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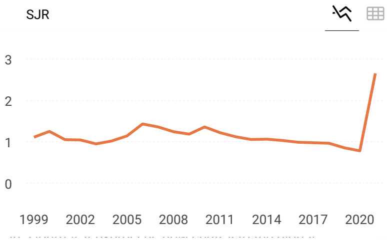

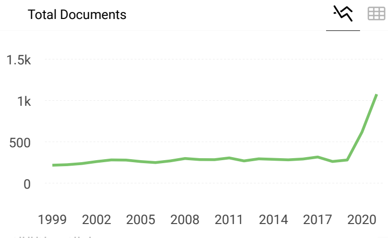

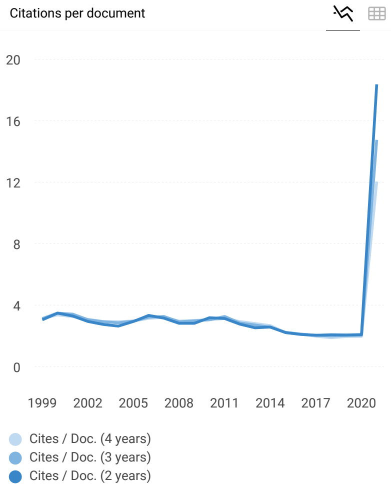

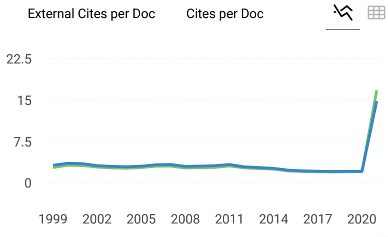

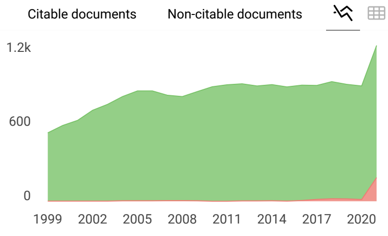

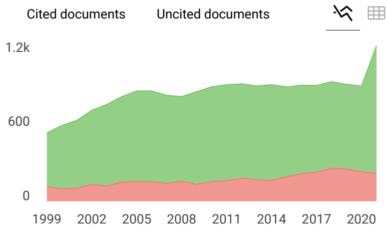

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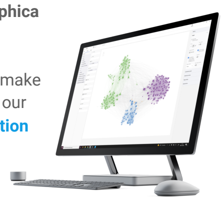

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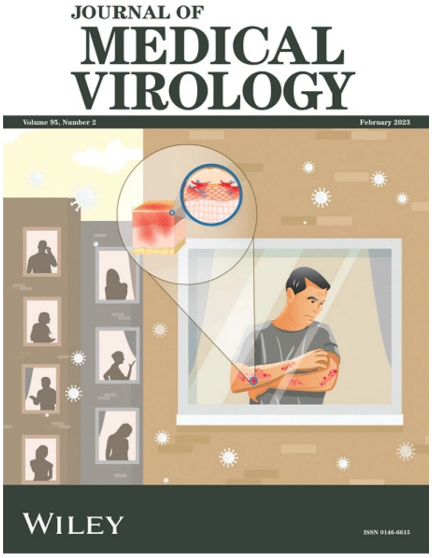

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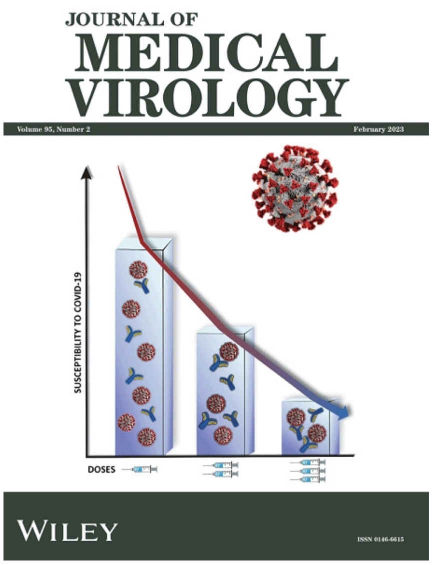

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A systematic review and clinical atlas on mucocutaneous presentations of the current monkeypox outbreak: With a comprehensive approach to all dermatologic and nondermatologic aspects of the new and previous monkeypox outbreaks

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Cross-reactivity of SARS-CoV-2 with other pathogens, especially dengue virus: A historical perspective

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mRNA vaccines: The future of prevention of viral infections?

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Coronavirus disease 2019 rebounds following nirmatrelvir/ritonavir treatment

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Animal host range of mpox virus

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It is time to improve the acceptance of COVID-19 vaccines among people with chronic diseases: A systematic review and meta-analysis

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RESEARCH ARTICLES

Predictors of severity in severe respiratory infection in children with COVID-19 respiratory infection in a developing country

Daniel Mauricio Beltran, Milena Villamil Osorio, Sara Liliana Goyeneche Fonseca, Sonia M. Restrepo-Gualteros, María José Rosero Garcia, Carlos E. Rodriguez-Martinez

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Nirmatrelvir-ritonavir therapy and COVID-19 vaccination improve clinical outcomes of SARS-CoV-2 Omicron variant infection

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Monkeypox awareness and low vaccination hesitancy among men who have sex with men in China

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Safety and immunogenicity of a recombinant receptor-binding domain-based protein subunit vaccine (Noora vaccine™) against COVID-19 in adults: A randomized, double-blind, placebo-controlled, Phase 1 trial

Jafar Salimian, Ali Ahmadi, Jafar Amani, Gholamreza Olad, Raheleh Halabian, Ali Saffaei, Masoud Arabfard, Mojtaba Nasiri, Shahram Nazarian, Hassan Abolghasemi, Gholamhossein Alishiri

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Analysis of the reliability of rapid diagnostic tests for varicella, including breakthrough cases

Yuki Higashimoto, Fumihiko Hattori, Yoshiki Kawamura, Kei Kozawa, Aoi Hamano, Mizuki Kato, Sayaka Kato, Asuka Hosokawa, Yasuko Enya, Masaru Ihira, Tetsushi Yoshikawa

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Comparable humoral and cellular immunity against Omicron variant BA.4/5 of once-boosted BA.1/2 convalescents and twice-boosted COVID-19-naïve individuals

Chang Kyung Kang, Min-Gang Kim, Seong-wook Park, Yong-Woo Kim, Chan Mi Lee, Pyoeng Gyun Choe, Wan Beom Park, Nam Joong Kim, Minji Kim, Soojin Lee, Ik Soo Kim, Chang-Han Lee, Hyun Mu Shin, Hang-Rae Kim, Myoung-don Oh

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Immunogenicity of novel DNA vaccines encoding receptor-binding domain (RBD) dimer-Fc fusing antigens derived from different SARS-CoV-2 variants of concern

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Tumor cell vaccine combined with Newcastle disease virus promote immunotherapy of lung cancer

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Discovery of Isojacareubin as a covalent inhibitor of SARS-CoV-2 main protease using structural and experimental approaches

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Inhibition of PIKFYVE kinase interferes ESCRT pathway to suppress RNA virus replication

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Head-to-head comparison of genotyping of human papillomavirus by real-time multiplex PCR assay using type-specific primers and SPF10-PCR-based line probe assay

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---

Analysis on the physiological changes of residents before and during the COVID-19 pandemic: A cross-sectional study

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Dysregulation of memory B cells and circulating T follicular helper cells is a predictor of poor immune recovery in HIV-infected patients on antiretroviral therapy

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Monitoring of SARS-CoV-2 concentration and circulation of variants of concern in wastewater of Leuven, Belgium

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Oxidative stress—A key determinant of complications and negative outcome in hepatitis E virus infected pregnancies: A comprehensive account involving cases from northeast India

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High C-reactive protein to lymphocyte ratio predicts mortality outcomes of patients with severe fever with thrombocytopenia syndrome: A multicenter study in China

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Dysbiosis of the stool DNA and RNA virome in Crohn's disease

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HBsAg (−)/HBsAb (−)/HBeAg (−)/HBeAb (+)/HBcAb (+) predicts a high risk of hepatitis B reactivation in patients with B-cell lymphoma receiving rituximab based immunochemotherapy

Li-Ping Shui, Yan Zhu, Xiao-Qin Duan, Yu-Ting Chen, Li Yang, Xiao-Qiong Tang, Hong-Bin Zhang, Qing Xiao, Li Wang, Lin Liu, Xiao-Hua Luo

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Investigating the effect of ribavirin treatment on genetic mutations in Crimean–Congo haemorrhagic fever virus (CCHFV) through next-generation sequencing

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Impact of alcohol consumption on coronavirus disease 2019 severity: A systematic review and meta-analysis

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Treatment with integrase inhibitors alters SARS-CoV-2 neutralization levels measured with HIV-based pseudotypes in people living with HIV

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Disentangling the common genetic architecture and causality of rheumatoid arthritis and systemic lupus erythematosus with COVID-19 outcomes: Genome-wide cross trait analysis and bidirectional Mendelian randomization study

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Receptor-binding domain-based SARS-CoV-2 vaccine adjuvanted with cyclic di-adenosine monophosphate enhances humoral and cellular immunity in mice

María José Germanó, Constanza Giai, Diego Esteban Cargnelutti, María Isabel Colombo, Sebastián Blanco, Brenda Konigheim, Lorena Spinsanti, Javier Aguilar, Sandra Gallego, Hugo Alberto Valdez, Juan Pablo Mackern-Oberti, Maria Victoria Sanchez

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Twelve-month clinical, functional, and radiological outcomes in patients hospitalized for SARS-CoV-2 pneumonia

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A new glutamine synthetase index to evaluate hepatic lobular restoration in advanced fibrosis during anti-HBV therapy

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Enhanced recombination among Omicron subvariants of SARS-CoV-2 contributes to viral immune escape

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Persistent circulation of soluble and extracellular vesicle-linked Spike protein in individuals with postacute sequelae of COVID-19

Vaughn Craddock, Aatish Mahajan, Leslie Spikes, Balaji Krishnamachary, Anil K. Ram, Ashok Kumar, Ling Chen, Prabhakar Chalise, Navneet K. Dhillon

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Factors affecting prolonged SARS-CoV-2 infection and development and validation of predictive nomograms

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Impact of air pollutants on influenza-like illness outpatient visits under COVID-19 pandemic in the subcenter of Beijing, China

Xin−Yao Lian, Lu Xi, Zhong−Song Zhang, Li−Li Yang, Juan Du, Yan Cui, Hong−Jun Li, Wan−Xue Zhang, Chao Wang, Bei Liu, Yan−Na Yang, Fuqiang Cui, Qing−Bin Lu

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“Mitochondrial pathogenic mutations and metabolic alterations associated with COVID-19 disease severity”

Diksha Kumari, Yamini Singh, Sayar Singh, Vikas Dogra, Ashish Kumar Srivastava, Swati Srivastava, Iti Garg, Mona Bargotya, Javid Hussain, Lilly Ganju, Rajeev Varshney

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---

Nonpharmaceutical interventions reduce the incidence and mortality of COVID-19: A study based on the survey from the International COVID-19 Research Network (ICRN)

Seung Hyun Park, Sung Hwi Hong, Kwanghyun Kim, Seung Won Lee, Dong Keon Yon, Sun Jae Jung, Ziad Abdeen, Ramy Abou Ghayda, Mohamed Lemine Cheikh Brahim Ahmed, Abdulwahed Al Serouri, Waleed Al-Herz, Humaid O. Al-Shamsi, Sheeza Ali, Kosar Ali, Oidov Baatarkhuu, Henning Bay Nielsen, Enrico Bernini-Carri, Anastasiia Bondarenko, Ayun Cassell, Akway Cham, Melvin L. K. Chua, Sufia Dadabhai, Tchin Darre, Hayk Davtyan, Elena Dragioti, Barbora East, Robert Jeffrey Edwards, Martina Ferioli, Tsvetoslav Georgiev, Lilian A. Ghandour, Harapan Harapan, Po-Ren Hsueh, Saad I. Mallah, Aamer Ikram, Shigeru Inoue, Louis Jacob, Slobodan M. Janković, Umesh Jayarajah, Milos Jesenak, Pramath Kakodkar, Nathan Kapata, Yohannes Kebede, Yousef Khader, Meron Kifle, David Koh, Višnja Kokić Maleš, Katarzyna Kotfis, Ai Koyanagi, James-Paul Kretchy, Sulaiman Lakoh, Jinhee Lee, Jun Young Lee, Maria da Luz Lima Mendonça, Lowell Ling, Jorge Llibre-Guerra, Masaki Machida, Richard Makurumidze, Ziad A. Memish, Ivan Mendoza, Sergey Moiseev, Thomas Nadasdy, Chen Nahshon, Silvio A. Ñamendys-Silva, Blaise Nguendo Yongsi, Amalea Dulcene Nicolasora, Zhamilya Nugmanova, Hans Oh, Atte Oksanen, Oluwatomi Owopetu, Zeynep Ozge Ozguler, Konstantinos Parperis, Gonzalo Emanuel Perez, Krit Pongpirul, Marius Rademaker, Nemanja Radojevic, Anna Roca, Alfonso J. Rodriguez-Morales, Enver Roshi, Khwaja Mir Islam Saeed, Ranjit Sah, Boris Sakakushev, Dina E. Sallam, Brijesh Sathian, Patrick Schober, P. Shaik Syed Ali, Zoran Simonović, Tanu Singhal, Natia Skhvitaridze, Marco Solmi, Kannan Subbaram, Kalthoum Tizaoui, John Thato Tlhakanelo, Julio Torales, Junior Smith Torres-Roman, Dimitrios Tsartsalis, Jadamba Tsolmon, Duarte Nuno Vieira, Sandro G. Viveiros Rosa, Guy Wanghi, Uwe Wollina, Ren-He Xu, Lin Yang, Kashif Zia, Muharem Zildzic, Jae Il Shin, Lee Smith

