 468:647-652.

c. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrel CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Ali Khan S, Hosseini P, Bogich TL, Olival KJ, Sanchez-Leon MD, Karesh W, Goldstein T, Luby SP, Morse SS, Mazet JAK, **Daszak P***, Lipkin WI. (2013). A strategy to estimate unknown viral diversity in mammals. **MBio** 4(5): e00598-13.

d. Mandl JN, Ahmed R, Barreiro LB, **Daszak P**, Epstein JH, Virgin HW, Feinberg MB. (2015). Reservoir host immune responses to emerging zoonotic viruses. **Cell** 160: 20-35

4. National and international leadership in infectious disease research. I have tried to use my research to promote multidisciplinary collaboration among medical doctors, veterinarians and ecologists. In addition

to primary data and analysis papers, I have published editorials, reviews, book chapters to highlight these linkages, including 5 Policy Forums and editorials in *Science*. I have served as a member of the NASEM Forum on Microbial Threats for over 10 years, and now Chair, where I help set the agenda on EID threats. I am a new and active member of the National Academy of Medicine, and represent the health sciences on the NRC Committee to Advise the US Global Change Research Program. I have served on advisory and review boards at CSIRO, Australia and on the Australian Biosecurity CRC, and on all annual meetings of the WHO R&D Blueprint Pathogen Prioritization Committee. I have managed meetings among senior leadership of the US NSF and NSF-China to promote US-China collaboration, and am an active member of a series of One Health editorial boards and international organization boards, as well as a Commissioner of *The Lancet Commission on One Health*.

- a. Womack JE, Anderson LC, Bull LS, Capen CS, Cheville NF, **Daszak P**, Dodds WJ, Doyle MP, Franz DR, Shadduck JA, Shaw DH, Swayne DE, Tolwani RJ (2005). Critical needs for research in veterinary science. **National Academies Press**, 222 pp.
- b. Rodríguez JP, Taber AB, **Daszak P**, Sukumar R, Valladares-Padua C, Padua S, Aguirre LF, Medellín R, Acosta M, Aguirre AA, Bonacic C, Bordino P, Bruschini J, Buchori D, González S, Mathew T, Mendez M, Mugijca L, Pacheco LF, Dobson AP, Pearl M (2007). Policy Forum: The globalization of conservation: A view from the South. **Science** 317: 755-756.
- c. Smith KF*, Behrens M, Schloegel LM, Marano N, Burgiel S & **Daszak P*** (2009). Reducing the risks of the wildlife trade. **Science** 324: 594-595.
- d. **Daszak P** (2012). Anatomy of a pandemic. **Lancet** 380: 1883-1884. Lead article as Guest Editor for a **Lancet Series** on Zoonoses.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats PREDICT-2	Mazet (PI)	10/01/14 – 09/30/19
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The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries
Role: PI on Subcontract

2R01 AI110964	Daszak (PI)	06/01/19 – 05/31/24
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Understanding the Risk of Bat Coronavirus Emergence
The goal of this work is to characterize the virological, behavioral and demographic factors that present a high risk of future emergence of SARSr-CoVs in people in southern China, and identify any clinical outcomes.
Role: PI

Completed Research Support (last 3 years only) out of 14 prior awards

1R01 AI110964	Daszak (PI)	06/01/14 – 05/31/19
---------------	-------------	---------------------

Understanding the Risk of Bat Coronavirus Emergence
The goal was to conduct ecological and virological studies on bat-origin SARSr-CoVs in China, behavioral risk surveys and testing in people, to identify risk of future spillover of these viruses.
Role: PI

USAID 1414374 (RDMA, Thailand)	Daszak (CoP)	10/01/13 - 03/30/19
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Infectious Disease Emergence and Economics of Altered Landscapes (IDEEAL)
Cooperative agreement to analyze how land use change affects economics of disease risk in SE Asia.
Role: Chief of Party

NSF DEB 1414374	Perrings (PI)	10/15/14 - 04/14/18
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US-UK Collab: Risks of Animal and Plant Infectious Diseases through Trade (RAPID Trade)
The goal is to analyze and model how policy changes to trade affect emerging disease risk globally.
Role: Co-Investigator

HDTRA1 Allen (PI) 04/15/15 - 04/14/17
Global Rapid Identification of undiagnosed EID Events
The goal was to design software for the DoD biosurveillance ecosystem to diagnose novel EID events.
Role: Co-Investigator

1R01GM100471 (NIGMS) Perrings (PI) 09/15/11-06/30/15
MASpread: Modeling Anthropogenic Effects in the Spread of Infectious Disease
The goal was to analyze the social decisions involved in disease spread through trade.
Role: Co-Investigator

NSF Daszak (PI) 07/01/10-06/30/15
EcoHealthNet - a Research Coordination Network
Funding for student exchange and workshops to fuse veterinary science, ecology and human medical sciences
Role: PI

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Olival, Kevin James

eRA COMMONS USER NAME: (b) (6)

POSITION TITLE: Vice President for Research

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Colorado State University, Fort Collins, CO	B.S	05/1997	Biology
Columbia University, New York, NY	M.A	10/2003	Conservation Biology
Columbia University, New York, NY	Ph.D.	05/2008	Ecology & Evolution
American Museum of Natural History, New York	Post Doctoral	08/2009	Molecular Parasitology
NIH Fogarty US Global Health Fellow, New York	Post Doctoral	08/2011	International Emerging Infectious Diseases

A. Personal Statement

The goal of our proposal is to establish an Emerging Infectious Disease Research Center in Southeast Asia to better understand the risk of zoonotic viral emergence, and to strengthen regional capacity to identify, characterize, and rapidly respond to novel infectious diseases threats. I have 17 years of experience managing zoonotic disease surveillance projects, primarily in Southeast Asia, and leading cutting-edge research on pathogen discovery, disease ecology, and modeling the risk of viral spillover that are strongly complementary to our project's aims. As a PhD student and then NIH-Fogarty Global Health Post-Doc Fellow, I investigated the ecology of Nipah virus in Malaysia and Bangladesh, respectively, using phylogeographic approaches to integrate wildlife host and virus data. Over the last 10 years, I have served as the global lead for USAID-PREDICT activities in Thailand and Indonesia managing all human and animal surveillance, and coordinated training and other project activities in Malaysia, Myanmar, Bangladesh, and India. I have managed field-based disease investigations around the world, leading to the following significant discoveries: the wildlife origin of Ebola Reston in the Philippines, first evidence of Ebola Zaire infection in Asian wildlife, MERS-CoV in Saudi Arabian bats, and the first isolation of Nipah virus from the large flying fox in Malaysia. I currently serve as the Modeling & Analytics coordinator under the USAID PREDICT-2 project, leading a team analyzing combined human, animal, and laboratory surveillance data to predict and prevent zoonoses. As part of this effort, I developed a new approach that combines phylogenetic, ecological, and life-history traits to predict viral diversity, host/reservoir range, and spillover potential, leading to a recent first author paper in *Nature*.

1. Rahman SA, Hassan SS, **Olival KJ**, Mohamed M, Chang L-Y, Hassan L, Saad NM, Shohaimi SA, Mamat ZC, Naim MS, Epstein JH, Suri AS, Field HE, Daszak P and HERG (2010). Characterization of Nipah virus from Naturally Infected *Pteropus vampyrus* Bats, Malaysia. **EID** 16(12): 1990-1993.
2. **Olival KJ***, Islam A, Yu M, Anthony SJ, Epstein JH, Khan SA, Khan SU, Crameri G, Wang LF, Lipkin WI, Luby SP, and Daszak P (2013). Ebolavirus Antibodies in Fruit Bats, Bangladesh. **EID** 19(2): 270-273.

3. Memish ZA, Mishra N, **Olival KJ**, Fagbo SF, Kapoor V, Epstein JH, AlHakeem R, Al Asmari M, Islam A, Kapoor A, Briese T, Daszak P, Al Rabeeah AA, Lipkin WI (2013). Middle East Respiratory Syndrome Coronavirus in Bats, Saudi Arabia. **EID** 19(11): 1819-1823.
4. **Olival KJ***, Hosseini P, Zambra-Torrellio C, Ross N, Bogich T, Daszak P* (2017). Host and viral traits predict zoonotic spillover from mammals. **Nature** 546(7660): 646-650.

*corresponding author

B. Positions and Honors

Positions and Employment

- 1999 -02 Research Associate, Kewalo Marine Laboratory, University of Hawaii
- 2003 -07 US Environmental Protection Agency STAR Fellow
- 2006 -13 Instructor, Columbia University Secondary School Summer Program
- 2010 -12 NIH Fogarty US Global Health Post-Doc Fellow
- 2012 -15 Senior Research Scientist, EcoHealth Alliance
- 2015 -17 Associate Vice President for Research, EcoHealth Alliance
- 2009 - Visiting Scientist, American Museum of Natural History
- 2009 - Adjunct Faculty, Earth Institute Center for Environmental Sustainability, Columbia University
- 2017 - Vice President for Research, EcoHealth Alliance

Other Experience and Professional Memberships

- 1998 -00 Member, American Association for the Advancement of Science
- 2000 -02 Mentor, NSF Undergraduate Mentoring in Environmental Biology (UMEB), University of Hawaii
- 2003 -05 Member, American Society of Mammalogists
- 2005 -06 Member, New York Academy of Sciences
- 2011 - Scientific Steering Committee Member, Southeast Asian Bat Conservation Research Unit
- 2011 - Scientific Advisory Board Member, Lube Bat Conservancy, FL
- 2011 - Scientific Advisor, Bat Conservation International
- 2011 - Review Editor, EcoHealth
- 2015 - US White-Nose Syndrome Stakeholder Committee and Communications Committee Member
- 2017 - DoD DTRA: Steering Committee Member, Bat One Health Research Network
- 2017 - Founder, Western Asia Bat Research Network