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Emerging Omicron subvariants evade neutralizing immunity elicited by vaccine or BA.1/BA.2 infection

Zehui Chen, Jiaming Li, Jing Zheng, Yifei Jin, Yidun Zhang, Fei Tang, Jingjing Li, Hongliang Cheng, Lina Jiang, Huixin Wen, Chao Hong, Xiaohong Zeng, Shijie Huang, Bing Lu, Li Li, Zhongyi Wang

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---

Appearance of extrapyramidal symptoms in adolescent psychiatry patients during COVID-19 infection

Aysegul Tonyali, Gul Karacetin, Celal Yesilkaya, Feyza Nur Tas Arik, Binay Kayan Ocakoglu

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---

Association of *ESR1* gene polymorphisms with the susceptibility to Hepatitis B virus infection and the clinical outcomes

Jiaxin Xie, Yibo Ding, Xiaopan Li, Rui Pu, Wenbin Liu, Peng Li, Jianhua Yin

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Cocirculation of A(H3N2) and B/Victoria increased morbidity in hospitalized patients in the 2019–2020 A(H1N1)pdm09 predominant influenza season in Israel

Menucha Jurkowicz, Ital Nemet, Nofar Atari, Ilana S. Fratty, Limor Kliker, Hilda Sherbany, Nathan Keller, Eugene Leibovitz, Ella Mendelson, Michal Mandelboim, Michal Stein

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---

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Delayed cutaneous hypersensitivity reactions following the use of infliximab or adalimumab in patients with coronavirus disease 2019

Jing Wang, Xuedong Yin, Linlin Yu, Weiwei Cheng, Ling Wang, Bin Zhao, Zhiling Li, Xiaoping Jing

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---

The case fatality rate of COVID-19 during the Delta and the Omicron epidemic phase: A meta-analysis

Kisong Kim, Kyuyeon Cho, Junmin Song, Masoud Rahmati, Ai Koyanagi, Seung Won Lee, Dong Keon Yon, Jae Il Shin, Lee Smith

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---

Developmental outcomes in children born to women with possible subclinical rubella exposures during pregnancy

Jill Hutton

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Pharmaco-virological algorithm to target risk of drug resistance among a population of HIV-infected key populations in Togo

Valentine M. Ferré, Alexandra M. Bitty-Anderson, Gilles Peytavin, Minh P. Lê, Claver A. Dagnra, Romain Coppée, Fifonsi A. Gbeasor-Komlanvi, Diane Descamps, Charlotte Charpentier, Didier K. Ekouevi

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---

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Torque teno virus (TTV): A gentle spy virus of immune status, predictive marker of seroconversion to COVID-19 vaccine in kidney and lung transplant recipients

Piergiorgio Roberto, Lilia Cinti, Anna Napoli, Daniele Paesani, Rodolfo J. Riveros Cabral, Fabrizio Maggi, Manuela Garofalo, Renzo Pretagostini, Anastasia Centofanti, Carolina Carillo, Federico Venuta, Aurelia Gaeta, Guido Antonelli

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---

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Surveillance for SARS-CoV-2 and its variants in wastewater of tertiary care hospitals correlates with increasing case burden and outbreaks

Nicole Acosta, Maria A. Bautista, Barbara J. Waddell, Kristine Du, Janine McCalder, Puja Pradhan, Navid Sedaghat, Chloe Papparis, Alexander Buchner Beaudet, Jianwei Chen, Jennifer Van Doorn, Kevin Xiang, Leslie Chan, Laura Vivas, Kashtin Low, Xuewen Lu, Jangwoo Lee, Paul Westlund, Thierry Chekouo, Xiaotian Dai, Jason Cabaj, Srijak Bhatnagar, Norma Ruecker, Gopal Achari, Rhonda G. Clark, Craig Pearce, Joe J. Harrison, Jon Meddings, Jenine Leal, Jennifer Ellison, Bayan Missaghi, Jamil N. Kanji, Oscar Larios, Elissa Rennert-May, Joseph Kim, Steve E. Hrudey, Bonita E. Lee, Xiaoli Pang, Kevin Frankowski, John Conly, Casey R. J. Hubert, Michael D. Parkins

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Abstract | Full text | PDF | References | Request permissions

---

Persistent effects of COVID-19 in patients hospitalized during the first wave of the pandemic: The impact of persistent fatigue on quality of life in a cross-sectional study

Joseph P. Skinner, Lauren V. Moran

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---

Molecular characterization of rotavirus infections in children less than 5 years of age with acute gastroenteritis in Tehran, Iran, 2021–2022: Emergence of uncommon G9P[4] and G9P[8] rotavirus strains

Atefeh Kachooei, Ahmad Tava Koli, Sara Minaeian, Mahdieh Hosseini, Somayeh Jalilvand, Tayebeh Latifi, Arash Arashkia, Angila Ataei-Pirkooh, Zabihollah Shoja

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Ultrastructural analysis of monkeypox virus replication in Vero cells

Amanda Stéphanie Arantes Witt, Giliane de Souza Trindade, Fernanda Gil de Souza, Mateus Sá Magalhães Serafim, Alana Vitor Barbosa da Costa, Marcos Vinícius Ferreira Silva, Felipe Campos de Melo Iani, Rodrigo Araújo Lima Rodrigues, Erna Geessien Kroon, Jônatas Santos Abrahão

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---

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ELISPOT assays with pp65 peptides or whole HCMV antigen are reliable predictors of immune control of HCMV infection in seropositive kidney transplant recipients

Federica Zavaglio, Francesca Rivela, Irene Cassaniti, Francesca Arena, Elisa Gabanti, Anna L. Asti, Daniele Lilleri, Teresa Rampino, Fausto Baldanti, Marilena Gregorini

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---

Immune-dysregulation in subacute sclerosing panencephalitis: An exploratory case–control study

Vijayaragavan Vijayavarman, Hardeep S. Malhotra, Imran Rizvi, Neeraj Kumar, Shweta Pandey, Mili Jain, Wahid Ali, Vinay Suresh, Ravindra K. Garg, Amita Jain, Rajesh Verma, Praveen Sharma, Ravi Uniyal

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---

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Evolution and emergence of primate-specific interferon regulatory factor 9

Sam Drury, Grace Claussen, Allison Zetterman, Hideaki Moriyama, Etsuko N. Moriyama, Luwen Zhang

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---

Identification of two proposed novel human rhinovirus types: Bpat107 and Cpat58

Qiang Zhang, Zhibo Xie, Baicheng Xia, Yage Wang, Wenbo Xu, Yan Zhang

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Abstract | Full text | PDF | References | Request permissions

---

Inhibition of influenza A virus replication by a marine derived quinolone alkaloid targeting virus nucleoprotein

Yang Zhang, Wei-Feng Xu, Yunjia Yu, Qun Zhang, Lianghao Huang, Cui Hao, Chang-Lun Shao, Wei Wang

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Abstract | Full text | PDF | References | Request permissions

---

Two-year impact of COVID-19 pandemic on hospitalized patients with skin diseases in China

Jie Pan, Songchun Yang, Xiaozhen Chen, Xuanlin Che, Wenrui Lin, Mingliang Chen, Xiang Chen, Guangtong Deng, Juan Su

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Abstract | Full text | PDF | References | Request permissions

---

SERTAD3 induces proteasomal degradation of ZIKV capsid protein and represents a therapeutic target

Nina Sun, Rong-Rong Zhang, Guang-Yuan Song, Qiaomei Cai, Saba R. Aliyari, Karin Nielsen-Saines, Jae U. Jung, Heng Yang, Genhong Cheng, Cheng-Feng Qin

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---

A hepatitis B virus core antigen-based virus-like particle vaccine expressing SARS-CoV-2 B and T cell epitopes induces epitope-specific humoral and cell-mediated immune responses but confers limited protection against SARS-CoV-2 infection

Anna M. Hassebroek, Harini Sooryanarain, Connie L. Heffron, Seth A. Hawks, Tanya LeRoith, Thomas E. Cecere, William B. Stone, Debra Walter, Hassan M. Mahsoub, Bo Wang, Debin Tian, Hannah M. Ivester, Irving C. Allen, Albert J. Auguste, Nisha K. Duggal, Chenming Zhang, Xiang-Jin Meng

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---

Higher clearance rates of multiple HPV infections may explain their lower risk of HSIL: A retrospective study in Wenzhou, China

Xinyu Ni, Jiaming Hu, Yin Huang, Jinxin Tao, Hua Zhu

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---

Contribution of genotypes in Prothrombin and Factor V Leiden to COVID-19 and disease severity in patients at high risk for hereditary thrombophilia

Aslıhan Kiraz, Ozlem Sezer, Adem Alemdar, Sezin Canbek, Nilgun Duman, Atıl Bisgin, Tulin Cora, Hatice Ilgın Ruhi, Mahmut Cerkez Ergoren, Bilgen Bilge Geçkinli, Sebnem Ozemri Sag, Hilmi Erdem Gözden, Ozlem Oz, Zuhal Mert Altıntaş, Sinem Yalcıntepe, Adem Keskin, Ayşegül Yabacı Tak, Şeyma Aktaş Paskal, Uğur Fahri Yürekli, Mercan Demirtas, Emine Unal Evren, Abdullah Hanta, Müşerref Başdemirci, Kaya Suer, Burhan Balta, Nadir Kocak, Halil Gürhan Karabulut, Havva Cobanogulları, Esra Arslan Ateş, Sevcan Tuğ Bozdoğan, Damla Eker, Sadiye Ekinci, Süleyman Nergiz, Timur Tuncalı, Serap Yagbasan, Ceren Alavanda, Nuket Yurur Kutlay, Hakan Evren, Murat Erdoğan, Sule Altıner, Tamer Sanlidag, Gizem Akıncı Gonen, Arzu Vicdan, Nazan Eras, Hatice Koçak Eker, Ozgür Balasar, Gulten Tuncel, Munis Dundar, Hakan Gurkan, Sehime Gulsun Temel

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---

Needle-free injection system delivery of ZyCoV-D DNA vaccine demonstrated improved immunogenicity and protective efficacy in rhesus macaques against SARS-CoV-2

Pragya D. Yadav, Sanjay Kumar, Kshitij Agarwal, Mukul Jain, Dilip R. Patil, Kapil Maithal, Basavaraj Mathapati, Suresh Giri, Sreelekshmy Mohandas, Anita Shete, Gajanan Sapkal, Deepak Y. Patil, Ayan Dey, Harish Chandra, Gururaj Deshpande, Nivedita Gupta, Priya Abraham, Himanshu Kaushal, Rima R. Sahay, Anuradha

Tripathy, Dimpal Nyayanit, Rajlaxmi Jain, Abhimanyu Kumar, Prasad Sarkale, Shreekant Baradkar, Chozhavel Rajanathan, Hari Prasad Raju, Satish Patel, Niraj Shah, Pankaj Dwivedi, Dharmendra Singh

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---

Analysis of long noncoding RNAs and messenger RNAs expression profiles in the hearts of mice with acute viral myocarditis

Yimin Xue, Jun Ke, Jiuyun Zhang, Mingguang Chen, Lijuan Zeng, Qiaolian Fan, Chunfu Zheng, Feng Chen

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---

Complete genome analyses of G12P[8] rotavirus strains from hospitalized children in Surabaya, Indonesia, 2017–2018

Laura Navika Yamani, Takako Utsumi, Yen Hai Doan, Yoshiki Fujii, Zayyin Dinana, Rury Mega Wahyuni, Emily Gunawan, Soegeng Soegijanto, Alpha Fardah Athiyyah, Subijanto Marto Sudarmo, Reza Gunadi Ranuh, Andy Darma, Soetjipto, Juniastuti, Rheza Gandi Bawono, Chieko Matsui, Lin Deng, Takayuki Abe, Hiroyuki Shimizu, Koji Ishii, Kazuhiko Katayama, Maria Inge Lusida, Ikuo Shoji

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---

Machine learning-driven blood transcriptome-based discovery of SARS-CoV-2 specific severity biomarkers

Pandikannan Krishnamoorthy, Athira S Raj, Himanshu Kumar

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---

Efficacy of serum apelin and galectin-3 as potential predictors of mortality in severe COVID-19 patients

Nurcan Kırıcı Berber, Ayşegül Altıntop Geçkil, Nazife Özge Altan, Tuğba Raika Kıran, Önder Otlu, Mehmet Erdem, Erdal İn

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---

Inhibiting cardiac autophagy suppresses Zika virus replication

Xin Ma, Yinnong Jia, Jing Yuan, Qiu-Ju Tang, Wen-Cong Gao, Guang-Feng Zhou, Ren-Hua Yang, Wei Pang, Chang-Bo Zheng

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---

How does SARS-CoV-2 infection impact on immunity, procession and treatment of pan cancers

Nan Xiong, Qiangming Sun

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---

A decrease in the incidence of encephalitis in South Korea during the COVID-19 pandemic: A nationwide study between 2010 and 2021