Honors

- 1993 -97 Colorado State University Distinguished Scholar Award
- 2003 NSF Graduate Student Fellowship, Honorable Mention
- 2005 -07 Bat Conservation International Student Award and Scholarship
- 2004 -07 US EPA STAR Fellowship Award
- 2008 PhD Dissertation *with Distinction*, Columbia University
- 2013 Plenary Speaker, 11th Annual ASM Biodefense and EID Research Meeting
- 2013 -14 Institute of Medicine, Forum on Microbial Threats. Invited speaker, briefings on MERS-CoV and Emerging Viral Diseases
- 2016 Plenary Speaker, NYC Medtech conference – Global Virome Project
- 2017 -18 Three papers awarded the InCites Highly Cited Paper™ designation (top 1% in field) for Immunology and Microbiology
- 2019 Keynote Speaker, World-Wide Human Geography Data Working Group, Harvard University, MA
- 2019 Keynote Speaker, 18th International Bat Research Conference, Phuket, Thailand

C. Contribution to Science

1. **Characterizing viral diversity in people and wildlife.** A large body of my research has focused on the discovery and characterization of viruses in wildlife populations to better anticipate viral emergence. This includes over 10 studies in South and Southeast Asia, generating sequence data for 100s of novel viral strains. These include: molecular evidence for MERS-related coronaviruses circulating in bats at guano mining sites in Thailand; Ebola Reston sequences from multiple bat species in the Philippines captured near pig farms where outbreaks first occurred; and novel virus discovery using metagenomic approaches in Saudi Arabian bats collected at the site of the first human MERS-CoV case. Lastly, follow-up human viral surveillance in guano miner populations from Thailand yielded a full-genome sequence of HKU-1 coronavirus. Most of these research studies were conducted and published jointly with in-country colleagues on the current proposal.
 - a. Wacharapluesadee S, Sintunawa C, Kaewpom T, Khongnomnan K, **Olival KJ**, Epstein JH, Rodpan A, Sangsri P, Intarut N, Chindamporn A, Suksawa K, Hemachudha T (2013). Group C Betacoronavirus in Bat Guano Fertilizer, Thailand. **EID** 19(8): 1349-1352.
 - b. Jayme S, Yu M, Jong Cd, **Olival KJ**, Tagtag A, Hughes T, Foord A, Marsh G, Crameri G, Epstein JH, Santos I, Catbagan D, Lim M, Benigno C, Wang L, Daszak P, Field H, Newman S (2015). Molecular evidence of Ebola Reston virus infection in Philippine bats. **Virology Journal** 12(1): 107.
 - c. Mishra N, Fagbo S, Alagaili AN, Nitido A, Williams SH, Ng J, Lee B, Durosini A, Garcia JA, Jain K, Kapoor V, Epstein JH, Briese T, Memish Z, **Olival KJ**, Lipkin WI (2019). A viral metagenomic survey identifies known and novel mammalian viruses in bats from Saudi Arabia. **PLOS ONE** 14(4): e0214227.
 - d. Joyjinda Y, Rodpan A, Charpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, **Olival KJ**, Stokes MM, Hemachudha T, Wacharapluesadee S (2019). First complete genome sequence of Human Coronavirus HKU1 (HCoV-HKU1) from a non-ill bat guano miner, Thailand. **Microbiol Resour Announc** 8:e01457-18.

2. **Analyses to better target zoonotic disease surveillance.** For the last 5 years, I have led the development of new strategies to better target the geographic regions, transmission pathways, host species, and sample types to make zoonotic surveillance more effective. (b) (4)

Previous work includes the first use of species accumulation curves to estimate viral diversity from longitudinal surveillance data in wildlife (Bangladesh bats); two meta-analyses using pathogen-specific transmission and host range data from all known zoonotic EIDs to refine disease surveillance targets; and analysis of data from 100 viral discovery studies in bats to optimize surveillance.

 - a. Anthony SJ, Epstein JH, Murray KA, Navarrete-Macias I, Zambrana-Torrel CM, Solovyov A, Ojeda-Flores R, Arrigo NC, Islam A, Khan SA, Hosseini P, Bogich TL, **Olival KJ**, Sanchez-Leon MD, Karesh WB, Goldstein T, Luby SP, Morse SS, Mazet JAK, Daszak P, Lipkin WI (2013). A Strategy To Estimate Unknown Viral Diversity in Mammals. **Mbio** 4(5): e00598-13.
 - b. Levinson J, Bogich TL, **Olival KJ**, Epstein JH, Johnson CK, Karesh WB, and Daszak P (2013). Targeting surveillance for zoonotic virus discovery. **EID** 19(5): 743-747.
 - c. Loh EH, Bogich TL, **Olival KJ**, Johnson CK, Mazet JAK, Karesh W, Daszak P (2015). Targeting emergence pathways for zoonotic disease surveillance and control. **Vector Borne and Zoonotic Diseases** 15(7):432-437.
 - d. Young CC and **Olival KJ*** (2016). Optimizing Viral Discovery in Bats. **PLOS ONE** 11(2): e0149237.

- 3. Modeling global disease emergence and spillover risk.** I have used my applied ecology background to develop new models that help explain zoonotic spillover and disease circulation. This includes studies of the environmental drivers of bat virus spillover to humans, cross-species transmission among bat species, spatial analysis of emerging zoonotic disease hotspots, and novel phylo-factorization approaches to estimating viral host range. These models explicitly use data from PCR- and serology-based field studies, combined with an understanding of wildlife biology, ecology, and host phylogenetics and evolution, to assess the environmental and demographic drivers of disease transmission -- bridging the gap between field investigations and transmission risk.
- Brierley L, Vonhof MJ, **Olival KJ**, Daszak P, Jones KE (2016). Quantifying global drivers of zoonotic bat viruses: a process-based perspective. **American Naturalist** 187(2): E53-64.
 - Willoughby AR, Phelps K, PREDICT Consortium, **Olival KJ*** (2017). A Comparative Analysis of Viral Richness and Viral Sharing in Cave-Roosting Bats. **Diversity** 9(3): 35.
 - Allen T, Murray KA, Zambrana-Torrel C, Morse SS, Rondinini C, Di Marco M, Breit N, **Olival KJ**, Daszak P (2017). Global hotspots and correlates of emerging zoonotic diseases. **Nature Comm** 8(1124): 1-10.
 - Washburne A, Crowley DE, Becker DJ, **Olival KJ**, Taylor M, Munster VJ, Plowright RK (2018). Taxonomic patterns in the zoonotic potential of mammalian viruses. **PeerJ** 6:e5979.
- 4. Elucidating host-vector-pathogen interactions using evolutionary biology.** I started using evolutionary and phylogenetic tools to improve the understanding of host and vector disease biology during my PhD dissertation. I continued this through my NIH post-doctoral fellowship research on Nipah virus dynamics using host phylogeographic analyses of *Pteropus* spp. fruit bats and their associated bat fly vectors. Other examples include DNA barcoding analysis of mosquito bloodmeals to understand bunyavirus vertebrate host range; co-phylogenetic mapping of bacterial pathogens in bats and rodents to identify host-switching events; and analyzing patterns of coronavirus diversification in bat communities in Eastern Thailand.
- Murdock C, **Olival KJ**, and Perkins SL (2010). Feeding preference of snow-melt mosquitoes (Culicidae: *Culiseta* and *Ochlerotatus*) show a link between cervid amplifying hosts for Jamestown Canyon Virus (Bunyaviridae: Orthobunyavirus) and humans. **Journal of Medical Entomology**. 47(2): 226-229.
 - Olival KJ***, Dick CW, Simmons NB, Morales JC, Melnick DJ, Dittmar K, Perkins SL, Daszak P, DeSalle R (2013). Lack of population genetic structure and host specificity in the bat fly, *Cyclopodia horsfieldi*, across species of *Pteropus* bats in Southeast Asia. **Parasites & Vectors**. 8(6): e231.
 - Lei BR, **Olival KJ*** (2014). Contrasting Patterns in Mammal-Bacteria Coevolution: *Bartonella* and *Leptospira* in Bats and Rodents. **PLOS NTD**. 8(3): e2738.
 - Wacharapluesadee S, Duengkae P, Rodparn A, Kaewpom T, Maneeorn P, Kanchanasaka B, Yinsakmongkon S, Sittidetboripat N, Chareesaen C, Khlangsap N, Pidthong A, Leadprathom K, Ghai S, Epstein JH, Daszak P, **Olival KJ**, Blair PJ, Callahan MV, Hemachudha T (2015). Diversity of Coronavirus in Bats from Eastern Thailand. **Virology Journal** 12:57.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

HDTRA11710064

Olival (PI)

10/02/17-10/01/22

Understanding the Risk of Bat-Borne Zoonotic Disease Emergence in Western Asia

The goal of this project is to characterize pathogen diversity, strengthen zoonotic disease surveillance capacity, and test key hypotheses about the risk of bat-borne zoonotic disease emergence in Western Asia.

Role: PI

USAID Emerging Pandemic Threat Mazet (PI) 10/01/14-09/30/19
PREDICT 2

The goal of this project is to create and implement a global virus surveillance system in animals and humans and analyze spillover risk.

Role: Modeling and Analytics Coordinator; Country lead for Indonesia and Thailand.

Completed Research Support

R01 AI110964 Daszak (PI) 06/01/14-05/31/19
Understanding Risk of Bat Coronaviruses

The goal of this study is to analyze the risk of coronavirus spillover from bats to humans in Southern China

Role: co-PI

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Baric, Ralph Steven

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Professor, Kenan Distinguished Professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
N.C. State University, Raleigh, NC	B.S.	1977	Zoology
N.C. State University, Raleigh, NC	Ph.D.	1982	Microbiology
University of Southern CA, School of Med., Los Angeles, CA	Post-Doc	1986	Microbiology

A. Personal Statement

We use systems genetic, biochemical, molecular and immunologic approaches to study the molecular mechanisms regulating viral evolution, virus immunity, virus-host interactions, virus pathogenesis and vaccine mediated protective immunity primarily using coronaviruses (SARS-CoV, MERS-CoV), noroviruses (GI.4 and related strains) and flaviviruses (Dengue, Zikv) as models. Additional studies have focused on the pathogenesis of influenza and Ebola viruses. My major contributions include publications describing: **a)** emerging coronavirus, Dengue 1-4 and Zikv reverse genetic platforms, **b)** the identification of human host susceptibility alleles that regulate norovirus infection and pathogenesis, **c)** the identification of host susceptibility alleles that regulate SARS-CoV and Ebola virus pathogenesis and immunity using the Collaborative Cross Genetic Reference Population, **d)** the development of platform strategies and animal models to identify and culture emerging, pre-epidemic human viruses from outbreak samples or in silico sequences, **e)** the functional mapping of human monoclonal antibodies and their epitopes against all of the viruses described above, **f)** pioneering approaches in structure guided immunogen design to develop bivalent vaccine and immune diagnostic viruses and VLPs to all three virus families noted above, **e)** the mapping and characterization of the primary targets of polyclonal neutralizing antibodies following infection and vaccination, **g)** the design and testing of broadly cross protective coronavirus, norovirus and dengue virus vaccines, **h)** the identification novel antivirals targeting the emerging human, contemporary and prepandemic threat viruses and **i)** structure-function studies of viral genes involved in replication, pathogenesis, innate immune evasion and cross species transmission. We also helped to demonstrate the existence of the first proof-reading enzyme in an RNA virus. I have extensively collaborated with Dr. Daszak and his team in the past including joint publications and grants. I have considerable experience managing large cooperative centers and program project grants and also study human DENV vaccine outcomes and human norovirus challenge studies.

1. Lindesmith L, Moe C, Marionneau S, Ruvoen N, Jiang X, Lindblad L, Stewart P, LePendou J, **Baric R** (2003). Human susceptibility and resistance to Norwalk virus infection. **Nat Med** 9(5):548-53.
2. Graham RL, Becker MM, Eckerle LD, Bolles M, Denison MR, **Baric RS**. 2012. A live, impaired-fidelity coronavirus vaccine protects in an aged, immunocompromised mouse model of lethal disease. **Nat Med** 6;18(12):1820-6.
3. Menachery VD, Yount BL, Debbink K, Agnihothram S, Gralinski LE, Plante JA, Graham RL, Scobey T, Ge S-Y, Donaldson EF, Randell SH, Lanzavecchia A, Marasco WA, Shi Z-L, **Baric RS** (2015). Novel

platform identifies threat posed by a SARS-like cluster of circulating bat coronavirus. **Nature Med** 21(12):1508-13.

4. Cockrell AS, Yount BL, Scobey T, Jensen K, Douglas M, Beall A, Tang XC, Marasco WA, Heise MT, **Baric RS** (2016). A mouse model for MERS coronavirus-induced acute respiratory distress syndrome. **Nat Microbiol** 28;2:16226.

B. Position and Honors

Positions and Employment

1986 -1992	Assistant Professor, Department of Parasitology and Laboratory Practice and Department of Epidemiology, University of North Carolina (UNC), Chapel Hill, NC
1992 -2001	Associate Professor, Departments of Epidemiology and Microbiology & Immunology, UNC Chapel Hill
2001 -	Professor, Departments of Epidemiology and Microbiology and Immunology, UNC Chapel Hill

Other Experience and Professional Membership

2005 -09	Permanent Member, NIH VirB Study Section
2005 -15	Review Board, J. Virology
2006 -07	Acting Chair and Chair, Division T RNA Viruses, American Society of Microbiology
2007 -08	Associate Editor, Plos Pathogens
2008	Nat'l Acad Sci: Working Group: Gene Sequence Methods for Classification of Select Agents
2008 -17	Senior Editor, Plos Pathogens
2014	National Academy of Sciences: Working Group on Risks and Benefits of Gain of Function Research
2015	MERS-CoV Stakeholders Workshop, Organizer and Invited panelist, NIH
2015	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" September 28-30 in Beijing, China
2017	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" Jan 16-18 th in Galveston-Texas.
2018	Natl. Acad. Of Sciences "China-U.S. Workshop on the Challenges of Emerging Infections, Laboratory Safety, and Global Health Security" Jan 6-10 th in Harbin China.

Honors

1984 -86	Harvey Weaver Scholar, National Multiple Sclerosis Society
1984 -87	Established Investigator: American Heart Association
2003	Finalist/Runner-up, World Technology Award
2011	Innovation/Inspiration Award for Faculty Research, UNC Gillins School of Public Health
2019	Kenan Distinguished Professor

C. Contributions to Science

1. **Contributions to Virology:** My group studies coronavirus, norovirus and flavivirus immunology, molecular biology, virus-host interactions, genetics, pathogenesis, vaccine and therapeutic design, using traditional and new technologies like structure guided immunogen design, synthetic genome design, and systems genetics. We developed new approaches to identify and recover pre-pandemic viruses.
 - a. Yount B, Curtis K, Fritz L, Hensley L, Jahrling P, Prentice E, Denison M, Geisbert T, **Baric RS** (2003). Reverse Genetics with a full-length infectious cDNA for the SARS Coronavirus. **Proc Natl Acad Sci USA** 100(22):12995-13000.
 - b. Lindesmith LC, Donaldson EF, Lobue AD, Cannon JL, Zheng DP, Vinje J, **Baric RS** (2008). Mechanisms of GII.4 NoV persistence in humans. **PLoS Med** 5(2):e31.
 - c. Sheahan TP, Sims AC, Graham RL, Menachery VD, Gralinski LE, Case JB, Leist SR, Pirc K, Feng JY, Trantcheva I, Bannister R, Park Y, Babusis D, Clarke MO, Mackman RL, Spahn JE, Palmiotti CA, Siegel D, Ray AS, Cihlar T, Jordan R, Denison MR, **Baric RS** (2017). Broad-spectrum antiviral GS-5734 inhibits both epidemic and zoonotic CoV. **Sci Transl Med** 28;9(396).

- d. Menachery VD, Yount BL Jr, (+15 other authors) and **Baric RS** (2016). SARS-like WIV1-CoV poised for human emergence. **Proc Natl Acad Sci USA** 113:3048-3053.
- 2. Viral Immunity.** New diagnostic metrics are needed to identify precise correlates of protective immunity at the molecular level. Our group has pioneered the use of structure-guided immunogen design, coupled with reverse genetic strategies, to transfer complex conformational immunogen epitopes between viruses (or viral proteins), using noroviruses and dengue/zikv virus as model platforms.
- a. Lindesmith LC, Ferris MT, Mullan CW, Ferreira J, Debbink K, Swanstrom J, Richardson C, Goodwin RR, Baehner F, Mendelman PM, Bargatze RF, **Baric RS** (2015). Broad blockade antibody responses in human volunteers after immunization with a multivalent norovirus VLP candidate vaccine: immunological analyses from a phase I clinical trial. **PLoS Med** 24;12(3):e1001807.
- b. Gallichotte EN, Baric TJ, Yount BL Jr, Widman DG, Durbin A, Whitehead S, **Baric RS**, de Silva AM (2018). Human dengue virus serotype 2 neutralizing antibodies target two distinct quaternary epitopes. **PLoS Pathog** 26;14(2):e1006934.
- c. Gallichotte EN, Baric TJ, Nivarthi U, Delacruz MJ, Graham R, Widman DG, Yount BL, Durbin AP, Whitehead SS, de Silva AM, **Baric RS** (2018). Genetic Variation between Dengue Virus Type 4 Strains Impacts Human Antibody Binding and Neutralization. **Cell Rep** 30;25(5):1214-1224.
- d. Lindesmith LC, McDaniel JR, Changela A, Verardi R, Kerr SA, Costantini V, Brewer-Jensen PD, Mallory ML, Voss WN, Boutz DR, Blazeck JJ, Ippolito GC, Vinje J, Kwong PD, Georgiou G, **Baric RS**. Sera Antibody Repertoire Analyses Reveal Mechanisms of Broad and Pandemic Strain Neutralizing Responses after Human Norovirus Vaccination. *Immunity*. 2019 Jun 18;50(6):1530-1541.e8.
- 3. Virus Molecular Genetics/Immunity.** My group has pioneered strategies for performing reverse genetic analyses in coronaviruses and flaviviruses, including recently emerged strains like SARS-CoV, MERS-CoV, PEDV, conventional human and model coronaviruses like MHV and HCoV NL63, and several bat coronaviruses. We have also built full length infectious cDNA clones for DENV1-4 serotypes, several Zikv strains, as well as panels of isogenic DENV serotypes encoding genotype distinct E glycoproteins. We demonstrated that coronaviruses and influenza viruses regulate host expression, by epigenetics.
- a. Douglas G, Widman DG, Ellen Young E, Yount BL, Plante K, Carbaugh D, Gallichotte EN, Peck KM, Plante J, Swanstrom J, Heise MT, Lazear HM, **Baric RS** (2017). A reverse genetics platform that spans the Zika virus family tree. **MBio** 7;8(2). pii: e02014-16.
- b. Swanstrom JA, Plante JA, Plante KS, Young EF, McGowan E, Gallichotte EN, Widman DG, Heise MT, de Silva AM, **Baric R** (2016). Dengue Virus Envelope Dimer Epitope Monoclonal Antibodies Isolated from Dengue Patients Are Protective against Zika Virus. **MBio** 19;7(4). pii: e01123-16.
- c. Lindesmith LC, Beltramello M, Donaldson EF, Corti D, Swanstrom J, Debbink K, Lanzavecchia A, **Baric RS** (2012). Immunogenetic mechanisms driving norovirus GII.4 antigenic variation. **PLoS Pathog** 8(5):e1002705.
- d. Menachery VD, Einfeld AJ, (+23 other authors) and Baric RS. Pathogenic influenza viruses and coronaviruses utilize similar and contrasting approaches to control interferon-stimulated gene responses. **Mbio** 5:e01174-14, 2014.
- 4. Host Susceptibility/Innate Immune Antagonism.** Coronaviruses, noroviruses and DENV are major causes of human morbidity and mortality worldwide. We have used the Collaborative Cross Mice to identify host susceptibility alleles that regulate SARS-CoV and EBoV pathogenesis, and demonstrated common epigenetic control mechanisms that antagonize antigen presentation after infection.
- a. Gralinski LE, Ferris MT, (+16 other authors) and **Baric RS** (2015). Genome Wide Identification of SARS-CoV Susceptibility Loci Using the Collaborative Cross. **PLoS Genet** 11:e1005504,
- b. Gralinski L, Menachery V, (+9 other authors) and **Baric RS** (2017). *Ticam2* contributes to SARS-CoV pathogenesis. **G3** 7;7(6):1653-1663.
- c. Rasmussen AL, Okumura A, (**Baric RS** + 18 others) and Katze MG (2014). Host genetic diversity enables Ebola hemorrhagic fever pathogenesis and resistance. **Science** 346:987-991, PMC4241145.