Se Hee Kim, Jee Yeon Baek, Minkyung Han, Myeongjee Lee, Sung Min Lim, Ji Young Lee, Ji-Man Kang, Inkyung Jung, Hoon-Chul Kang, Jong Gyun Ahn

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---

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Colchicine and risk of hospitalization due to COVID-19: A population-based study

María Sáenz-Aldea, Ángel Salgado-Barreira, Margarita Taracido Trunk, María Piñeiro-Lamas, Maria T. Herdeiro, Manuel Portela-Romero, Marc Saez, Adolfo Figueiras

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---

Development and validation of a deep learning model to diagnose COVID-19 using time-series heart rate values before the onset of symptoms

Heewon Chung, Hoon Ko, Hooseok Lee, Dong Keon Yon, Won Hee Lee, Tae-Seong Kim, Kyung Won Kim, Jinseok Lee

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---

Memory impairment among recovered COVID-19 patients: The prevalence and risk factors, a retrospective cohort study

Muayad A. Merza, Hind B. Almufty, Heewa A. Younis, Suzan O. Rasool, Shinah A. Mohammed

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---

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Integrative systems immunology uncovers molecular networks of the cell cycle that stratify COVID-19 severity

Caroline Aliane de Souza Prado, Dennyson Leandro M. Fonseca, Youvika Singh, Igor Salerno Filgueiras, Gabriela Crispim Baiocchi, Desirée Rodrigues Plaça, Alexandre H. C. Marques, Raquel Costa Silva Dantas-Komatsu, Júlia N. Usuda, Paula Paccielli Freire, Ranieri Coelho Salgado, Sarah Maria da Silva Napoleao, Rodrigo Nalio Ramos, Vanderson Rocha, Guangyan Zhou, Rusan Catar, Guido Moll, Niels Olsen Saraiva Camara, Gustavo Cabral de Miranda, Vera Lúcia Garcia Calich, Lasse M. Giil, Neha Mishra, Florian Tran, Andre Ducati Luchessi, Helder I. Nakaya, Hans D. Ochs, Igor Jurisica, Lena F. Schimke, Otavio Cabral-Marques

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Upregulation of PD-L1 by SARS-CoV-2 promotes immune evasion

Hsiang-Chi Huang, Shih-Han Wang, Guo-Chen Fang, Wen-Cheng Chou, Chun-Che Liao, Cheng-Pu Sun, Jia-Tsrong Jan, Hsiu-Hua Ma, Hui-Ying Ko, Yi-An Ko, Ming-Tsai Chiang, Jian-Jong Liang, Chun-Tse Kuo, Te-An Lee, Diego Morales-Scheihing, Chen-Yang Shen, Shih-Yu Chen, Louise D. McCullough, Lu Cui, Gerlinde Wernig, Mi-Hua Tao, Yi-Ling Lin, Yao-Ming Chang, Shu-Ping Wang, Yun-Ju Lai, Chia-Wei Li

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Jéssica P. Farias, Josilene R. Pinheiro, Robert Andreata-Santos, Mayanna M. C. Fogaça, Ruth D. da Silva Brito, Edgar F. da Cruz, Maria F. de Castro-Amarante, Samuel S. Pereira, Shirley dos Santos Almeida, Ludimila M. Moreira, Rafael da Conceição Simões, Wilson B. Luiz, Alexander Birbrair, Aline Belmok, Bergmann M. Ribeiro, Juliana T. Maricato, Carla T. Braconi, Luís C. de Souza Ferreira, Luiz M. R. Janini, Jaime Henrique Amorim

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---

Genetic analysis and biological characterization of H10N3 influenza A viruses isolated in China from 2014 to 2021

Yuancheng Zhang, Jianzhong Shi, Pengfei Cui, Yaping Zhang, Yuan Chen, Yujie Hou, Liling Liu, Yongping Jiang, Yuntao Guan, Hualan Chen, Huihui Kong, Guohua Deng

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> **Importance**
> Avian influenza virus, which frequently jumps to humans and causes severe illness and death, poses a continuing threat to public health. Understanding the genesis and characteristics of avian influenza viruses will help prevent future human influenza pandemics. In this study, we provide evidence that the human-infecing H10N3 viruses are reassortants with internal genes from chicken H9N2 viruses and surface genes from duck viruses, suggesting a critical role for ducks in the generation of viruses with human-infecting potential. Our findings demonstrate that some H10N3 viruses exhibit higher affinity for human-type receptors than for avian-type receptors, and some can transmit via direct contact and/or respiratory droplets in the guinea pig model, suggesting the potential risk posed by H10N3 viruses.

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Low prevalence of influenza viruses and predominance of A(H3N2) virus with respect to SARS-CoV-2 during the 2021–2022 season in Bulgaria

Neli Korsun, Ivelina Trifonova, Veselin Dobrinov, Iveta Madzharova, Iliyana Grigorova, Iva Christova

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Baricitinib or imatinib in hospitalized COVID-19 patients: Results from COVINIB, an exploratory randomized clinical trial

Alejandro Morales-Ortega, Ana Isabel Farfán-Sedano, Juan Víctor San Martín-López, Almudena Escribá-Bárcena, Beatriz Jaenes-Barrios, Elena Madroñal-Cerezo, Cristina Llarena-Barroso, Nieves Mesa-Plaza, Begoña Frutos-Pérez, José Manuel Ruiz-Giardín, Miguel Ángel Duarte-Millán, Sara Isabel Piedrabuena-García, Lorena Carpintero-García, Eduardo Canalejo-Castrillero, Belén Mora-Hernández, Carlos Javier García-Parra, Héctor Agustín Magro-García, Alicia Algaba-García, Belén Hernández-Muniesa, Berta Nasarre-López, Ana Ontañón-Nasarre, María Jesús Domínguez-García, Dulce Gómez-Santos, Santiago Prieto-Menchero, Jaime García de Tena, Fernando Bermejo, Mario García-Gil, Sonia Gonzalo-Pascua, David Bernal-Bello, the COVINIB Study Group investigators

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---

Isolation and characterization of mammalian orthoreovirus from bats in the United States

Liping Wang, Baoliang Zheng, Zhenyu Shen, Nirmalendu Deb Nath, Yonghai Li, Timothy Walsh, Yan Li, William J. Mitchell, Dongchang He, Jinhwa Lee, Susan Moore, Suxiang Tong, Shuping Zhang, Wenjun Ma

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Rapid detection of monkeypox virus by multiple cross displacement amplification combined with nanoparticle-based biosensor platform

Juan Zhou, Fei Xiao, Jin Fu, Nan Jia, Xiaolan Huang, Chunrong Sun, Chunyan Liu, Hui Huan, Yi Wang

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Single-cell transcriptomics dissects epithelial heterogeneity in HPV$^+$ cervical adenocarcinoma

Cong Wang, Lei Li, Fuhao Wang, Xia Li, Jujie Sun, Xiaohui Li, Tianyu Lei, Qingyu Huang, Guangyu Zhang, Hongqing Wang, Dapeng Li, Jue Jia, Chunyan Li, Feng Geng, Jinbo Yue, Chao Liu

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---

Characterization of cross-reactive monoclonal antibodies against SARS-CoV-1 and SARS-CoV-2: Implication for rational design and development of pan-sarbecovirus vaccines and neutralizing antibodies

Shibo Li, Jianbo Wu, Weiyu Jiang, Haiyan He, Yunjiao Zhou, Wei Wu, Yidan Gao, Minxiang Xie, Anqi Xia, Jiaying He, Qianqian Zhang, Yuru Han, Nan Wang, Guangqi Zhu, Qiujing Wang, Zheen Zhang, Christian T. Mayer, Kang Wang, Xiangxi Wang, Junqing Wang, Zhenguo Chen, Shibo Jiang, Lei Sun, Rong Xia, Qiao Wang

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Real-world effectiveness of sotrovimab and remdesivir for early treatment of high-risk hospitalized COVID-19 patients: A propensity score adjusted retrospective cohort study

Lin Pin Koh, Siang Li Chua, Shawn Vasoo, Matthias Paul Han Sim Toh, Jeremy Nicholas Cutter, Puay Hoon Nah, Yee-Sin Leo, Jun Xin Tay, Barnaby Edward Young, David C. Lye, Sean W. X. Ong

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---

ACE2 PET to reveal the dynamic patterns of ACE2 recovery in an infection model with pseudocorona virus

Xiao Li, Wei Yin, Ao Li, Danni Li, Xiaolong Gao, Ruizhi Wang, Bin Cui, Shuang Qiu, Rou Li, Lina Jia, Changjing Zuo, Lan Zhang, Ming Li

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Establishment of a diverse head and neck squamous cancer cell bank using conditional reprogramming culture methods

Daniel Li, Carlos Thomas, Nitisha Shrivastava, Adam Gersten, Nicholas Gadsden, Nicolas Schlecht, Nicole Kawachi, Bradley A. Schiff, Richard V. Smith, Gregory Rosenblatt, Stelby Augustine, Evripidis Gavathiotis, Robert Burk, Michael B. Prystowsky, Chandan Guha, Vikas Mehta, Thomas J. Ow

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Omicron infection increases IgG binding to spike protein of predecessor variants

Gokulnath Mahalingam, Yogapriya Periyasami, Porkizhi Arjunan, Rajesh K. Subaschandrabose, Tamil V. Mathivanan, Roshlin S. Mathew, Ramya K. T. Devi, Prasanna S. Premkumar, Jayaprakash Muliyil, Alok Srivastava, Mahesh Moorthy, Srujan Marepally

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Head-to-head comparison of genotyping of human papillomavirus by GP5+/6+-PCR-based reverse dot blot hybridization assay and SPF10-PCR-based line probe assay

Jian Yin, Siying Peng, Xinyue Li, Changning Zhang, Fangfang Hu, Wen Chen, Youlin Qiao

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---

Efficacy and safety of nirmatrelvir/ritonavir (Paxlovid) for COVID-19: A rapid review and meta-analysis

Behnam Amani, Bahman Amani

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The pattern of cytokines expression and dynamic changes of renal function at 6 months in patients with Omicron COVID-19

Lanbo Teng, Xinyuan Song, Miaomiao Zhang, Yingying Han, Ge Chang, Wenxiu Chang, Zhongyang Shen

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A novel, ultrafast, ultrasensitive diagnosis platform for the detection of SARS-COV-2 using restriction endonuclease-mediated reverse transcription multiple cross displacement amplification

Junfei Huang, Xinggui Yang, Lijuan Ren, Weijia Jiang, Yan Huang, Ying Liu, Chunting Liu, Xu Chen, Shijun Li

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The salivary and nasopharyngeal microbiomes are associated with SARS-CoV-2 infection and disease severity

Josh G. Kim, Ai Zhang, Adriana M. Rauseo, Charles W. Goss, Philip A. Mudd, Jane A. O'Halloran, Leyao Wang

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Dynamics of nosocomial SARS-CoV-2 transmissions: Facing the challenge of variants of concern in a Brazilian reference hospital

Andressa Taíz Hoffmann, Mariana Soares da Silva, Juliana Schons Gularte, Alessandro Comaru Pasqualotto, José Luiz Proença Módena, Alana Witt Hansen, Claudio Marcel Berdún Stadñik, Teresa Cristina Teixeira Sukienik, Meriane Demoliner, Fágner Henrique Heldt, Micheli Filippi, Vyctoria Malayhka de Abreu Góes Pereira, Cristiani Gomes de Marques, Ionara Ines Kohler, Daniela Muller De Quevedo, Fernando Rosado Spilki

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Surveillance, isolation and genomic characterization of *Pteropine orthoreovirus* of probable bat origin among patients with acute respiratory infection in Malaysia

Kok Keng Tee, Po Qhuan Chan, Alson Mun-Khin Loh, Sarbhan Singh, Chee How Teo, Thevambiga Iyadorai, Jack Bee Chook, Kim Tien Ng, Yutaka Takebe, Kok Gan Chan, I-Ching Sam, Kenny Voon

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Impact of nonalcoholic fatty liver disease status change on antiviral efficacy of nucleos(t)ide analogues in HBeAg-positive chronic hepatitis B

Yanhua Tang, Rong Fan, Zhixian Lan, Qing Xie, Jiping Zhang, Xieer Liang, Hao Wang, Deming Tan, Jun Cheng, Shijun Chen, Qin Ning, Xuefan Bai, Min Xu, Xinyue Chen, Junqi Niu, Junping Shi, Hong Ren, Zhiliang Gao, Maorong Wang, Xiaoguang Dou, Jinlin Hou, Jian Sun

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Weekly symptom profiles of nonhospitalized individuals infected with SARS-CoV-2 during the Omicron outbreak in Hong Kong: A retrospective observational study from a telemedicine center

Jingyuan Luo, Jialing Zhang, Hiu To Tang, Hoi Ki Wong, Yanfang Ma, Duoli Xie, Bo Peng, Aiping Lyu, Chun Hoi Cheung, Zhaoxiang Bian

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Microglia innate immune response contributes to the antiviral defense and blood–CSF barrier function in human choroid plexus organoids during HSV-1 infection

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Disparities in survival outcomes among Black patients with HPV-associated oropharyngeal cancer

Sujith Baliga, Darrion Mitchell, Vedat O. Yildiz, Emile Gogineni, David J. Konieczkowski, John Grecula, Dukagjin M. Blakaj, Xuefeng Liu, Mauricio E. Gamez

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Prophylactic tenofovir alafenamide for hepatitis B virus reactivation and reactivation-related hepatitis

Goki Suda, Masaru Baba, Yoshiya Yamamoto, Takuya Sho, Koji Ogawa, Megumi Kimura, Shunichi Hosoda, Sonoe Yoshida, Akinori Kubo, Qingjie Fu, Zijian Yang, Yoshimasa Tokuchi, Takashi Kitagataya, Osamu Maehara, Shunsuke Ohnishi, Ren Yamada, Masatsugu Ohara, Naoki Kawagishi, Mitsuteru Natsuizaka, Masato Nakai, Kenichi Morikawa, Ken Furuya, Kazuharu Suzuki, Takaaki Izumi, Takashi Meguro, Katsumi Terashita, Jun Ito, Tomoe Kobayashi, Izumi Tsunematsu, Naoya Sakamoto

e28452 | First Published: 04 January 2023

> **Lay Summary**
> Hepatitis B virus (HBV) reactivation during antitumor or immunosuppressive therapy could be fatal. Tenofovir alafenamide (TAF) is a novel prodrug of tenofovir with high efficacy and safety for hepatitis B infection. Nonetheless, there exist no prospective studies on the efficacy of TAF prophylaxis for the prevention of HBV reactivation. This prospective multicenter study is the first to show the high efficacy of TAF prophylaxis for the prevention of HBV reactivation.

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RSV-CLASS —Clinical Assessment Severity Score: An easy-to-use clinical disease severity score for respiratory syncytial virus infection in hospitalized children

Julia Gsenger, Thomas Bruckner, Clara Marlene Ihling, Rebecca Marie Rehbein, Sarah Valerie Schnee, Johannes Hoos, Britta Manuel, Johannes Pfeil, Paul Schnitzler, Julia Tabatabai

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Usefulness of dried blood spot samples for monitoring hepatitis C treatment outcome and reinfection among people who inject drugs in a test-and-treat program

Anna Not, Verónica Saludes, Mont Gálvez, Anna Miralpeix, Antoni E. Bordoy, Noemí González, Sara González-Gómez, Laura Muntané, Juliana Reyes-Urueña, Xavier Majó, Joan Colom, Xavier Forns, Sabela Lens, Elisa Martró

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Cross-sectional analysis reveals autoantibody signatures associated with COVID-19 severity

Gabriela C. Baiocchi, Aristo Vojdani, Avi Z. Rosenberg, Elroy Vojdani, Gilad Halpert, Yuri Ostrinski, Israel Zyskind, Igor S. Filgueiras, Lena F. Schimke, Alexandre H. C. Marques, Lasse M. Giil, Yael B. Lavi, Jonathan I. Silverberg, Jason Zimmerman, Dana A. Hill, Amanda Thornton, Myungjin Kim, Roberta De Vito, Dennyson L. M. Fonseca, Desireé R. Plaça, Paula P. Freire, Niels O. S. Camara, Vera L. G. Calich, Carmen Scheibenbogen, Harald Heidecke, Miriam T. Lattin, Hans D. Ochs, Gabriela Riemekasten, Howard Amital, Yehuda Shoenfeld, Otavio Cabral-Marques

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Local immune dysregulation and subsequent inflammatory response contribute to pulmonary edema caused by *Enterovirus* infection in mice

Tiantian Sun, Dong Li, Xinchen Dai, Caiyun Meng, Yi Li, Cheng Cheng, Wangquan Ji, Peiyu Zhu, Shuaiyin Chen, Haiyan Yang, Yuefei Jin, Weiguo Zhang, Guangcai Duan

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Association between trans fatty acids and COVID-19: A multivariate Mendelian randomization study

Xuxu Liu, Zhiwei Du, Jing Wang, Qiang Wang, Yi Zheng, Le Niu, Chenjun Hao, Dongbo Xue, Yingmei Zhang

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An integrated strategy to identify COVID-19 causal genes and characteristics represented by LRRC37A2

Zijun Zhu, Xinyu Chen, Chao Wang, Sainan Zhang, Rui Yu, Yubin Xie, Shuofeng Yuan, Liang Cheng, Lei Shi, Xue Zhang

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The effect of synbiotic adjunct therapy on clinical and paraclinical outcomes in hospitalized COVID-19 patients: A randomized placebo-controlled trial

Mahsa Vaezi, Sahar Ravanshad, Mina Akbari Rad, Hossein Zarrinfar, Mona Kabiri

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SHORT COMMUNICATIONS

First report of coinfection and whole-genome sequencing of norovirus and sapovirus in an acute gastroenteritis patient from Pakistan

Massab Umair, Zaira Rehman, Syed Adnan Haider, Muhammad Usman, Muhammad Suleman Rana, Aamer Ikram, Muhammad Salman

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Risk stratification for cervical precancer and cancer by DH3-HPV partial genotyping and cytology in women attending cervical screening: A retrospective cohort study

Yunfeng Fu, Ying Li, Xiao Li, Xinyu Wang, Weiguo Lü

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Infection by SARS-CoV-2 with alternate frequencies of mRNA vaccine boosting

Jeffrey P. Townsend, Hayley B. Hassler, Alex Dornburg

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SARS-CoV-2 infection of kidney tissues from severe COVID-19 patients

Shawn Radovic, Wen Meng, Luping Chen, Alberto E. Paniz Mondolfi, Clare Bryce, Zachary Grimes, Emilia M. Sordillo, Carlos Cordon-Cardo, Haitao Guo, Yufei Huang, Shou-Jiang Gao

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Whole-genome sequencing of hMPXV1 in five Italian cases confirms the occurrence of the predominant epidemic lineage

Diego Forni, Chiara Moltrasio, Manuela Sironi, Alessandra Mozzi, Eleonora Quattri, Luigia Venegoni, Marzia Zamprogno, Andrea Citterio, Mario Clerici, Angelo Valerio Marzano, Rachele Cagliani

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Significant neutralizing escapes of Omicron and its sublineages in SARS-CoV-2-infected individuals vaccinated with inactivated vaccines

Fan Shen, Cui-Xian Yang, Ying Lu, Mi Zhang, Ren-Rong Tian, Xing-Qi Dong, An-Qi Li, Yong-Tang Zheng, Wei Pang

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Clustered cases of human adenovirus types 4, 7, and 14 infections in US Department of Defense Beneficiaries during the 2018–2019 season

Adam R. Pollio, Anthony C. Fries, Yu Yang, Jerry J. Hughes, Christian K. Fung, Matthew A. Conte, Robert A. Kuschner, Natalie D. Collins, Elizabeth A. Macias, Jun Hang

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Erratum

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Sung-Woon Kang,Ji Yeun Kim,Heedo Park,So Yun Lim,Jeonghun Kim,Euijin Chang,Seongman Bae,Jiwon Jung,Min Jae Kim,Yong Pil Chong,Sang-Oh Lee,Sang-Ho Choi, Yang Soo Kim,Man-Seong Park,Sung-Han Kim

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Chuan Kok Lim,Jason Roberts,Michael Moso,Kwee Chin Liew,Mona L. Taouk,Eloise Williams,Thomas Tran,Eike Steinig,Leon Caly,Deborah Ann Williamson

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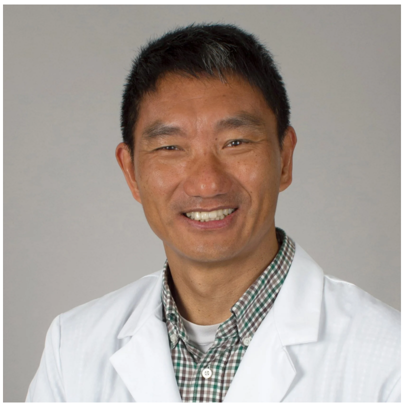

Shou-Jiang Gao

Editor-in-Chief

Dr. Gao received his Ph.D. in Microbiology and Health from the University of Bordeaux, Bordeaux (1993), France, and Postdoctoral training in Parasitology with Dr. John Burand in the University of Massachusetts at Amherst (1993-1994) and in Tumor Virology with Drs. Yuan Chang and Patrick Moore in Columbia University (1994-1997). He was a faculty member at the University of Texas Health Science Center at San Antonio (1997-2001: Assistant Professor; 2002-2006: Associate Professor; 2007-2011: Professor; 2009-2011: HEB Endowed Chair for Cancer Research), then at the University of Southern California (2011-20018: Professor). He is currently a Professor in the Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, and the Director of Cancer Virology Program of the University of Pittsburgh Medical Center (UPMC) Hillman Cancer Center and the Pittsburgh Foundation Endowed Chair for Cancer Therapy. Dr. Gao is an Elected Fellow of the American Academy of Microbiology (2014-). Dr. Gao is an expert in viral oncogenesis. His laboratory studies the oncogenic mechanisms of tumor viruses with current focus on Kaposi's sarcoma-associated herpesvirus (KSHV), which is associated with several AIDS-related malignancies including Kaposi's sarcoma, primary effusion lymphoma and a subset of multicentric Cattleman's disease. The research areas include mechanism of viral oncogenesis, metabolic reprogramming, cancer inflammation, cancer angiogenesis, epigenetic and epitranscriptomic reprogramming, functions of viral microRNAs, mechanism of persistent infection and reactivation, viral entry, trafficking and signaling, microbiome in cancer and infection, identification of therapeutic targets, development of therapeutic agents, and KSHV epidemiology.

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RESEARCH ARTICLE

JOURNAL OF MEDICAL VIROLOGY WILEY

Complete genome analyses of G12P[8] rotavirus strains from hospitalized children in Surabaya, Indonesia, 2017–2018

Laura Navika Yamani[1,2,3] | Takako Utsumi[1,4] | Yen Hai Doan[5] | Yoshiki Fujii[6] | Zayyin Dinana[1,3] | Rury Mega Wahyuni[1] | Emily Gunawan[1] | Soegeng Soegijanto[1] | Alpha Fardah Athiyyah[1,7] | Subijanto Marto Sudarmo[1,7] | Reza Gunadi Ranuh[1,7] | Andy Darma[1,7] | Soetjipto[1,3] | Juniastuti[1,3] | Rheza Gandi Bawono[4] | Chieko Matsui[4] | Lin Deng[4] | Takayuki Abe[4] | Hiroyuki Shimizu[6] | Koji Ishii[8] | Kazuhiko Katayama[9] | Maria Inge Lusida[1,3] | Ikuo Shoji[4]

[1]Laboratory of Viral Diarrhea, Indonesia-Japan Collaborative Research Center for Emerging and Re-emerging Infectious Diseases, Institute of Tropical Disease, Universitas Airlangga, Surabaya, Indonesia

[2]Department of Epidemiology, Biostatistics, Population Studies and Health Promotion, Faculty of Public Health, Universitas Airlangga, Surabaya, Indonesia

[3]Laboratory of Viral Diarrhea, Research Center on Global Emerging and Re-emerging Infectious Diseases, Institute of Tropical Disease, Universitas Airlangga, Surabaya, Indonesia

[4]Division of Infectious Disease Control, Center for Infectious Diseases, Kobe University Graduate School of Medicine, Hyogo, Japan

[5]Laboratory VIII, Center for Emergency Preparedness and Response, National Institute of Infectious Diseases, Tokyo, Japan

[6]Department of Virology II, National Institute of Infectious Diseases, Tokyo, Japan

[7]Department of Child Health, Soetomo Hospital, Universitas Airlangga, Surabaya, Indonesia

[8]Department of Quality Assurance and Radiological Protection, National Institute of Infectious Diseases, Tokyo, Japan

[9]Laboratory of Viral Infection I, Department of Infection Control and Immunology, Ōmura Satoshi Memorial Institute, Graduate School of Infection Control Sciences, Kitasato University, Tokyo, Japan

Correspondence

Ikuo Shoji, Centre for Infectious Diseases, Kobe University Graduate School of Medicine, 7-5-1 Kusunoki-Cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan.
Email: ishoji@med.kobe-u.ac.jp

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Abstract

Rotavirus A (RVA) is a major viral cause of acute gastroenteritis (AGE) worldwide. G12 RVA strains have emerged globally since 2007. There has been no report of the whole genome sequences of G12 RVAs in Indonesia. We performed the complete genome analysis by the next-generation sequencing of five G12 strains from hospitalized children with AGE in Surabaya from 2017 to 2018. All five G12 strains were Wa-like strains (G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1) and were clustered into lineage-III of VP7 gene phylogenetic tree. STM430 sample was observed as a mixed-infection between G12 and G1 strains: G12/G1-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1. A phylogenetic tree analysis revealed that all five Indonesian G12 strains (SOEP379, STM371, STM413, STM430, and STM433) were genetically close to each other in all 11 genome segments with 98.0%–100% nucleotide identities, except VP3 and NSP4 of STM430, suggesting that these strains have originated from a similar ancestral G12 RVA. The VP3 and NSP4 genome segments of STM430-G12P[8] were separated phylogenetically from those of the other four G12 strains, probably due to intra-genotype reassortment between the G12 and G1 Wa-like strains. The change from G12P[6] lineage-II in 2007 to G12P[8] lineage-III 2017–2018 suggests the evolution and diversity of G12 RVAs in Indonesia over the past approximately 10 years.