- d. Menachery VD, Schäfer A, (+12 other authors), Sims AC, Kawaoka Y, **Baric RS** (2018). MERS-CoV and H5N1 influenza virus antagonize antigen presentation by altering the epigenetic landscape. **Proc Natl Acad Sci USA** 30;115(5):E1012-E1021.
- 5. Pathogenesis and Intervention Studies.** Our group has studied the role of virus-host interactions in susceptibility, pathogenesis and vaccine design.
- a. Adams Waldorf KM, Nelson BR, Stencel-Baerenwald JE, Studholme C, Kapur RP, Armistead B, Walker CL, Merillat S, Vornhagen J, Tisoncik-Go J, Baldessari A, Coleman M, Dighe MK, Shaw DWW, Roby JA, Santana-Ufret V, Boldenow E, Li J, Gao X, Davis MA, Swanstrom JA, Jensen K, Widman DG, **Baric RS et al** (2018). Congenital Zika virus infection as a silent pathology with loss of neurogenic output in the fetal brain. **Nat Med** 24(3):368-374.
- b. Tang XC, Agnihothram SS, Jiao Y, Stanhope J, Graham RL, Peterson EC, Avnir Y, Tallarico AS, Sheehan J, Zhu Q, **Baric RS**, Marasco WA (2014). Identification of human neutralizing antibodies against MERS-CoV and their role in virus adaptive evolution. **PNAS USA** 13;111(19):E2018-26.
- c. de Alwis R, Smith SA, Olivarez NP, Messer WB, Huynh JP, Wahala WM, White LJ, Diamond MS, **Baric RS**, Crowe JE Jr, de Silva AM (2012). Identification of human neutralizing antibodies that bind to complex epitopes on dengue virions. **PNAS USA** 8;109(19):7439-44.
- d. Zhang S, Kostyuchenko VA, Ng TS, Lim XN, Ooi JS, Lambert S, Tan TY, Widman DG, Shi J, **Baric RS**, Lok SM (2016). Neutralization mechanism of a highly potent antibody against Zika virus. **Nat Commun** 24;7:13679.

Complete List of Publications in MyBibliography:

<http://www.ncbi.nlm.nih.gov/sites/myncbi/ralph.baric.1/bibliography/40583903/public/?sort=date&direction=ascending>. 328 total publications, >120 since 2014, overall H-index:86; 22625 total citations.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

- | | | |
|---|---|-------------------------------------|
| U19 AI 142759 CETR | Whitley (PI) | 03/07/19-02/28/24 |
| UAB/NIH/NIAID | Antiviral Drug Discovery and Development Center | Role: Baric Co-Director: Project 2. |
| The specific aims of the proposal will identify small molecule inhibitors of CoV replication and pathogenesis. | | |
| U19 AI109761 CETR | Lipkin (PI) | 03/01/14-02/28/19 |
| (NCE) Columbia/NIH/NIAID | Diagnostic and Prognostic Biomarkers for Viral Severe Lung Disease | |
| The goal is to develop new platform technologies that use functional genomics as diagnostic and prognostic indicators of severe end stage lung disease following virus infection. Role: Project 1 Leader. | | |
| R01 AI110700 | Baric/Li(MPIs) | 04/20/15-03/31/20 |
| NIH/NIAID | Mechanisms of MERS-CoV Entry, Cross-species Transmission and Pathogenesis | |
| The overall goal is to build a comprehensive understanding of the molecular mechanisms guiding group 2c CoV receptor recognition, entry and pathogenesis. | | |
| P01 AI106695 | Harris (PI) | 07/1/2015-6/30/20 |
| NIH/NIAID | Protective immunity following dengue virus natural infections and vaccination | |
| Project 2: Aravinda deSilva and Ralph S. Baric (Co-PI). The goal of these studies is to identify natural correlates of protective immunity following natural infection and or vaccination. | | |
| R01 AI125198 | de Silva (PI) | 05/01/16-04/30/21 |
| NIH/NIAID | Preclinical assays to predict dengue vaccine efficacy | |
| We use samples from DENV tetravalent vaccine clinical trials to identify mechanisms and correlates of protective immunity or breakthrough infections in vaccines. Role: Co-investigator | | |
| R01 AI 089728 | Fang Li (PI) | 07/01/16-06/30/21 |
| NIH/NIAID | Receptor recognition and cell entry of coronaviruses | |
| The program studies receptor usage and cell entry mechanisms of emerging coronaviruses, focused on PEDV, MHV and SARS-like Coronaviruses. Role: Co-Investigator | | |
| U19 AI00625 | Baric/Heise (MPIs) | 9/01/17-8/31/22 |
| NIH/NIAID | Systems Immunogenetics of Biodefense Pathogens in the Collaborative Cross | |

We use the Collaborative Cross (CC) to identify genes and gene interactions which regulate the induction, kinetics, and magnitude of the innate, inflammatory and adaptive immune response after infection.

R01 AI132178 Baric/Sheahan (PI) 08/15/17-8/14/22
NIH/NIAID Broad-spectrum antiviral GS-5734 to treat MERS-CoV and related emerging CoV.
The goal of this proposal is to obtain GS-5734 preclinical data for IND development and translational studies, all designed to move the therapeutic into human trials.

Not Assigned Baric (PI) 07/01/16-12/30/19
(b) (4) Breadth of Blockade Antibody Responses Following Norovirus Vaccination.
(b) (4) and UNC will collaborate to evaluate the breadth of the antibody blockade response following norovirus vaccination of about 14,000 samples in various human volunteer populations.

R01 AI108197 Baric/Denison (MPIs) 05/01/18-04/30/23
NIH/NIAID Determinants of Coronavirus Fidelity in Replication and Pathogenesis
We test if nsp14 functions in maintaining high replication fidelity and antagonizes innate immunity.

R21 AI135682 Baric/Georgiou (MPIs) 04/01/18-03/30/20
NIH/NIAID Molecular Analysis of Serum Antibody Constituents in Zika Virus Infection.
The goal of this application is to identify antibodies that make up the serologic repertoire after Zikv infection of naive and DENV preimmune individuals. Role: Co-investigator.

NIH R01AI127845 Becker-Dreps (PI) 09/01/16-08/31/21
NIH/NIAID Natural history, immunity, and transmission patterns of sapovirus in a Nicaraguan birth cohort
We study sapovirus gastroenteritis and immunity in early childhood development. We also study the potential impact of maternal immunity on infection. Role: Investigator.

R01 AI 107731 de Silva (PI) 03/01/19-02/27/24
NIH/NIAID Molecular Basis of Dengue Virus Neutralization by Human Antibodies
These studies proposed here are directly relevant to developing simple assays to predict the performance, safety and efficacy of the leading dengue vaccine candidates. Role: Co-Investigator.

48415 de Silva (PI) 06/30/16-12/31/19
(b) (4) UNC- (b) (4) study to characterize human antibody response to DENVax
The de Silva and Baric laboratories will jointly characterize the properties of neutralizing antibodies using competition assays with monoclonal antibodies and neutralization assays. Role: Investigator

D43 TW010923 Becker-Dreps/Meshnick (MPIs) 05/10/18-02/28/23
NIH/NIAID Nicaraguan Emerging and Endemic Diseases (NEED)
The goals of this program are to 1) train young Nicaraguan scientists in Infectious Disease Epidemiology at the UNC, 2) create a sustainable supply of scientists in Nicaragua and 3) foster professional growth and development among trainees and local faculty. Role: Investigator

R21 AI137887 Moorman/Heise (MPIs) 02/05/18-01/31/20
NIH/NIAID Molecular Characterization of Functional RNA Structures in the ZikV genome
The proposed studies will identify new viral virulence determinants that can be targeted to generate safer and more effective Zika virus vaccines and therapeutics. Role: Investigator

K24 AI141744 Becker-Dreps (PI) 12/06/18-11/30/23
NIH/NIAID. The Development of Norovirus Immunity in Early Childhood and Implications for Norovirus Vaccines. To acquire new research skills and carry out a research plan that will allow guidance of the development of pediatric norovirus vaccines. Role: Investigator.

U01AI149644 Baric (PI) 05/01/2019-4/30/2024
NIH/NIAID Respiratory Virus Vaccine and Adjuvant Exploration
To use systems genetic approaches to map susceptibility alleles that regulate vaccine and adjuvant performance in genetic reference models of outbred populations.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Wang, Linfa

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Professor and Programme Director

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
East China Normal University, Shanghai, China	B.S.	02/1982	Biology
University of California, Davis, USA	Ph.D.	06/1986	Molecular Biology

A. Personal Statement

My research group focuses on the investigation of emerging infectious diseases, especially those caused by zoonotic agents or with unknown etiology. Trained as a biochemist and molecular biologist, I have been working in the field of virology and infectious diseases for more than 25 years and played a key role in identification of animal links with several high-profile zoonotic agents, including Hendra virus in Australia, Nipah virus in Malaysia and SARS virus in China. In my current role as director of the Program in Emerging Infectious Diseases at Duke-NUS Medical School, I have initiated several major projects to develop cutting edge technological platforms for investigation of human infections of unknown etiology using both molecular and serological approaches. We have also started a new area of research into the interplay of immunity, inflammation, apoptosis, DNA damage repair and tumor suppression of bats as part of an ambitious goal to learn from bats on their ability to live long and co-exist with viruses largely free of clinical diseases. Over the years, I have established an extensive collaborative network with scientists all around the world, covering research and surveillance work into infections of human, animal and wildlife in a truly OneHealth approach. I have been invited by international organizations including WHO, FAO, OIE and CEPI for investigation of major disease outbreaks and for playing a consultation role in several committees in the area of zoonotic infections. My research experience and track record fit extremely well with the proposed project.

- Li W, Shi Z, Yu M, Ren W, Smith C, Epstein JH, Wang H, Crameri G, Hu Z, Zhang H, Zhang J, McEachern J, Field H, Daszak P, Eaton BT, Zhang S, Wang L-F (2005). Bats are natural reservoir of SARS-like coronaviruses. *Science* 310: 676-679.
- Ge XY, Li JL, Yang XL, Chmura AA, Zhu G, Epstein JE, Mazet JK, Hu B, Zhang W, Peng C, Zhang YJ, Luo CM, Tan B, Wang N, Zhu Y, Crameri G, Zhang SY, Wang L-F, Daszak P, Shi Z (2013). Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. *Nature* 503: 535-8.
- Zhang G, Cowled C, Shi, Z, Huang Z, Bishop-Lilly KA, Fang X, Wynne JW, Xiong Z, Baker ML, Zhao W, Tachedijan M, Zhu Y, Zhou P, Jiang X, Ng J, Yang L, Wu L, Xiao J, Feng Y, Chen Y, Sun X, Zhang Y, Marsh GA, Crameri G, Broder CC, Frey KG, **Wang L-F.** and Wang, J (2013). Comparative Analysis of Bat Genomes Provides Insight into the Evolution of Flight and Immunity. *Science* 339: 456-60.
- Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, Zhu Y, Zhang YW, Xie QM, Mani S, Zheng XS, Li B, Li JM, Guo H, Pei GQ, An XP, Chen JW, Zhou L, Mai KJ, Wu ZX, Li D, Anderson DE, Zhang LB, Li SY, Mi ZQ, He TT, Cong F, Guo PJ, Huang R, Luo Y, Liu XL, Chen J, Huang Y, Sun Q, Zhang XL,

Wang YY, Xing SZ, Chen YS, Sun Y, Li J, Daszak P, **Wang L-F**, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556: 255-258.

B. Positions and Honors

Positions and Employment

1982 -86 Doctoral Candidate, Department of Biochemistry, University of California, Davis, USA
1986 -89 Post-doctoral Fellow, Department of Biochemistry, University of California, Davis, USA
1990 Senior Research Officer, Ctr for Molecular Bio. and Med., Monash University, Clayton, Australia
1990 -92 Research Scientist, CSIRO Australian Animal Health Laboratory (AAHL), Geelong, Australia
1992 -96 Senior Research Scientist, CSIRO AAHL, Geelong, Australia
1996 -04 Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2004 -08 Senior Principal Research Scientist, CSIRO AAHL, Geelong, Australia
2008 - OCE Science Leader, CSIRO AAHL, Geelong, Australia
2012 - Professor and Director, Program in Emerging Infectious Diseases, Duke-NUS Medical School, Singapore

Other Experience and Professional Membership

1996 - Editorial Board, Asia Pacific Journal of Molecular Biology and Biotechnology
2003 WHO SARS Scientific Research Advisory Committee
2005 - Honorary Professor, Wuhan Institute of Virology, Chinese Academy of Sciences
2006 - Editorial Board, Chinese Journal of Virology
2006 - Editorial Board, Zoonoses and Public Health
2006 -07 NH&MRC Grant Review Panel
2008 -15 Chair, ICTV Study Group, Paramyxoviridae
2009 - Honorary Professor, The University of Melbourne, Australia
2010 - Editorial Board, Frontiers in Virology
2012 - Editor-in-Chief, Virology Journal
2012 - Board of Directors, Singapore Eye Research Institute
2012 - Executive Committee, Australasian Society of Virology
2013 - WHO International Health Regulations Roster of Experts
2015 - Editorial Board, Scientific Reports

Honors

2006 CSIRO Award for Excellence in Partnership
2007 Finalist, Eureka Prize for Scientific Research
2008 CSIRO CEO Science Leader Award
2010 Elected fellow of the Australian Academy of Technological Sciences and Engineering
2011 Gardner Lecture Award, European Society of Clinical Virologist
2013 CSIRO Chairman's Medal for Research
2014 Winner, Eureka Prize for Infectious Disease Research

C. Contributions to Science

1. Identification of bats as major reservoir of emerging zoonotic viruses. I have used surveillance in wildlife, livestock and humans, coupled with experimental infections under BSL-2, -3, and -4, and laboratory assays to identify evidence that bats are the reservoir for a series of emerging viruses in people, including Hendra virus, Nipah virus, SARS-CoV, and others. This work has been one of the foundations for current interest in bats in EID research globally.

- a. Chua KB, Crameri C, Hyatt A, Yu M, Tompang MR, Rosli J, McEachern J, Crameri S, Kumarasamy V, Eaton BT, **Wang L-F** (2007). A previously unknown reovirus of bat origin is associated with an acute respiratory disease in humans. **Proc. Natl. Acad. Sci. USA** 27: 11424-11429.
- b. Mahalingam S, Herrero LJ, Playford G, Spann K, Herring B, Rolph R, Middleton D, McCall B, Field H, **Wang L-F** (2012). Hendra virus: an emerging paramyxovirus in Australia. **Lancet Infectious Diseases** 12: 799-807.
- c. Zhou P, Fan H, Lan T, Yang X-L, Shi W-F, Zhang W, Zhu Y, Zhang Y-W, Xie Q-M, Mani S, Zheng X-S, Li B, Li J-M, Guo H, Pei G-Q, An X-P, Chein J-W, Zhou L, Mai K-J, Wu Z-X, Li D, Anderson DE, Zhang L-B, Li S-Y, Mi Z-Q, He T-T, Cong F, Guo P-J, Huang R, Luo Y, Liu X-L, Chen J, Huang Y, Sun Q, Zhang H-L, Wang Y-Y, Xing S-Z, Chen Y-S, Sun Y, Li J, Daszak P, **Wang L-F**, Shi ZL, Tong YG, Ma JY (2018). Fatal swine acute diarrhoea syndrome caused by an HKU2-related coronavirus of bat origin. **Nature** 556:255-258.
- d. Yang XL, Tan CW, Anderson DE, Jiang RD, Li B, Zhang W, Zhu Y, Lim XF, Zhou P, Liu XL, Guan W, Zhang L, Li SY, Zhang YZ, **Wang L-F**, Shi ZL (2019). Characterization of a filovirus (Mengla virus) from Rousettus bats in China. **Nat Microbiol.** 4:390-395.

2. Establishment of bats as a new mammalian model system to study virus-host interaction and evolutionary biology.

Working with collaborators around the world, my lab has amassed an unprecedented collection of serological, tissue and other samples from bat surveillance programs. I have used these to develop and disseminate primary and immortalized bat cell lines, and a host of reagents which my team and collaborators are using to test hypotheses about why bats are able to host so many distinct viruses. Current projects include bat genomics and proteomics; examining the bat MHC, using gene knockout technology to identify links between flight, viral resistance, and longevity.

- a. Wynne JW, Shiell BJ, Marsh G, Boyd V, Monaghan P, Zhou P, Klein R, Todd S, Mok L, Green D, Tachedjian M, Baker M, Matthews D, **Wang L-F** (2014). Proteomics informed by transcriptomics reveals Hendra virus sensitizes bat cells to TRAIL mediated apoptosis. **Genome Biology** 15: 532.
- b. Xie J, Li Y, Shen X, Goh G, Zhu Y, Cui J, **Wang L-F**, Shi ZL, Zhou P (2018). Dampened STING-Dependent Interferon Activation in Bats. **Cell Host Microbe** 23(3):297-301.e4.
- c. Ahn M, Anderson DE, Zhang Q, Tan CW, Lim BL, Luko K, Wen M, Chia WN, Mani S, Wang LC, Ng JHJ, Sobota RM, Dutertre C-A, Ginhoux F, Shi Z-L, Irving A, **Wang L-F** (2019). Dampened NLRP3-mediated inflammation in bats and implications for a special viral reservoir host. **Nat Microbiol.** 4:789-799.

3. Application of both molecular and serological platforms to pathogen discovery.

My work at CSIRO AAHL, and now at Duke-NUS has focused on the development and use of PCR and serological assays to identify novel pathogens in wildlife, livestock and people, often under outbreak conditions. This includes the discovery of bats as a reservoir for SARS-CoV, using novel serological assays and PCR techniques I developed.

- a. Bossart KN, McEacherna JA, Hickey AC, Choudhry V, Dimitrov DS, Eaton BT, **Wang L-F** (2007). Neutralization assays for differential henipavirus serology using Bio-Plex Protein Array Systems. **J. Virol. Meth.** 142: 29-40.
- b. Kaku Y, Noguchi A, Marsh G, Barr JA, Okutani A, Hotta K, Bazarzeren B, Fukushi S, Broder CC, Yamada A, Inoue I, **Wang L-F** (2012). Second generation of pseudotype-based serum neutralization assay for Nipah virus antibodies: Sensitive and high-throughput analysis utilizing secreted alkaline phosphatase. **J. Virol. Meth.** 179: 226-232.
- c. Mani S, Tan CW, **Wang L-F**, Anderson DE (2018). Serological Cross Reactivity between Zika and Dengue Viruses in Experimentally Infected Monkeys. **Virol Sin.** 33:378-381.

- d. Uehara A, Tan CW, Mani S, Chua KB, Leo YS, Anderson DE, **Wang L-F** (2018). Serological evidence of human infection by bat orthoreovirus in Singapore. **J Med Virol.** 91(4).

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

9016102060 Wang (PI) 29/09/16 - 28/09/19

Ministry of Defense, Singapore

Pathogen Finder

Role: PI

NRF2016NRF-NSFC002-013 Wang (PI) 01/01/17 - 31/12/19

National Research Foundation (NRF, Singapore)

Combating the next SARS-or MERS-like emerging infectious disease outbreak by active surveillance

Role: PI

R01 AI121378 Wang (Co-PI) 01/01/16 - 31/12/20

Investigating Febrile Deaths in Tanzania (INDITe)

NIH (Sub-award from Duke University)

Role: Co-PI

NRF2018NRF-NSFC003SB-002 Wang (PI) 01/04/19 - 31/03/22

National Research Foundation (NRF, Singapore)

Synthetic biology-driven smart virus sensors for prevention and control of emerging zoonotic viral diseases

Role: PI

Completed Research Support (last 3 years only)

NRF2012NRF-CRP001-056 Wang (PI) 01/11/13 - 31/10/18

National Research Foundation (NRF, Singapore)

Learning from bats: from genomics to controlling viral infection and combating cancer

Role: Leading PI

(b) (4)

Development of multiple serological platforms for differentiation of Zika and dengue virus infections

Role: PI

CDPHRG12NOV003 Wang (PI) 01/02/14 - 31/01/17

Ministry of Health, Singapore

Establishment of serological diagnostic capability for highly virulent zoonotic viral infections in Singapore

Role: PI

DP150102569 Moseley (PI) 01/01/15 - 31/12/18

Australia Research Council, Australia

Nucleolus targeting by negative strand RNA viruses

Role: Co-PI

BIOGRAPHICAL SKETCH

NAME: Anderson, Danielle Elizabeth

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Research Assistant Professor

EDUCATION/TRAINING

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Deakin University, Australia	BSc (Hons)	12/2000	Biology
Curtain University of Technology, Australia	PhD	02/2007	Virology

A. Personal Statement

As a Research Assistant Professor in the Emerging Infectious Diseases (EID) program at Duke-NUS Medical School, my research aims to identify host factors important for paramyxovirus and coronavirus replication. I serve as Scientific Director of the Duke-NUS ABSL3 laboratory, which provides infrastructure, expertise and support for research with pathogens requiring high containment. I have a background in virology, with specific training and expertise in high throughput screening. In my current role, my vision for the Duke-NUS ABSL3 is to create a world class containment research lab with an impeccable safety record. A facility that not only Duke-NUS, but Singapore can be proud of, and that enhances the biomedical research activities in Singapore by providing the opportunity for *in vitro* and *in vivo* experimentation with BSL3 pathogens. I was involved in the design and accreditation process of commissioning the Duke-NUS ABSL3, so I am intimately familiar with capacities of the facility and the regulatory framework it is embedded in. In addition to my laboratory expertise, I have extensive experience in designing animal experiments with ferrets, non-human primates and bats. As I have trained and worked at BSL3 facilities in Singapore (Duke-NUS Medical School) and the USA (Duke University), and the BSL4 facility in China (Wuhan Institute of Virology), I believe that I have the necessary broad expertise and the international network to continue my research. The current application not only builds logically on my prior work and expertise in this field but is aligned with my future research program.