KEYWORDS
complete genome, G12 strains, Indonesia, NGS, Rotavirus

1 | INTRODUCTION

Rotavirus A (RVA) is a major viral cause of acute gastroenteritis (AGE) worldwide, and RVAs continue to be the leading cause of diarrhea-related mortality among children <5 years of age which is estimated to be approximately 20% of the affected population. Low-income countries with no RVA vaccination programs are particularly affected by the RVA diarrhea.[1,2] The World Health Organization has been recommending the use of RVA vaccines in all national immunization programs since 2009. To date, 114 countries have introduced RVA vaccines.[3] Systematic review reports revealed vaccine effectiveness with reductions of ≥32% in diarrhea-associated morbidity and mortality in all countries. Although the introduction of vaccines has reduced the number of RVA-associated deaths, the effectiveness of licensed vaccines in low-income countries at 30%–40% lower than the effectiveness in high-income countries, is suboptimal[4,5] and showed that RVA gastroenteritis still results in >200 000 deaths annually.[6] These phenomenon remains incompletely understood.[7,8] In Asia, only a few countries have introduced the vaccine nationally or sub-nationally.[9] Indonesia has not yet implemented a RVA vaccine as a universal immunization program, but two RVA vaccines, Rotarix® (GSK) and RotaTeq® (Merck & Co.) have been commercially available in the private market in Indonesia since 2011. In Indonesia, diarrhea is the leading cause of child mortality, and approximately 38%–67% of hospitalized children in Indonesia have diarrhea due to RVA infection.[10,11] Indonesia is one of the countries with the greatest number of RVA deaths as a proportion of all global RVA deaths in children under 5 in 2017.[12]

RVA is a nonenveloped virus consisting of 11 gene segments of double-stranded RNA encoding six structural proteins (VP1, VP2, VP3, VP4, VP6, and VP7genes) and five or six nonstructural proteins (NSP1, NSP2, NSP3, NSP4, and NSP5/NSP6).[13] The RVA genotypes are determined based on the nucleotide sequence identity in the open reading frame of each gene and are designated using a letter and a number. Two genes encoding VP7 (a glycoprotein) and VP4 (a protease-sensitive protein) are referred to as G and P types, respectively, and both proteins play crucial roles in recognition and neutralization by the immune system. To date, RVAs have been classified into 42G and 58P genotypes by the RVA Classification Working Group (https://rega.kuleuven.be/cev/viralmetagenomics/virus-classification/rcwg). Molecular epidemiological studies have identified the widespread circulation of various genotypes of RVAs, showing that five G-genotypes, i.e., G1–G4 and G9 and three P-genotypes, i.e., P[4], P[6], and P[8] are commonly associated with human infection.[14,15]

G12 rotaviruses have received little attention until recently. Since 1998, a decade after their first detection in the Philippines, G12 strains have been detected in Asia, Europe, South America, and North America, suggesting their possible emergence worldwide.[16] G12 genotype was the sixth major human G-genotype.[16,17] There have been reports of outbreaks in parts of West Africa such as Nigeria with G12 RVA strains[18,19] and some other countries identified G12 RVA as a prevalent genotype.[16,17] The vast majority of G12 strains have been isolated in Asia and more specifically in Southeast Asia.[16] G12 RVA has a very large genetic diversity caused mainly by genetic reassortments.[16,18]

The geographical region may contribute to the variation of G12 strains isolated around the world. Four different combinations of the G12 genotype and a P-genotype have been detected: G12P[4], G12P[6], G12P[8], and G12P[9].[16,17] Thus far, G12 strains were clustered into three lineages: I, II, and III. The first G12 strain, L26 (G12P[4]), isolated from a diarrheic child in the Philippines in 1987, was classified into lineage-I. More than 10 years after the isolation of strain L26, the G12P[9] strain named T152 was isolated in Thailand and was clustered into lineage-II. Many G12 strains isolated in the 2000s were clustered into lineage-III.[16]

In Indonesia, the first detection of a G12 strain, G12P[6], was obtained from a 14-day-old febrile infant with diarrhea, vomiting, moderate dehydration and malnutrition who was brought to Sumber Waras Hospital in West Jakarta in December, 2007. The strain isolated from this patient's stool was genotyped by semi-nested reverse transcription-polymerase chain reaction (RT-PCR) targeting the VP7 and VP4 genes, which are two of the 11 segments in the RVA genome.[20] There has been no other reports about G12 RVA strains in Indonesia, and the whole genome sequence of G12 strains in Indonesia has not been reported.

A whole genome-based genotyping method using the analysis of all 11 gene segments has been used for RVA epidemiology, with classification into genogroups based on the overall genomic RNA homology. Three genogroups of human RVA have been defined: Wa-like, DS-1-like, and AU-1-like. Of these three constellations, the Wa-like strains are the most predominant followed by the DS-1-like strains, and the AU-1-like strains are the least numerous strains in humans globally.[21] It is urgently necessary to fully sequence and characterize G12 RVA strains, as this information will contribute to our understanding of the evolutionary pattern and the diversity of emerging G12 strains. In this study, we performed a whole genome analysis of five G12 RVA strains detected in Indonesia in 2017–2018 by using the next-generation sequencing (NGS) technique.

2 | MATERIALS AND METHODS

2.1 | Specimens

During the RVA surveillance in 2017–2018 among hospitalized children with AGE in Surabaya, Indonesia, 67 RVA-positive stool samples were detected by an immunochromatography assay and RT-PCR. We used these RVA-positive samples for the whole genome analyses by NGS. The most commonly observed RVA genotypes were G1 and G3, and 62 of the 67 samples were excluded from this study; G12 RVA strains were detected in only five samples, all of which were included in the present investigation.

We thus analyzed the whole genome sequences of G12 RVA strains isolated from five stool specimens of ≤5-year-old children with AGE treated as inpatients at Dr. Soetomo hospital and Soerya hospital in Surabaya, East Java, Indonesia in 2017–2018. SOEP379 was isolated from an inpatient child treated at Soerya hospital, and STM371, STM413, STM430, and STM433 were isolated from children treated at Dr. Soetomo hospital. AGE was defined as the occurrence of three times looser than normal stools during a 24-h period. This study was approved by the Research Ethics Board of both hospitals, Universitas Airlangga (ethics approval number 2054/UN3.14/LT/2015) in Indonesia and Kobe University (ethics approval number 1857) in Japan. Written informed consent was obtained from the children's parents or guardians.

2.2 | Isolation of RNA virus and RT-PCR genotyping

Stool specimens were 10-fold diluted with phosphate-buffered saline (PBS; pH 7.4) and clarified by centrifugation at 10 000*g* for 10 min. Aliquots of all of the samples were then stored at −80°C before use. Viral RNA was extracted using Trizol LS Reagent (Life Technologies). In brief, 80 µl of the aliquot of a stool suspension in PBS was mixed with 240 µl of Trizol LS reagent and incubated for 5 min at room temperature. Then, 320 µl of 100% ethanol was added to the mixture. The mixture was placed into a Zymo-Spin IIC column (Zymo Research) and was centrifugated at 12 000*g* for 1 min, and washed with the prewash buffer and the wash buffer following the manufacturer's instructions. The viral RNAs were eluted with DNase/RNase-free water and used for RT-PCR genotyping and the whole genome analysis by NGS.

Viral extracted were subjected to genotyping in the VP7 (G typing) and VP4 genes (P typing) by multiplex RT-PCR. The VP7 and VP4 primer sets used had been previously described.[22] In particular, the VP7 primer set allowed us to correctly identify equine-like G3 among the other epidemic strains (G1, G2, typical human G3, G4, G8, G9, and G12).[23] The RNA samples were initially incubated at 65°C for 5 min with the first PCR primers. Subsequently, reverse transcription reaction was performed at 45°C for 10 min and at 94°C for 2 min, followed by 40 cycles of amplification (at 98°C for 10 s, at 50°C for 15 s, and at 68°C for 40 s), with a final extension at 68°C for 3 min. A total of 1 µl of diluted (50-fold) first PCR products was then used for a second PCR. The initial denaturation step was conducted at 98°C for 10 min, followed by 20 cycles of amplification (at 98°C for 10 s, at 50°C for 15 s, and at 68°C for 60 s), with a final extension at 68°C for 3 min. Both negative and positive controls were included in each experiment. Then, RT-PCR products were run in the agarose gel electrophoresis and D1000 ScreenTape assay on 4150 TapeStation (Agilent Technologies) was performed to visualize the size of PCR pruducts.

2.3 | Complementary DNA (cDNA) library building and Illumina Miseq sequencing for NGS analysis

The preparation of the cDNA library and the Illumina Miseq sequencing were performed as previously described.[24,25] Briefly, a 200-bp fragment library ligated with bar-coded adapters was constructed for individual strains using an NEBNext Ultra RNA library Prep Kit for Illumina ver. 1.2 (New England Biolabs) according to the manufacturer's instructions. Library purification was performed using Agencourt AMPure XP magnetic beads (Beckman Coulter). The quality of the purified DNA libraries was assessed on a MultiNa MCE-202 bioanalyzer (Shimadzu Corporation). Nucleotide sequencing was performed on an Illumina Miseq sequencer (Illumina) using the Miseq Reagent Kit ver. 2 (Illumina) to generate 151 paired-end reads.

2.4 | Nucleotide analysis and determination of RVA genotypes detected by NGS analysis

The sequence data were analyzed and assembled in the CLC Genomics Workbench Software ver. 7.0.3 (CLC Bio). A de novo assembly was carried out for all samples and the resulting contigs were identified using the Nucleotide Basic Local Alignment Search Tool (NCBI BLAST). The mixed infection between RVAs was defined as when two or more sequences were present in the same genome segment and they were of the same or different genotypes. The different titers of RVA genomic RNA extracted from the stool specimen will reflect the number of copies in the library, and therefore, the number of reads obtained for the genes of each strain. Thus, genome constellation of each RVA strain in mixed infection sample was defined as all sequences for 11 genome segments have a similar rate between total read count and length of obtained sequences.

The genotype of each of 11 gene segments of G12P[8] strains were determined using the online database Virus pathogen Database and Analysis Resource (ViPR).[23] The sequence results were deposited in the DDBJ/GenBank database with accession numbers LC581220 to LC581275.

2.5 | Phylogenetic tree analyses

Sequence comparisons were carried out with the references retrieved from GenBank. Alignment between the study and reference strains was performed using a Multiple Sequence Comparison by Log Expectation alignment.[26] Phylogenetic trees were constructed in MEGA version 10.0 software using Maximum likelihood method.[27] The best substitution models were selected based on the corrected Akaike information criterion value as implemented in MEGA10. Models used in this study were Tamura 3-parameter (T92) + G + I (VP7, NSP3, NSP4, and NSP5), (T92) + G + I (NSP2), Tamura-Nei (TN93) + G + I (VP1 and VP3), General Time Reversible (GTR) + G + I (VP4, VP2, and NSP1). The reliability of the branching order was estimated from 1000 bootstrap replicates. Lineages of G12 RVA strains were assigned according to the literature.[16,28]

3 | RESULTS

3.1 | Genotype constellation of Indonesian G12 strains

Five G12 RVA strains isolated from stool samples of pediatric patients with AGE were used: SOEP379, STM371, STM413, STM430, and STM433. The patients were 6–24 months old (average 12.6 months old), consisting of two boys and three girls. The clinical symptoms of the patients were diarrhea (5/5, 100%), waterly diarrhea (1/5, 20%), vomitting (2/5, 40%), fever (2/5, 40%), abdominal pain (1/5, 20%), some dehydration (3/5, 60%), and severe dehydration (1/5, 20%). We analyzed the whole genome of all five strains by NGS. The open reading frames of the 11 genome segments of SOEP379, STM371, STM413, STM430, and STM433 strains were successfully determined using the Illumina MiSeq technology. The genotype constellation of all five strains revealed to be G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1, i.e., typical Wa-like strains. Of these, STM430 sample was observed as mixed-infection sample between G12 and G1 strains with two genome constellations: G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1 and G11-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1. No reassortment event with inter-genogroups or inter-species of RVA strains was detected (Table 1).

3.2 | Phylogenetic tree analysis

The analysis demonstrated that all of the Indonesian G12 strains have a close relationship with each other, as depicted by the single clade in the phylogenetic tree of VP7 gene (Figure 1). They were clustered into lineage-III. The VP7 gene of these strains were closely associated with the VP7 gene of strain RVA/Human-wt/USA/2013774166/2013/G12P8 and shared 99.14%–99.24% nucleotide identity (Table 2). In the phylogenetic tree of VP7 genes, we also identified the mixed-genotype strain with RVA G1 (STM430-G1P[8]), which

TABLE 1 RVA genotype constellations of five human G12 RVA study strains compared to the published human G12 RVA strains

G12 strain	Year	Genogroup	VP7 (Lineage)	VP4	VP6	VP1	VP2	VP3	NSP1	NSP2	NSP3	NSP4	NSP5	Reference
L26	1987	DS-1-like	G12 (I)	P[4]	I2	R2	C2	M1/M2	A2	N1	T2	E2	H1	Previous study[16]
T152	1998	AU-1-like	G12 (II)	P[9]	I3	R3	C3	M3	A12	N3	T3	E3	H6	
RV161-00	2000–2002	DS-1-like	G12 (III)	P[6]	I2	R2	C2	M2	A2	N2	T2	E1	H2	
RV176-00	2000–2002	DS-1-like	G12 (III)	P[6]	I2	R2	C2	M2	A2	N2	T2	E6	H2	
N26-02	2000–2002	DS-1-like	G12 (III)	P[6]	I2	R2	C2	M2	A2	N1	T2	E6	H2	
Dhaka25-02	2002–2005	Wa-like	G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	
Dhaka12-03	2002–2005	Wa-like	G12 (III)	P[6]	I1	R1	C1	M1	A1	N1	T1	E1	H1	
Matlab13-03	2002–2005	Wa-like	G12 (III)	P[6]	I1	R1	C1	M1	A1	N1	T2	E1	H1	
SOEP379-18	2017–2018	Wa-like	G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	Present study
STM371-17	2017–2018	Wa-like	G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	
STM413-17	2017–2018	Wa-like	G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	
STM433-17	2017–2018	Wa-like	G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	
STM430-17	2017–2018	Wa-like	G1/G12 (III)	P[8]	I1	R1	C1	M1	A1	N1	T1	E1	H1	

Note: The Wa-, DS-1-, and AU-1-like genogroups were assigned to human strains if at least seven gene segments belonged to the Wa-, DS-1, and AU-1-like genotype, respectively. Colors were added to visualize patterns or gene constellations. Green: Wa-like, red: DS-1-like, and yellow: AU-like gene segments. Gray: Subtype 4A, and blue: RVA gene from animals. *Green is Wa-like strain. *Red is DS-1-like strain. *Yellow is AU-1-like strain. *Gray is an ST3-like strain. *Blue is a RVA gene from an animal.