1. **DE Anderson***, K Pfeffermann*, SY Kim, B Sawatsky, J Pearson, M Kovtun, DL Corcoran, Y Krebs, K Sigmundsson, SF Jamison, ZZJ Yeo, LJ Rennick, L-F Wang, PJ Talbot, WPDuprex, MA Garcia-Blanco and V von Messling (*Authors contributed equally). Comparative Loss-of-Function Screens Reveal ABCe1 as an Essential Cellular Host Factor for Efficient Translation of *Paramyxoviridae* and *Pneumoviridae*. **mBio**. 10(3) e00826-19; DOI: 10.1128/mBio.00826-19, **2019**.
2. X-L Yang, CW Tan, **DE Anderson**, R-D Jiang, B Li, W Zhang, Y Zhu, XF Lim, P Zhou, X-L Liu, W Guan, L Zhang, S-Y Li, Y-Z Zhang, L-F Wang and Z-L Shi. Characterization of a filovirus (Měnglà virus) from *Rousettus* bats in China. **Nature Microbiology**. doi: 10.1038/s41564-019-0398-5, **2019**.
3. **DE Anderson***, A Islam*, G Cramer*, S Todd, A Islam, MSU Khan, A Foord, MZ Rahman, IH Mendenhall, SP Luby, ES Gurley, P Daszak, JH Epstein and L-F Wang (*Authors contributed equally). Isolation and full-genome characterization of multiple Nipah viruses from bats, Bangladesh. **Emerging Infectious Diseases**. 25(1):166-170, **2019**.
4. P Zhou, H Fan, T Lan, X-L Yang, W-F Shi, W Zhang, Y Zhu, Y-W Zhang, Q-M Xie, S Mani, X-S Zheng, B Li, J-M Li, H Guo, G-Q Pei, X-P An, J-W Chen, Li Zhou, K-j Mai, Z-X Wu, D Li, **DE Anderson**, L-B Zhang, S-Y Li, Z-Q Mi, T-T He, F Cong, P-J Guo, R Huang, Y Luo, X-L Liu, J Chen, Y Huang, Q Sun, X-L-L Zhang, Y-Y Wang, S-Z Xing, Y-S Chen, Y Sun, J LI, P Daszak, L-F Wang, Z-L Shi, Y-G Tong, J-

Y Ma. Fatal Swine Disease Outbreak Caused by a Novel HKU2-related Coronavirus of Bat Origin. **Nature**. 556(7700), 255-258., 2018.

B. Positions and Honors

Positions and employment

- 2001 -03 Research Technician, Dana-Farber Cancer Institute, Harvard Medical School, Boston, Massachusetts, USA.
- 2006 -07 Research Technician, CSIRO Australian Animal Health Laboratory, Geelong, Australia.
- 2007 -10 Postdoctoral Fellow, INRS-Institut Armand-Frappier / Université du Québec, Montréal, Canada.
- 2010 -10 Research Scientist, INRS-Institut Armand-Frappier / World Anti-Doping Agency. Vancouver 2010 Winter Olympic Games (Feb 12-28, 2010), Vancouver, Canada.
- 2012 -12 Visiting Scientist, Duke University Medical Center, Department of Molecular Genetics and Microbiology, RNAi Facility (May 9- July 27, 2012), Durham, USA
- 2011 -17 Senior Research Fellow, Duke Medical School / National University of Singapore, Singapore.
- 2017 - Research Assistant Professor, Scientific Director of ABSL3 Laboratory, Duke Medical School/National University of Singapore, Singapore.

Other Experience and Professional Membership

- 2012 -14 Committee Member, Duke-NUS Early Career Scientists Association
- 2014 -19 Editorial Board Member, Journal of General Virology
- 2017 - Committee Member, Duke-NUS ABSL3 Biosafety Committee
- 2017 - Committee Member, NUS Institutional Biosafety Committee
- 2017 - Committee Member, National Large Animal Research Facility (NLARF) User Committee

Honors

- 2003 CSIRO Postgraduate Scholarship
- 2007 Canadian Louis Pasteur Postdoctoral Fellowship
- 2008 Fondation J.-Louis Lévesque Postdoctoral Fellowship
- 2009 Fonds de la Recherche en Santé Québec (FRSQ) Postdoctoral Fellowship
- 2018 National Centre for Infectious Disease short-term fellowship

C. Contributions to Science

- 1. Characterization of novel paramyxoviruses.** I received my PhD from Curtin University of Technology, Australia, for work undertaken at the Australian Animal Health Laboratory on the characterization of new paramyxoviruses.
 - DE Anderson**, EJ Dubovi, M Yu, L-F Wang and RW Renshaw. Genome characterization of Salem virus reveals its evolutionary intermediate status in the subfamily *Paramyxovirinae*. **Archives of Virology**, 157(10), 1989-93, 2012.
 - L Lambeth*, M Yu*, **DE Anderson***, G Crameri, BT Eaton, L-F Wang. (*Authors contributed equally). Complete genome sequence of Nariva virus, a rodent paramyxovirus. **Archives of Virology**, 154(2), 199-207, 2009.
 - DE Magoffin**, JS Mackenzie and L-F Wang. Genetic analysis of J-virus and Beilong virus using minireplicons. **Virology** 364(1), 103-111, 2007.
 - Z Li, M Yu, H Zhang, **DE Magoffin**, PJM Jack, A Hyatt, H-Y Wang, and L-F Wang. Beilong virus, a novel paramyxovirus with the largest genome of non-segmented negative-stranded RNA viruses. **Virology** 346(1), 219-228, 2006.
- 2. Viral pathogenesis.** My post-doctoral studies at the INRS-Institut Armand-Frappier, University of Quebec, Canada, expanded my paramyxovirus research into the area of viral pathogenesis. I studied the pathogenesis of canine distemper virus in ferrets as a surrogate model for measles virus infection in humans and developed non-human primate pathogenesis models for several viruses.

- a. CW Tan, K Wittwer, XF Lim, A Uehara, S Mani, L-F Wang and **DE Anderson**. Serological evidence and experimental infection of cynomolgus macaques with pteropine orthoreovirus reveal monkeys as potential hosts for transmission to humans. **Emerging Microbes and Infections**. 8(1):787-795. doi: 10.1080/22221751.2019.1621668, 2019.
- b. S Mani, CW Tan, L-F Wang and **DE Anderson**. Serological Cross Reactivity Between Zika and Dengue Viruses in Experimentally Infected Monkeys. *Virologica Sinica*. 33(4), 378-381, 2018.
- c. **DE Anderson**, A Castan, M Bisailon, and V von Messling. Elements in the Canine Distemper Virus M 3' UTR Contribute to Control of Replication Efficiency and Virulence. *PLoS ONE*, 7(2): e31561. doi:10.1371/journal.pone.0031561, 2012.
- d. **DE Anderson**, and V von Messling. Region between the Canine Distemper virus M and F genes modulates virulence by controlling fusion protein expression. **Journal of Virology**, 82(21), 10510-10518, 2008.

3. **Pathogen discovery and outbreak investigation.** I am currently involved in developing novel diagnostic platforms for the identification of not only new paramyxoviruses, but also other clinically relevant emerging pathogens, such as MERS. Using these platforms, I was part of the team that discovered SADS coronavirus, and most recently, Mengla filovirus.

- a. US Kamaraj, JH Tan, OX Mei, L Pan, T Chawla, A Uehara, L-F Wang, EE Ooi, DJ Gubler, H Tissera, LC Ng, A Wilder-Smith, P Florez de Sessions, T Barkham, **DE Anderson** and OM Sessions. Application of a targeted-enrichment methodology for full-genome sequencing of Dengue 1-4, Chikungunya and Zika viruses directly from patient samples. **PLoS Neglected Tropical Diseases**. 13(4): e0007184. doi.org/10.1371/journal.pntd.0007184, 2019.
- b. S Ommeh, W Zhang, A Zohaib, J Chen, H Zhang, B Hu, X-Y Ge, X-L Yang, M Masika, V Obanda, Y Luo, S Li, C Waruhiu, B Li, Y Zhu, D Ouma, V Odendo, L-F Wang, **DE Anderson**, J Lichoti, E Mungube, F Gakuya, P Zhou, K-J Ngeiywa, B Yan, B Agwanda and Z-L Shi. Genetic evidence of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and widespread seroprevalence among camels in Kenya. **Virologica Sinica**, 33(6):484-492, 2018.
- c. A Uehara, CW Tan, S Mani, K Chua, YS Leo, **DE Anderson** and L-F Wang Serological evidence of human infection by bat orthoreovirus in Singapore. **Journal of Medical Virology**. 1-4, 2018.
- d. ZJM Ho, HC Hapuarachchi, T Barkham, A Chow, LC Ng, JMV Lee, YS Leo, K Prem, YHG Lim, PF de Sessions, MA Rabaa, CS Chong, CH Tan, J Rajarethinam, JH Tan, **DE Anderson**, XM Ong, AR Cook, CY Chong, LY Hsu, G Yap, YL Lai, T Chawla, L Pan, S Sim, I-CM Chen, KC Thoon, CF Yung, JH Li, HLD Ng, K Nandar, PL Ooi, RTP Lin, P Aw, A Uehara, PP De, W Soon, ML Hibberd, HH Ng, S Maurer-Stroh and OM Sessions. Outbreak of Zika in Singapore – An Epidemiological, Entomological, Virological and Clinical Account. **The Lancet Infectious Diseases**. 17(8), 813-21, 2017.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