Abbreviation: Rotavirus A.

was clustered together with RVA/Human-wt/IDN/STM457/2018/G1P[8] from Indonesia and near RVA/Human-wt/IND/RV1326/2013/G1 from India (Figure 1).

The VP4 genes of all five G12 strains were genotyped as P[8] (Figure 2). On the phylogenetic tree, all Indonesian G12 strains clustered closely to RVA/Human-wt/BGD/Bang-065/2008/G9P8 in VP4 gene and shared 99.08%–99.35% nucleotide identity (Table 2). STM430-G1 strain was also genotyped as P[8] but grouped as a different branch from the other G12 strains; it was found to be closely related to two strains of G1P[8] isolated from Indonesia, RVA/Human-wt/IDN/STM453/2018/G1P[8]. In addition, type P[8] of strain STM430-G1 is also phylogenetically close to RVA/Human-wt/JPN/Tokyo17-21/2017/G3P8 (Figure 2). The genetic backbone of all samples was Wa-like strain (Table 1 and Figure 2). The results of the phylogenetic analysis of the VP6, VP1–VP3, and NSP1–NSP5 genes of the five study strains are illustrated in Figures S1–S9.

Five Indonesian G12 strains were closely related to each other in all 11 genome segments with 98.0%–100% nucleotide identities, except VP3, and NPS4 gene of STM430-G12 strain (Figures 1 and 2, Figures S1–S9). The VP3 and NSP4 genes of STM430-G12 strain were separated into a different clade from the four other G12 study strains and clustered with other Indonesian strains RVA G1P[8] (RVA/Human-wt/IDN/STM387/2017/G1P8; RVA/Human-wt/IDN/STM453/2018/G1P8 or RVA/Human-wt/IDN/STM457/2018/G1P8) as described in the phylogenetic tree.

The VP4, VP6, VP1–VP3, and NSP1–NSP3 genes of all these Indonesian G12 strains, except VP3 and NSP4 of STM430-G12, were clustered with the closest reference G12 strains outside Indonesia, including strains from Bangladesh, Hungary, United States, Thailand, and Slovakia (Figures 1 and 2, Figures S1–S9). Interestingly, NSP4 genes in all five study strains were closest to RVA/Cow-wt/UGA/BUW-14-A035/2014/G12P8 isolated from a cow (i.e., a strain transmitted from a human to a cow) in Uganda (Figure S8).

The nucleotide sequence identities for the 11 genes between samples and closest references analyzed by NCBI homology BLAST are shown in Table 2. Within samples, some study strains exhibited

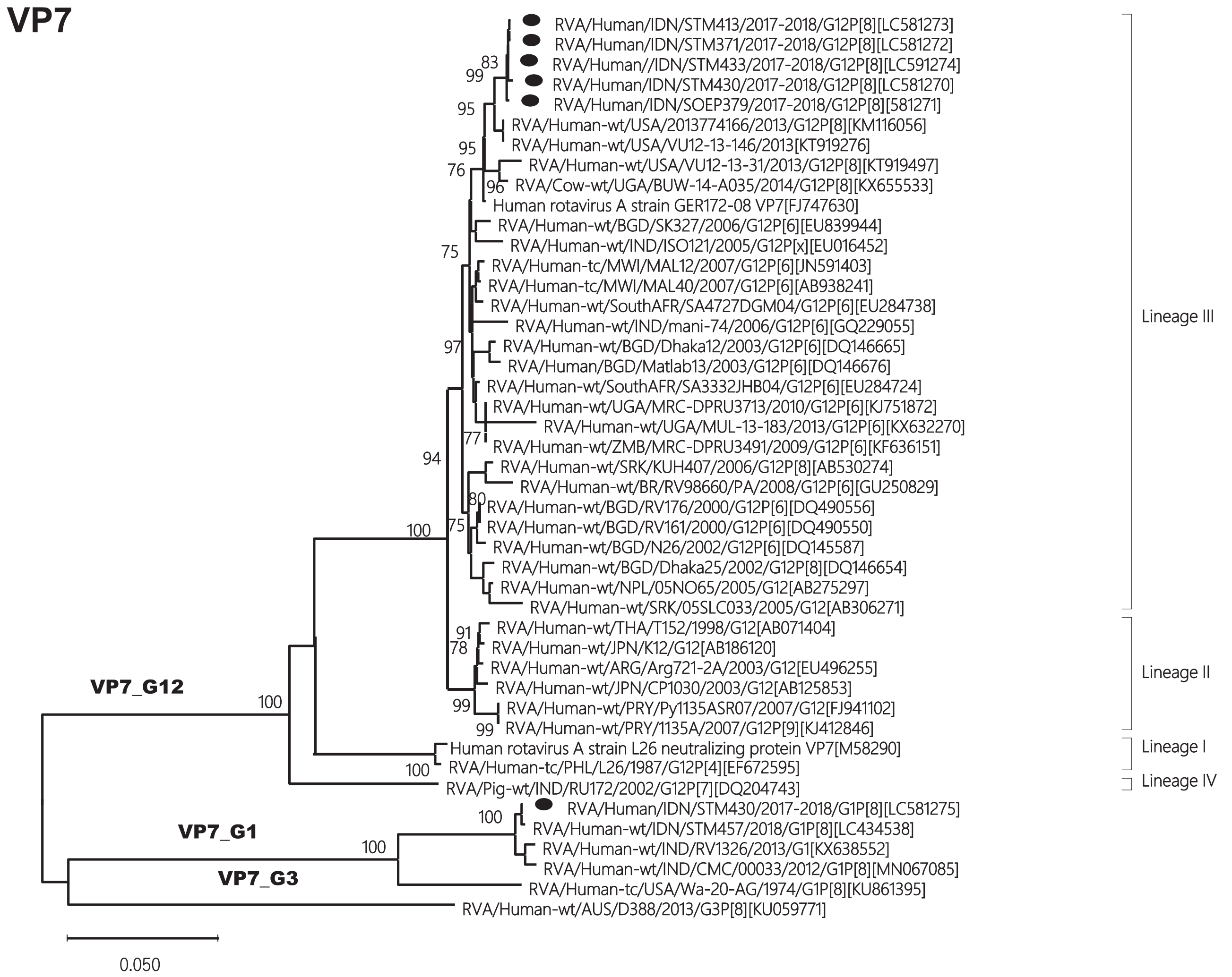

FIGURE 1 Phylogenetic tree analysis of VP7 genes for G12 RVA strains detected in five samples collected in Surabaya, Indonesia. *Black inverted triangles and Bullets:* The RVA strains sequenced in this study. The reference strains obtained from the GenBank database are represented by the accession number, strain name, country, and year of isolation. Scale bar: 0.050 substitutions per nucleotide. RVA, Rotavirus A

TABLE 2 Nucleotide sequence identity between G12 RVA genes obtained from Illumina MiSeq sequencing and the closest strains isolated from references based on NCBI homology BLAST

Gene	Accession no.	Genotype	Samples	Closest strain of NCBI homology (% nt identity)	Gene	Accession no.	Genotype	Samples	Closest strain of NCBI homology (% nt identity)
VP7	LC581270	G12P[8]	STM430	99.14% RVA/Human-wt/USA/2013774166/2013/G12P[8]	NSP1	LC721867	G12P[8]	STM430	99.45% Hungary human strain ERN5009 isolated 2012
	LC581271		SOEP379	99.24%		LC581221		SOEP379	99.38%
	LC581272		STM371	99.22%		LC581222		STM371	99.52%
	LC581273		STM413	99.24%		LC581223		STM413	99.59%
	LC581274		STM433	99.24%		LC581224		STM433	99.52%
	LC581275	G1P[8]	STM430	99.81% RVA/Human-wt/IDN/STM457/2018/G1P[8]		LC722500	G1P[8]	STM430	99.60% RVA/Human-wt/IDN/STM457/2018/G1P[8]
VP4	LC721862	G12P[8]	STM430	99.22% RVA/Human-wt/BGD/Bang-065/2008/G9P[8]	NSP2	LC721868	G12P[8]	STM430	98.80% RVA/Human-wt/USA/2013774165/2013/G12P[8]
	LC581261		SOEP379	99.08%		LC581226		SOEP379	98.84%
	LC581262		STM371	99.35%		LC581227		STM371	98.88%
	LC581263		STM413	99.26%		LC581228		STM413	98.94%
	LC721864		STM433	99.26%		LC581229		STM433	98.94%
	LC722498	G1P[8]	STM430	99.83% RVA/Human-wt/IDN/STM457/2017/G3P[8]		LC722501	G1P[8]	STM430	100% RVA/Human-wt/IDN/STM387/2017/G1P8 and RVA/Human-wt/IDN/STM453/2017/G1P[8]
VP6	LC721863	G12P[8]	STM430	99.76% RVA/human/SVK/2451/I1	NSP3	LC721869	G12P[8]	STM430	98.93% RVA/Human-wt/THA/DBM2018-111/2018/G9P[8]
	LC581266		SOEP379	99.76%		LC581231		SOEP379	98.77%
	LC581267		STM371	99.76%		LC581232		STM371	99.28%
	LC581268		STM413	99.76%		LC581233		STM413	98.88%
	LC581269		STM433	99.82%		LC581234		STM433	98.71%
	LC722499	G1P[8]	STM430	99.77% MN304727.1 RVA/Human-wt/NGR/2017		LC722502	G1P[8]	STM430	99.91% RVA/Human-wt/IDN/STM457/2017/G1P[8]
VP1	LC721864	G12P[8]	STM430	99.25% RVA/Human-wt/USA/VU12-13-39/2013/G12P[8]	NSP4	LC721870	G12P[8]	STM430	99.86% RVA/Human-wt/IDN/STM457/2018/G1P[8]
	LC581246		SOEP379	99.26%		LC581236		(like G1)	99.46% RVA/Cow-wt/UGA/BUW-14-A035/2014/G12P[8]
	LC581247		STM371	99.33%		LC581237		SOEP379	99.47%
	LC581248		STM413	99.23%		LC581238		STM371	99.31%
	LC581249		STM433	99.26%		LC581239		STM413	99.18%
								STM433	
	LC722495	G1P[8]	STM430	99.88% RVA/Human-wt/IDN/STM453/2018/G1P[8]		LC722503	G1P[8]	STM430 (like G12)	99.44% RVA/Cow-wt/UGA/BUW-14-A035/2014/G12P8
VP2	LC721865	G12P[8]	STM430	99.10% RVA/Human-wt/BGD/Bang-015/2008/G12P[6]	NSP5	LC722504	G12P[8]	STM430	99.39% RVA/Human-tc/USA/DC5685-40-AG/1991/G1P[8]
	LC581251		SOEP379	99.19%		LC581241		SOEP379	99.54%
	LC581252		STM371	99.44%		LC581242		STM371	99.52%
	LC581253		STM413	99.40%		LC581243		STM413	99.38%
	LC581254		STM433	99.33%		LC581244		STM433	99.54%
	LC722496	G1P[8]	STM430	99.89% RVA/Human-wt/IDN/STM453/2018/G1P8		LC721871	G1P[8]	STM430	100% RVA/Human-wt/IDN/STM457/2018/G1P[8]

TABLE 2 (Continued)

Gene	Accession no.	Genotype	Samples	Closest strain of NCBI homology (% nt identity)		Gene	Accession no.	Genotype	Samples	Closest strain of NCBI homology (% nt identity)
VP3	LC721866	G12P[8]	STM430 (like G1)	99.81%	RVA/Human-wt/IDN/STM387/2018/G1P[8]					
	LC581256		SOEP379	98.44%	RVA/Human-wt/USA/VU08-09-6/2008/G12P[8]					
	LC581257		STM371	98.33%						
	LC581258		STM431	98.48%						
	LC581259		STM433	98.48%						
	LC722497	G1P[8]	STM430 (like G12)	97.59%	RVA/Human-wt/USA/VU08-09-6/2008/G12P[8]					

Abbreviation: RVA, Rotavirus A.

100% similarity in several genes; for example, STM413 and STM433 in VP7 gene, as well as STM371 and SOEP379 in NSP4 gene (data not shown). A homology analysis using NCBI BLAST showed no evidence of inter-species reassortment events in any of the gene segments. Nevertheless, some animal strains were included in the phylogenetic tree of several genes because they are highly related to those of human RVAs and have homology with the study strains, suggesting that human RVA strains were also potentially transmitted to an animal and vice versa. The RVA strains isolated from animals that were observed in the present phylogenetic tree were RVA/Cow-wt/UGA/BUW-14-A035/2014/G12P in VP6, VP7, NSP1, and NSP4 genes (Figure 1, Figures S1, S5, and S8), RVA strain Rat-wt/ITA/Rat14/2015/G3P3 in VP6 (Figure S1), Porcine RV NSP3 (NS34) messenger RNA (strain PRICE) in NSP3 (Figure S7), RVA/Cow/B85/MP/India/2008 in NSP4 (Figure S8), and RVA/Donkey-wt/ZAF/MRC-DPRU1967/XXXX/GXPX in NSP5 (Figure S9). Their nucleotide sequence similarity compared to the study strains were around 96.9%–99.6%.

3.3 | Confirmation of mixed infection in STM430 sample

To confirm mixed infection for STM430 sample, the RNA was re-extracted from original clinical sample. RVA VP7 genotyping using the semi-nested multiplex PCR[23] were performed for both 1st and 2nd extracted RNA of STM430 together with other G1 (STM387) and G12 (STM413) samples. The size of PCR products was determined by D1000 ScreenTape assay on 4150 TapeStation (Agilent Technologies). The result revealed that all G12 samples contain 264 bp-band of G12 RVA. However, both 1st and 2nd STM430 samples contain two bands, 264 bp-band of G12 RVA and 636 bp-band of G1 RVA, indicating mixed infection of G12 RVA and G1 RVA (Figure 3).

4 | DISCUSSION

By using RT-PCR Genotyping and NGS analysis, we identified G12 RVAs as mono-infection in four samples (STM371, STM431, STM433, and SOEP379) and a co-infection of G12/G1 mixed-genotype in one sample (STM430). All strains were P[8] and showed a Wa-like genotype constellation, G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1. The single sample with the G12/G1 mixed-infection, exhibited two genotype constellations: G12-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1 and G1-P[8]-I1-R1-C1-M1-A1-N1-T1-E1-H1.

In Indonesia, the RVA genotypes G1P[8] and G3P[8] human strains are prevalent.[22,29,30] This may suggest co-infection between G1P[8]/G3P[8] and other G-types, such as the G12 isolated in this study. The finding of mixed-genotypes in this study showed that the NGS method is not only useful for whole genome-based analyses, but can also reveal the possibility of the occurrence of multiple isolates/strains/species. Other than, NGS analysis can also prove that there is

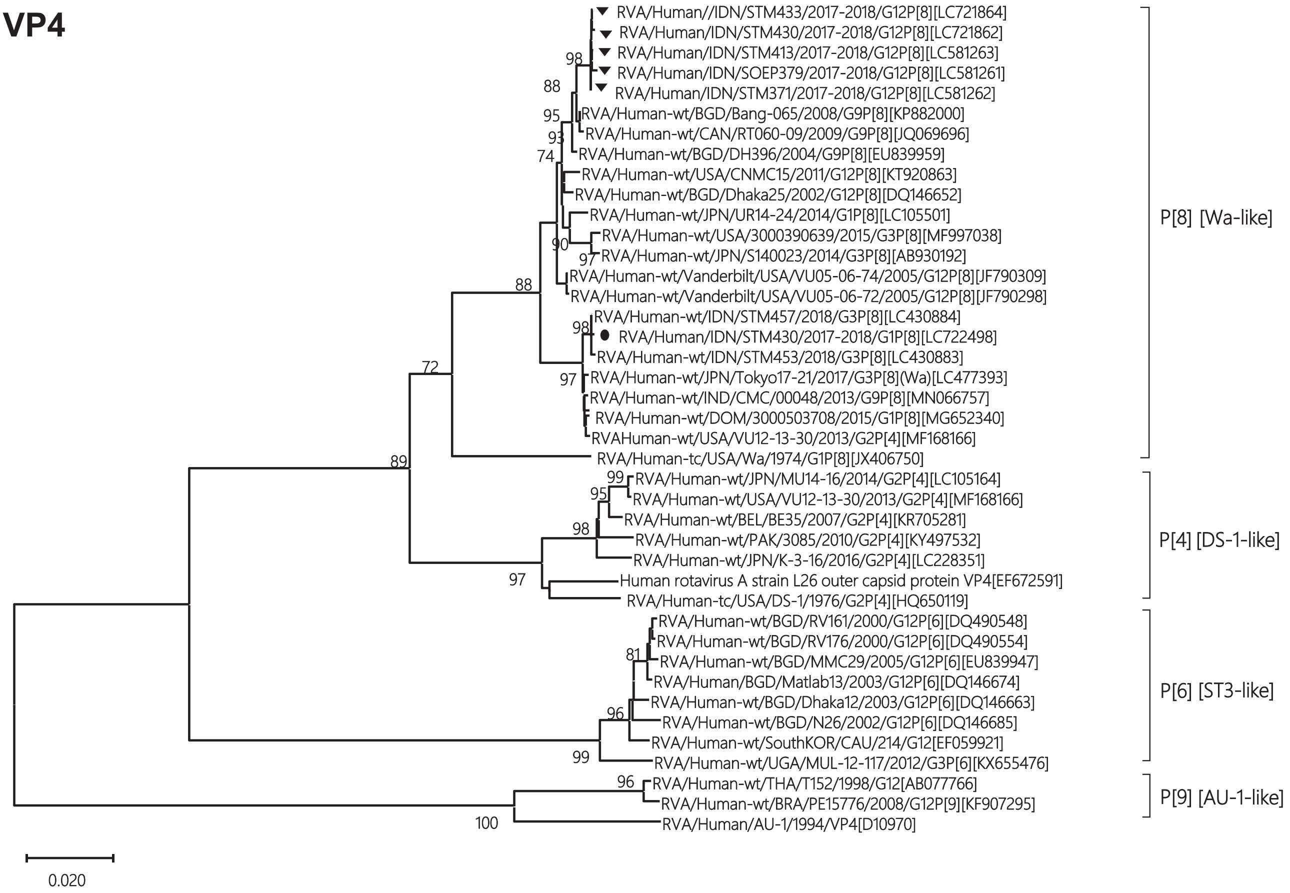

FIGURE 2 Phylogenetic tree analysis of VP4 genes detected in five samples collected in Surabaya, Indonesia. *Black inverted triangles and Bullets:* The G12 and G1 RVA strains sequenced in this study, respectively. The reference strains obtained from the GenBank database are represented by the accession number, strain name, country, and year of isolation. Scale bar: 0.020 substitutions per nucleotide. RVA, Rotavirus A.

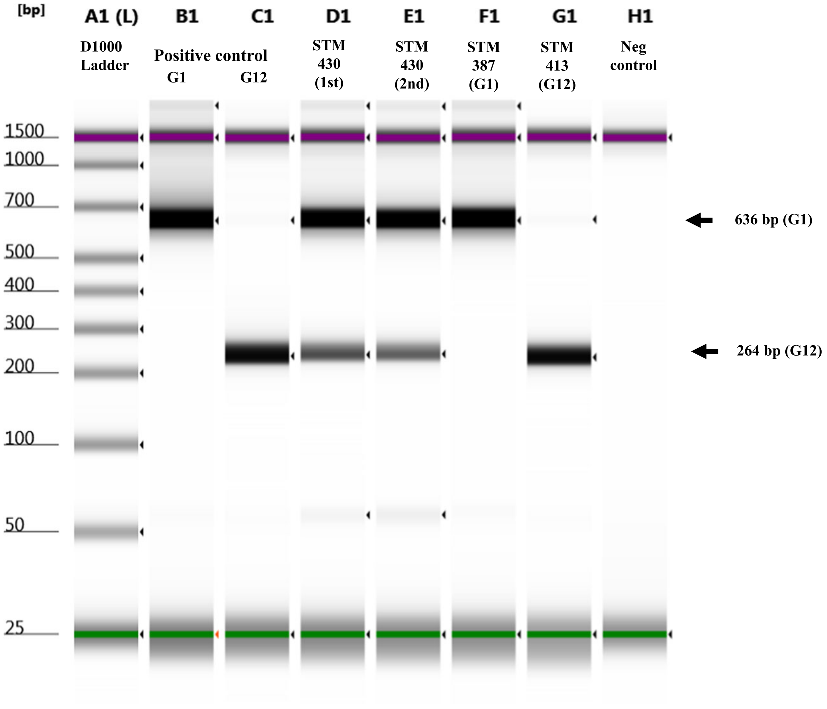

FIGURE 3 The VP7 genotyping of STM430. To confirm the mixed infection for STM430 sample, the RNA was re-extracted from original clinical sample. RVA genotyping using the semi-nested multiplex PCR were performed for both 1st and 2nd extracted RNA of STM430 together with other G1 (STM387) and G12 (STM413) samples. The size of PCR products was determined by D1000 ScreenTape assay on 4150 TapeStation (Agilent Technologies). RVA, Rotavirus A.

no contamination on RT-PCR Genotyping results with more than one band in the gel image of electrophoresis.

The RVA strains with rare or uncommon G/P types have been detected after the introduction of RVA vaccine and became dominant genotypes. It was reported that the emergence of G12P[8] RVA as a predominant genotype was newly observed in countries using RotaTeq,[31,32] whereas the dominance of G2P[4] and equine-like G3P[8] was found in countries using Rotarix.[33,34] These findings were obtained in countries with high vaccine coverage and effectiveness. However, emerging of previously rare or novel genotypes was observed in the vaccine era, indicating that the widespread vaccine use may accelerate strain diversities.[35] The RVA strains with new genotypes have also been found in countries with low coverage or no vaccination programs.[36,37]

Indonesia has not yet implemented a RVA vaccine national program. The use of Rotarix and RotaTeq in the private market at a relatively high price would have very limited coverage. We reported that uncommon equine-like G3 RVA strains were predominantly spread in Indonesia.[22,24] An isolate of an uncommon G12 RVA strain was firstly identified in Indonesia in December 2007 and was genotyped as G12P[6],[20] but there was no subsequent report about G12 RVA detection in Indonesia until 2016. During the RVA surveillance in 2017–2018, we detected five G12 RVA strains from hospitalized children. In the present study, we conducted a complete molecular characterization of these five G12 RVA Indonesian strains by NGS.

With the present phylogenetic analyses using the full-genome sequence of the 11 gene segments, we obtained direct evidence of the five strains' relatedness to other strains, even within the same genotype. The shifting of RVA genotypes was demonstrated by the difference in VP7 gene of G12 RVA between strain detected in 2007 classified in lineage-II and the present study strains isolated in 2017–2018, classified as lineage-III. The findings suggest an evolution of RVA genes may occur after ≥10 years, particularly regarding changes in VP4 gene and the lineage of VP7. The majority of RNA viruses have been reported to have an evolutionary rate of between 1.0×10^{-3} to 1.0×10^{-6} substitutions/site/year.[38] The evolutionary rate of the African G12 RVA sequences was 1.678×10^{-3}, (95% highest posterior density, 1.201×10^{-3} to 2.198×10^{-3}) substitutions/site/year.[39]

The nucleotide sequence divergence between lineage-II and lineage-III ranges from 2.6% to 3.2%.[16] However, lineage-II is a minority cluster when compared with lineage-III. G12 RVA lineage-I includes G12 strains from Japan, Argentina, Thailand, and Paraguay, whereas G12 RVA lineage-II consists of strains from the United States, India, Bangladesh, Germany, Uganda, and South Africa.[16,20] Hence, it was also suggested that the population mobility may contribute to genotype distribution.

The lineage-III G12 RVA strains in VP7 gene isolated in Indonesia were closely related to the United States strains, indicating that they might have originated in the United States. Indeed, each of the 11 genes of RVAs analyzed in this study showed the closest references from United States, Bangladesh, and Hungary (Table 2). This finding suggests that RVAs have genetically diverse population of segmented double-stranded RNA viruses due to the genomic reassortant ability between human strains or inter-species with animal strains.[40] The RVAs strains might be transported across the globe by the increasing mobility of humans and animals. Examples are seen in the RVA genome in the Belgian strain B4633-03, which was nearly identical to the Dhaka25-02 strain and the United Kingdom strain MV404-02, which was closely related to the Dhaka12-03 strain.[16] We compared our five study strains to other G12 strains that are Wa-, DS-1-, AU-1-, and ST3-like strains observed in Asian countries, such as the Philippines, Thailand, and Bangladesh (Table 1); the results indicate that all five study strains belong to Wa-like genogroups without reassortment with inter-genogroups or inter-species.