NRF2018NRF-NSFC003SB-002	in-Fa Wang (PI)	1/19 – 12/21
Synthetic biology-driven smart virus sensors for prevention and control of emerging zoonotic viral diseases.		
Role: Collaborator		

Y80506AYZ4	Anderson (PI)	9/18 – 9/19
Wuhan National Biosafety Laboratory, Chinese Academy of Sciences Advanced Customer Cultivation Project.		
Functional genomic strategies to discover antiviral mechanisms for Nipah and MERS in bats		
Role: PI		

(b) (4)/2018/0016	Anderson (PI)	9/18 – 9/19
Investigation of Flavivirus Immunity on the Vertical Transmission of Zika Virus		

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Wacharapluesadee, Supaporn

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Laboratory Chief

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
Chiang Mai University, Thailand	B.S.	02/1991	Medical Technology
Mahidol University, Thailand	M.S.	01/1994	Biochemistry
Chulalongkorn University, Thailand	Ph.D.	03/2006	Biomedical Sciences

A. Personal Statement

I have 20+ years in research and 15+ years of experience in emerging viral zoonoses. I have managed many internationally funded research projects, that involves working with and managing international and local interdisciplinary teams. Majority of my research projects are field surveillance in wild mammals, human behavioral risk surveys, and clinical sampling. I conduct workshops on development of novel diagnostic approaches, appropriate sample collection and handling for different pathogens, and viral characterization *in vitro* and *in vivo*. I am the Deputy Chief of Thai Red Cross Emerging Infectious Diseases Health Science Centre which conducts research on emerging zoonoses. My research background is focused on understanding the process of zoonotic disease emergence, particularly viral zoonoses. This includes identifying the bat origin of Nipah virus and MERS-CoV, and pathogenesis and diagnoses of Rabies. My study on the emergence of novel betacoronaviruses found in Thai bats, as well as Nipah virus have been published. Our centre was the first laboratory to correctly diagnose the first human MERS case in Thailand, which led to swift execution of containment measures preventing a MERS outbreak in Thailand. We are now the government's reference laboratory for emerging infectious diseases. I have been the PI on 5 multidisciplinary research projects that use epidemiology, laboratory, field science and bioinformatics to diagnose and monitor the emergence of wildlife-origin viral zoonoses, including SARS-CoV, Nipah and Hendra virus, Avian influenza and novel viruses from bats. I am also the Thailand country manager for large contracts from USAID involving successful management of teams of virologists, field biologists, veterinarians, epidemiologists, hospitals and laboratorians.

1. Phumea A, Buathong R, Boonserm R, Intayot P, Aungsananta N, Jittmittraphap A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Molecular Epidemiology and Genetic Diversity of Zika Virus from Field-Caught Mosquitoes in Various Regions of Thailand. **Pathogens** 8(1)pii:E30.
2. Joyjinda Y, Rodpan A, Charpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, Olival KJ, Stokes MM, Hemachudha T, **Wacharapluesadee S** (2019). First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6)pii:e01457-18.

3. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, Hemachudha T (2019). Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox (*Pteropus lylei*) in Thailand. **Virology** 20;15(1):38.
4. **Wacharapluesadee S**, Sintunawa C, Kaewpom T, Khongnomnan K, Olival KJ, Epstein JH, Rodpan A, Sangsri P, Intarut N, Chindamporn A, Suksawa K, Hemachudha T (2013). Group C betacoronavirus in bat guano fertilizer, Thailand. **Emerg Infect Dis** 19(8).

B. Positions and Honors

Positions and Employment

- 1994 -97 Biochemical Technician, Department of Entomology, AFRIMS, Thailand
- 1997 Researcher, Department of Immunology, Chulabhorn Research Institute, Thailand
- 1997 -00 Medical Technologist, The HIV/AIDS Collaboration Thai-US, Thailand
- 2000 -16 Laboratory Chief, Neuroscience Centre for Research and Development & WHO Collaborating Centre for Research and Training on Viral Zoonoses, Faculty of Medicine, Chulalongkorn University Hospital, Thai Red Cross Society, Thailand
- 2016 - Deputy Chief of Thai Red Cross Emerging Infectious Diseases Health Science Centre, Faculty of Medicine, Chulalongkorn University Hospital

Other Experience and Professional Membership

- 2010 -14 PREDICT Thailand Country Coordinator
- 2014 - Thai Ministry of Public Health (MOPH) Ebola Diagnostic Committee
- 2015 - PREDICT 2 Thailand Country Coordinator
- 2016 - Steering committee, Bat One Health Research Network, BTRP DTRA

C. Contribution to Science

1. Research on coronavirus prevalence in Thailand. Numerous high impact emerging viruses appear to have bat reservoirs. Our surveillance projects study the diversity of coronavirus (CoV) in bats in Thailand. We have isolated and characterized CoVs from many bat species, and detected and sequenced CoV in bat guano miner. Our surveillance studies continue to analyze the drivers of their emergence, and risk factors for spillover.

- a. Joyjinda Y, Rodpan A, Chartpituck P, Suthum K, Yaemsakul S, Cheun-Arom T, Bunprakob S, Olival KJ, Stokes MM, Hemachudha T, **Wacharapluesadee S** (2019). First Complete Genome Sequence of Human Coronavirus HKU1 from a Nonill Bat Guano Miner in Thailand. **Microbiol Resour Announc** 8(6).pii:e01457-18.
- b. **Wacharapluesadee S**, Duengkae P, Chaiyes A, Kaewpom T, Rodpan A, Yingsakmongkon S, Petcharat S, Phengsakul P, Maneeorn P, Hemachudha T (2019). Longitudinal study of age-specific pattern of coronavirus infection in Lyle's flying fox (*Pteropus lylei*) in Thailand. **Virology** 20;15(1):38.
- c. Pliapat T, Buathong R, **Wacharapluesadee S**, Siriarayapon P, Pittayawonganon C, Sangsajja C, Kaewpom T, Petcharat S, Ponpinit T, Jumpasri J, Joyjinda Y, Rodpan A, Ghai S, Jittmittraphap A, Khongwichit S, Smith DR, Corman VM, Drosten C, Hemachudha T (2017). Imported case of Middle East respiratory syndrome coronavirus (MERS-CoV) infection from Oman to Thailand, June 2015. **Euro Surveill** 22(33):pii: 30598.
- d. **Wacharapluesadee S**, Duengkae P, Rodpan A, Kaewpom T, Maneeorn P, Kanchanasaka B, Yingsakmongkon S, Sittidetboripat N, Chareesaen C, Khlangsap N, Pidthong A, Leadprathom K, Ghai S, Epstein JH, Daszak P, Olival KJ, Blair PJ, Callahan MV and Hemachudha T (2015). Diversity of Coronavirus in Bats from Eastern Thailand. **Virology** 12(1):57.

2. **Research on Nipah virus prevalence in Thai bats.** Nipah virus outbreaks, previously in Thailand's neighbouring country, Malaysia, and ongoing in Bangladesh have high mortality rate. Our surveillance projects study the characterization of Nipah Virus (NiV) in bats in Thailand. Our surveillance studies continue to analyze the drivers of their emergence, understanding their seasonal preference, and risk factors for spillover.
 - a. **Wacharapluesadee S**, Samseeneam P, Phermpool M, Kaewpom T, Rodpan A, Maneeorn P, Srongmongkol P, Kanchanasaka B, Hemachudha T (2016). Molecular characterization of Nipah virus from *Pteropus hypomelanus* in Southern Thailand. **Virology** 13(1):53
 - b. **Wacharapluesadee S**, Jittmittraphap A, Yingsakmongkon S, and Hemachudha T (2016). Molecular Detection of Animal Viral Pathogens. Nipah Virus. CRC Press.
 - c. **Wacharapluesadee S**, Ngamprasertwong T, Kaewpom T, Kattong P, Rodpan A, Wanghongsa S, Hemachudha T (2013). Genetic characterization of Nipah virus from Thai fruit bats (*Pteropus lylei*). **Asian Biomedicine** 7(6):813-819.
 - d. Breed AC, Meers J, Sendow I, Bossart KN, Barr JA, Smith I, **Wacharapluesadee S**, Wang L, Field HE (2013). The Distribution of Henipaviruses in Southeast Asia and Australasia: Is Wallace's Line a Barrier to Nipah Virus? **PLoS One** 8(4):e61316.
3. **Rabies Neuropathogenesis, diagnosis and management.** The centre worked many years on molecular analyses of rabies, including mutational effects, and designing primers to detect Thai street rabies virus. I regularly organize workshops to teach laboratories in the region on how to correctly collect specimen and test for rabies.
 - a. Hemachudha T, Ugolini G, Sungkarat W, Laothamatas J, Shuangshoti S, **Wacharapluesadee S** (2013). Human Rabies: neuropathogenesis, diagnosis and management. **Lancet Neurology** 498-513.
 - b. Shuangshoti S, Thepa N, Phukpattaranont P, Jittmittraphap A, Intarut N, Tepsumethanon V, **Wacharapluesadee S**, Thorner PS, Hemachudha T (2013). Reduced viral burden in paralytic compared to furious canine rabies is associated with prominent inflammation at the brainstem level. **BMC Vet Res** 14;9(1):31.
 - c. Virojanapirom P, Khawplod P, Sawangvaree A, **Wacharapluesadee S**, Hemachudha T, Yamada K, Morimoto K, Nishizono A (2012). Molecular analysis of the mutational effects of Thai street rabies virus with increased virulence in mice after passages in the BHK cell line. **Arch Virol** 157(11):2201-5.
 - d. Wilde H, Hemachudha T, **Wacharapluesadee S**, Lumlertdacha B, Tepsumethanon V (2013). Rabies in Asia: The Classical Zoonosis. **Curr Top Microbiol Immunol** 365:185-203.
4. **Investigating causes of encephalitis.** More than 50% of patients presenting with fever remain undiagnosed. Our centre has focused a lot of research into diagnosing fever of unknown origins (FUO). We study epidemiology, pathology and conduct surveillance studies into viral pathogens, and autoimmune diseases.
 - a. Hemachudha P, **Wacharapluesadee S**, Buathong R, Petcharat S, Bunprakob S, Ruchiseesarod C, Roeksomtawin P, Hemachudha T (2019). Lack of Transmission of Zika Virus Infection to Breastfed Infant. **Clin Med Insights Case Rep** 12:1179547619835179.
 - b. Phumee A, Buathong R, Boonserm R, Intayot P, Aungsananta N, Jittmittraphap A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Molecular Epidemiology and Genetic Diversity of Zika Virus from Field-Caught Mosquitoes in Various Regions of Thailand. **Pathogens** 8(1).pii: E30.
 - c. Phumee A, Chompoosri J, Intayot P, Boonserm R, Boonyasuppayakorn S, Buathong R, Thavara U, Tawatsin A, Joyjinda Y, **Wacharapluesadee S**, Siriyasatien P (2019). Vertical transmission of Zika virus in *Culex quinquefasciatus* Say and *Aedes aegypti* (L.) mosquitoes. **Scientific reports** 9(1):5257.

- d. Thanprasertsuk S, Pleumkanitkul S, **Wacharapluesadee S**, Ponpinit T, Hemachudha T, Suankratay C (2017). HTLV-1-Associated Myelopathy/Tropical Spastic Paraparesis: the First Case Report in Southeast Asia. **AIDS Res Hum Retroviruses**.

D. Additional Information: Research Support and/or Scholastic Performance

Ongoing Research Support

USAID Emerging Pandemic Threats Mazet (PI) 10/01/14 – 09/30/19
PREDICT-2

The goal is to conduct surveillance for novel pathogens in wildlife, livestock and people; characterize human risk behavior; analyze EID risk; and design interventions in >20 countries

Role: Thailand country coordinator

(b) (4) Wacharapluesadee (PI) 07/01/18 – 08/31/19

The goal is to support the Defense Threat Reduction Agency's (DTRA) (b) (4) evaluation program. Responsibilities include using the specified point-of-care diagnostic(s) through the procurement of supplies, enrollment of subjects according to inclusion and exclusion criteria, testing the samples, and reporting the data to the Naval Health Research Center (NHRC).

Pathogen Surveillance for Viral Zoonoses Wacharapluesadee (PI) 12/15/16 – 06/30/20

Disease surveillance analysis of wildlife-domestic animal-human interfaces, in coordination with PREDICT USAID project.

Surveillance for Emerging Infectious Disease Pathogens at the Animal-Human Interfaces in Thailand, in Coordination with PREDICT USAID Project and the Bat Serology Study

Wacharapluesadee (PI) 06/01/18 – 04/30/20

The goal of the study is to understand and mitigate zoonotic disease using multiplex serology developed by Utah State University (USU). This is also a disease surveillance analysis of wildlife-domestic animal-human interfaces, in coordination with PREDICT USAID project.

Completed Research Support (last 3 years only) out of 14 prior awards

(b) (4) Wacharapluesadee (PI) 04/01/16 – 03/31/19

The goal of this study was to establish a viral laboratory network in Thailand for Emerging Infectious Disease preparedness among the university laboratories and government public health laboratory.

BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors.
Follow this format for each person. **DO NOT EXCEED FIVE PAGES.**

NAME: Hughes, Tom

eRA COMMONS USER NAME (credential, e.g., agency login): (b) (6)

POSITION TITLE: Director, Conservation Medicine Ltd. Project Coordinator Malaysia, EcoHealth Alliance.

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
University of East Anglia, Norwich	B.S. (hons)	2002	Development Studies & Natural Resources
Capel Manor College, UK	City & Guilds (Distinction)	2003	Amenity Horticulture Phase 2 in Arboriculture
London School of Hygiene & Tropical Medicine, University of London	Post-Grad Dipl.	2009	Public Health
Mahidol-Oxford Tropical Medicine Research Unit, Open University, Bangkok	Ph.D.	Ongoing	Zoonotic Disease

A. Personal Statement

The current project brings the disciplines of virology, immunology and disease ecology together to understand and predict viral spillover. My background is a good fit for this work: I am trained in ecology, international development and public health. For the past 10 years I have acted as the Malaysian Project Coordinator for EcoHealth Alliance. I have designed, initiated and managed collaborative projects on surveillance, viral discovery and ecology of wildlife reservoirs of zoonoses. As the Malaysia country coordinator for the USAID-funded EPT/PREDICT project, which tests hundreds of wildlife, livestock and human samples annually, I will be able to support the PCR-serology data needs of the project. My current Ph.D research is focused on concurrent sampling and testing of human, wildlife and livestock in forest-inhabitant communities in Peninsular Malaysia. I am also co-PI on the DTRA funded Serological Biosurveillance study cited in this proposal. In support of EcoHealth Alliance in-country projects, I manage a staff of 13; oversee the Sabah Wildlife Health Unit (5 staff) and the Wildlife Health Genetic and Forensic laboratory which I designed, oversaw the building of, and help manage. In 2014, I incorporated and became director of Conservation Medicine Ltd. in Malaysia, to manage these and other projects.

1. Tambllyn A, O'Malley R, Turner C, **Hughes T** (2009). The Bat Fauna (Mammilla Chiroptera) of Palau Perhentian, Peninsular Malaysia. **Malayan Nature Journal** 61(1), 10-22.
2. de Jong C, Field H, Tagtag A, **Hughes T**, Dechmann D, Jayme S, Epstein J, Smith C, Santos I, Catbagan D, Lim M, Benigno C, Daszak P, Newman S (2013). Foraging Behaviour and Landscape Utilisation by the Endangered Golden-Crowned Flying Fox (*Acerodon jubatus*), The Philippines. **PLoS ONE** 8(11): e79665. doi:10.1371/journal.pone.0079665.
3. Salgado Lynn M, William T, Tanganuchitcharnchai A, Jintaworn S, Thaipadungpanit J, Lee M.H, Julius C, Daszak P, Goossens B, **Hughes T**, Blacksell SD (2018). Spotted Fever Rickettsiosis in a Wildlife Researcher in Sabah, Malaysia: A Case Study. **Trop. Med. Infect. Dis** 3, 29.

4. Satjanadumrong J, Robinson, MT, **Hughes T**, Blacksell SD (2019). Distribution and Ecological Drivers of Spotted Fever Group Rickettsia in Asia. **EcoHealth** <https://doi.org/10.1007/s10393-019-01409-3>.

B. Positions and Honors

Positions and Employment

- 2004 Expedition Leader, Tropical Forest Project Malaysia, Coral Cay Conservation
- 2005 -07 Field Officer, Malaysia, EcoHealth Alliance
- 2007 - Project Coordinator Malaysia, EcoHealth Alliance
- 2010 - PREDICT Country Coordinator Malaysia
- 2014 - Director, Conservation Medicine Ltd

Other Experience and Professional Memberships

- 2004 Lead, Community Education Program, Conservation Issues, The Perhentian Islands, Malaysia
- 2005 Member, The Henipavirus Ecology Research Group
- 2006 Lead, Community Education Program, Bat Ecology, Tioman Island, Malaysia
- 2008 Recipient, Scholarship to attend the International Ecology & Health Forum, Merida, Mexico
- 2008 - Reviewer, *EcoHealth* Journal
- 2010 Member, Philippine government/Food and Agriculture Organization of the United Nations mission to investigate Philippine bats as a possible reservoir of Reston Ebolavirus
- 2014 Invited Presenter, Disease Ecology, UN Special Rapporteur

C. Contributions to Science

1. Surveillance for emerging viruses in Southeast Asia

As project coordinator in Malaysia for EcoHealth Alliance, and now Director of Conservation Medicine Ltd, I have designed and led field programs that underpin advances in our understanding of wildlife-origin zoonoses (e.g. Macaques and Herpes B), risk factors for emergence (e.g. Nipah virus in fruit bats), the distribution of viruses (e.g. Ebola virus in the Philippines). Through the PREDICT project I currently lead a team that has found 71 novel viruses and 26 known viruses in wildlife reservoirs, livestock and humans. I have helped develop laboratory and personnel capacity for disease surveillance at the Department of Wildlife and National Parks (DWNP), Department of Veterinary Services and Ministry of Health in Malaysia. I have trained over 350 individuals from government partners, local universities and NGOs in surveillance and diagnostics techniques including sharing SOPs and protocols. In collaboration with Sabah Wildlife Department I established the Wildlife Health, Genetic and Forensic Laboratory that has all the equipment necessary to store samples, run extractions, PCR and analysis on biological samples for disease surveillance. The lab is used to screen samples for the PREDICT and to generate PCR and serological data for EcoHealth Alliance. I also establish the new molecular zoonosis laboratories at the DWNP's National Wildlife Forensic Laboratory. The lab is used to screen samples for the PREDICT & DTRA projects and to generate PCR and serological data for EcoHealth Alliance.

- a. Epstein JH, Olival KJ, Pulliam JRC, Smith C, Westrum J, **Hughes T**, Dobson AP, Zubaid A, Rahman SA, Basir MM, Field HE & Daszak P (2009). *Pteropus vampyrus*, a hunted migratory species with a multinational home-range and a need for regional management. **Journal of Applied Ecology** 46: 991-1002.
- b. Halpin K, Hyatt AD, Fogarty R, Middleton D, Bingham J, Epstein JH, Sohayati AR, **Hughes T**, Smith C, Field HE, Daszak P & HERG (2011). Pteropid bats are confirmed as the reservoir hosts of henipaviruses: A comprehensive experimental study of virus transmission. **Am J Trop Med Hyg** 85: 946-95.
- c. Rahman SA, Hassan L, Epstein JH, Mamat ZC, Yatim AM, Hassan SS, Field HE, **Hughes T**, Westrum J, Naim MS, Suri AS, Jamaluddin AA, Daszak P, Henipavirus Ecology Research Group (2013). Risk factors for Nipah virus infection among pteropid bats, Peninsular Malaysia. **EID** 19: 51-60.