The branch topology of the equivalent segments from all five Indonesian G12P[8] strains in this study fell within the same monophyletic lineage for all segments, except VP3 and NSP4 of STM430/G12P[8] strain. Clustering within same monophyletic lineage indicate that these G12 strains may have originated from the same ancestor. G12P[8] virus seems to be undergoing further intra-genotype reassortment with G1P[8] virus in a mixed infection STM430 sample. The reassortment events have occurred in its VP3, and NSP4 genes (proved by average coverage in NGS results almost similar to other genes of STM430 G12). However, it is possible that the reassortments also are undergoing in the VP2, NSP2, NSP3, and NSP5 genes (data not shown). In the future, we will conduct other experiments to confirm the undergoing reassortment events in the RVA mixed infection samples. RVA G1P[8] was also found to be predominant in Indonesia.[22] Circulating RVA mixed-genotypes may thus contribute to intra-genogroups events. Our present findings revealed that gene segments of STM430 were closely related to those of RVA G1 strains that we previously isolated in Indonesia.[22] No reassortment for inter-genogroups was observed, even though an equine-like G3P[8]/[6] DS-1-like RVA strain was predominant at a hospital in the suburbs of Surabaya in 2015–2018.[22]

The NSP4 gene of all five G12 strains isolated in this study was closest to RVA/Cow-wt/UGA/BUW-14-A035/2014/G12P which is isolated from domestic animals in Uganda and is human-to-animal RVA transmission.[41] This phenomenon suggests that NSP4 gene reassortment event easily occurs between human and animal strains. Importantly, there is no human possessing an animal strain. Our present findings demonstrate that the genotype constellation of G12 RVA strains are similar. This may be because only a few G12 strains were detected in the study; the further isolation of G12 RVAs throughout Indonesia is necessary.

The detection of G12P[8] RVA has also increased recently in countries with and without high vaccine coverage.[42,43] The G12 genotype was first detected in 1987 in the Philippines,[44] then remained undetected until it re-emerged in Thailand in 1998.[45] Although G12 was considered a rare genotype in the 2000s, G12P[8] is now common genotype in many countries including in Asian countries such as Bangladesh,[46] India,[47] Japan,[48] Korea,[49] Thailand,[45] and Vietnam.[50] The emergence of G12 RVA strains may also have an impact on the efficacy of RVA vaccines. The increasing frequency of

G12 RVAs raises questions about their origin and evolution and how they can spread all over the world. Characterizing the complete genomes may increase our understanding of the relatedness and the evolution of emerging G12 RVA strains, which could be the result of point mutations, genetic rearrangements or reassortment events, and inter-species transmission. Whole genome-based analyses are thus useful to understand the evolutionary dynamics of G12 strains.

5 | CONCLUSIONS

To our knowledge, this is the first research article of the complete genome analyses of the G12 strains that have re-emerged in Indonesia. Five G12 RVA strains were obtained in the samples collected in Indonesia in 2017–2018. The results of our analyses demonstrated that G12P[8] is a newly emerging genotype in Indonesia, with genetic backbone of all strains Wa-like; no reassortment event was observed in inter-genogroups or animal strains. Further surveillance studies are necessary to gain more information about the circulating genotypes of human RVA in Indonesia, especially new emerging strains, such as G12 RVA strains.

AUTHOR CONTRIBUTIONS

Laura Navika Yamani, Takako Utsumi, Yen Hai Doan, Maria Inge Lusida, and Ikuo Shoji: designed the study and wrote the manuscript. **Soegeng Soegijanto, Alpha Fardah Athiyyah, Subijanto Marto Sudarmo, Reza Gunadi Ranuh, Soetjipto, Juniastuti**: collected samples. **Zayyin Dinana, Rury Mega Wahyuni, and Emily Gunawan**: carried out RVA detection and genome analysis. **Laura Navika Yamani, Yen Hai Doan, Kazuhiko Katayama, and Chieko Matsui**: performed NGS sequencing. **Laura Navika Yamani, Yen Hai Doan, Chieko Matsui, Rheza Gandi Bawono**: conducted sequence data analysis. **Lin Deng, Takayuki Abe, Hiroyuki Shimizu, Koji Ishii, Kazuhiko Katayama, Maria Inge Lusida, Ikuo Shoji**: gave critical revision of the article. All the authors contributed to the interpretation of the data, writing of the manuscript, and approved the final manuscript.

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CONFLICTS OF INTEREST

The authors declare no conflict of interest.

DATA AVAILABILITY STATEMENT

The data that support the findings of this study will be available at Kernel-Kobe University Repository (https://da.lib.kobe-u.ac.jp/da/kernel/). The sequence results were deposited in the DDBJ/GenBank database with accession numbers LC581220 to LC581275.

ORCID

Hiroyuki Shimizu http://orcid.org/0000-0002-2987-2377
Ikuo Shoji http://orcid.org/0000-0002-0730-4379

REFERENCES

1. Crawford SE, Ramani S, Tate JE, et al. Rotavirus infection. *Nat Rev Dis Primers*. 2017;3:17083.
2. Zhang SX, Zhou YM, Tian LG, et al. Antibiotic resistance and molecular characterization of diarrheagenic *Escherichia coli* and non-typhoidal Salmonella strains isolated from infections in Southwest China. *Infect Dis Poverty*. 2018;7(1):53.
3. Global Introduction Status. 2020. https://preventrotavirus.org/vaccine-introduction/global-introduction-status/
4. Armah GE, Sow SO, Breiman RF, et al. Efficacy of pentavalent rotavirus vaccine against severe rotavirus gastroenteritis in infants in developing countries in sub-Saharan Africa: a randomised, double-blind, placebo-controlled trial. *The Lancet*. 2010;376(9741):606-614.
5. Madhi SA, Cunliffe NA, Steele D, et al. Effect of human rotavirus vaccine on severe diarrhea in African infants. *N Engl J Med*. 2010;362(4):289-298.
6. Tate JE, Burton AH, Boschi-Pinto C, Parashar UD, World Health Organization-Coordinated Global Rotavirus Surveillance N. Global, regional, and national estimates of rotavirus mortality in children <5 years of age, 2000–2013. *Clin Infect Dis*. 2016;62(Suppl 2):S96-S105.
7. Burnett E, Jonesteller CL, Tate JE, Yen C, Parashar UD. Global impact of rotavirus vaccination on childhood hospitalizations and mortality from diarrhea. *J Infect Dis*. 2017;215(11):1666-1672.
8. Tate JE, Parashar UD. Rotavirus vaccines in routine use. *Clin Infect Dis*. 2014;59(9):1291-1301.
9. Burnett E, Tate JE, Kirkwood CD, et al. Estimated impact of rotavirus vaccine on hospitalizations and deaths from rotavirus diarrhea among children <5 in Asia. *Expert Rev Vaccines*. 2018;17(5):453-460.
10. Nirwati H, Wibawa T, Aman AT, Wahab A, Soenarto Y. Detection of group A rotavirus strains circulating among children with acute diarrhea in Indonesia. *SpringerPlus*. 2016;5:97.
11. Soenarto Y, Sebodo T, Ridho R, et al. Acute diarrhea and rotavirus infection in newborn babies and children in Yogyakarta, Indonesia, from June 1978 to June 1979. *J Clin Microbiol*. 1981;14(2):123-129.
12. At Thobari J, Sutarman, Mulyadi AWE, et al. Direct and indirect costs of acute diarrhea in children under five years of age in Indonesia: health facilities and community survey. *The Lancet Regional Health - Western Pacific*. 2022;19:100333.
13. Hu L, Crawford SE, Hyser JM, Estes MK, Prasad BV. Rotavirus non-structural proteins: structure and function. *Current Opinion in Virology*. 2012;2(4):380-388.
14. Dennehy PH. Rotavirus vaccines: an overview. *Clin Microbiol Rev*. 2008;21(1):198-208.
15. Ursu K, Kisfali P, Rigó D, et al. Molecular analysis of the VP7 gene of pheasant rotaviruses identifies a new genotype, designated G23. *Arch Virol*. 2009;154(8):1365-1369.
16. Rahman M, Matthijnssens J, Yang X, et al. Evolutionary history and global spread of the emerging g12 human rotaviruses. *J Virol*. 2007;81(5):2382-2390.

17. Matthijnssens J, Bilcke J, Ciarlet M, et al. Rotavirus disease and vaccination: impact on genotype diversity. *Future Microbiol*. 2009;4(10):1303-1316.
18. Japhet MO, Adesina OA, Famurewa O, Svensson L, Nordgren J. Molecular epidemiology of rotavirus and norovirus in Ile-Ife, Nigeria: high prevalence of G12P[8] rotavirus strains and detection of a rare norovirus genotype. *J Med Virol*. 2012;84(9):1489-1496.
19. Japhet MO, Famurewa O, Iturriza-Gomara M, et al. Group A rotaviruses circulating prior to a national immunization programme in Nigeria: clinical manifestations, high G12P[8] frequency, intra-genotypic divergence of VP4 and VP7. *J Med Virol*. 2018;90(2): 239-249.
20. Wulan WN, Listiyaningsih E, Samsi KMK, Agtini MD, Kasper MR, Putnam SD. Identification of a rotavirus G12 strain, Indonesia. *Emerging Infect Dis*. 2010;16(1):159-161.
21. McDonald SM, Matthijnssens J, McAllen JK, et al. Evolutionary dynamics of human rotaviruses: balancing reassortment with preferred genome constellations. *PLoS Pathog*. 2009;5(10): e1000634.
22. Athiyyah AF, Utsumi T, Wahyuni RM, et al. Molecular epidemiology and clinical features of rotavirus infection among pediatric patients in east java, Indonesia during 2015-2018: dynamic changes in rotavirus genotypes from Equine-Like G3 to typical human G1/G3. *Front Microbiol*. 2019;10:940.
23. Fujii Y, Doan YH, Wahyuni RM, et al. Improvement of rotavirus genotyping method by using the semi-nested multiplex-PCR with new primer set. *Front Microbiol*. 2019;10:647.
24. Utsumi T, Wahyuni RM, Doan YH, et al. Equine-like G3 rotavirus strains as predominant strains among children in Indonesia in 2015-2016. *Infect Genet Evol*. 2018;61:224-228.
25. Doan YH, Haga K, Fujimoto A, et al. Genetic analysis of human rotavirus C: the appearance of Indian-Bangladeshi strain in far east asian countries. *Infect Genet Evol*. 2016;41:160-173.
26. Edgar RC. MUSCLE: multiple sequence alignment with high accuracy and high throughput. *Nucleic Acids Res*. 2004;32(5):1792-1797.
27. Kimura M. A simple method for estimating evolutionary rates of base substitutions through comparative studies of nucleotide sequences. *J Mol Evol*. 1980;16(2):111-120.
28. Doan YH, Nakagomi T, Agbemabiese CA, Nakagomi O. Changes in the distribution of lineage constellations of G2P[4] Rotavirus A strains detected in Japan over 32 years (1980-2011). *Infect Genet Evol*. 2015;34:423-433.
29. Mulyani NS, Prasetyo D, Karyana IPG, et al. Diarrhea among hospitalized children under five: a call for inclusion of rotavirus vaccine to the national immunization program in Indonesia. *Vaccine*. 2018;36(51):7826-7831.
30. Parwata WSS, Sukardi W, Wahab A, Soenarto Y. Prevalence and clinical characteristics of rotavirus diarrhea in Mataram, Lombok, Indonesia. *Paediatr Indones*. 2016;56(2):118-123.
31. Ogden KM, Tan Y, Akopov A, et al. Multiple introductions and antigenic mismatch with vaccines may contribute to increased predominance of G12P[8] Rotaviruses in the United States. *J Virol*. 2018;93(1):e01476-18.
32. Roczo-Farkas S, Kirkwood CD, Cowley D, et al. The impact of Rotavirus vaccines on genotype diversity: a comprehensive analysis of 2 decades of Australian surveillance data. *J Infect Dis*. 2018;218(4):546-554.
33. Roczo-Farkas S, Kirkwood CD, Bines JE. Australian Rotavirus surveillance program annual report, 2015. *Commun Dis Intell Q Rep*. 2016;40(4):E527-E538.
34. Zeller M, Rahman M, Heylen E, et al. Rotavirus incidence and genotype distribution before and after national rotavirus vaccine introduction in Belgium. *Vaccine*. 2010;28(47):7507-7513.
35. Sadiq A, Bostan N, Jadoon Khan P, Aziz A. Effect of rotavirus genetic diversity on vaccine impact. *Rev Med Virol*. 2022;32(1):e2259.
36. Dóró R, László B, Martella V, et al. Review of global rotavirus strain prevalence data from six years post vaccine licensure surveillance: is there evidence of strain selection from vaccine pressure? *Infect Genet Evol*. 2014;28:446-461.
37. Jain S, Vashistt J, Changotra H. Rotaviruses: is their surveillance needed? *Vaccine*. 2014;32(27):3367-3378.
38. Jenkins GM, Rambaut A, Pybus OG, Holmes EC. Rates of molecular evolution in RNA viruses: a quantitative phylogenetic analysis. *J Mol Evol*. 2002;54(2):156-165.
39. Motayo BO, Oluwasemowo OO, Olusola BA, Opayele AV, Faneye AO. Phylogeography and evolutionary analysis of African Rotavirus a genotype G12 reveals district genetic diversification within lineage III. *Heliyon*. 2019;5(10):e02680.
40. Patton JT. Rotavirus diversity and evolution in the post-vaccine world. *Discov Med*. 2012;13(68):85-97.
41. Bwogi J, Jere KC, Karamagi C, et al. Whole genome analysis of selected human and animal rotaviruses identified in Uganda from 2012 to 2014 reveals complex genome reassortment events between human, bovine, caprine and porcine strains. *PLoS One*. 2017;12(6):e0178855.
42. Markkula J, Hemming-Harlo M, Salminen MT, et al. Rotavirus epidemiology 5-6 years after universal rotavirus vaccination: persistent rotavirus activity in older children and elderly. *Infect Dis*. 2017;49(5):388-395.
43. Delogu R, Ianiro G, Camilloni B, Fiore L, Ruggeri FM. Unexpected spreading of G12P[8] rotavirus strains among young children in a small area of central Italy: unexpected spreading of G12P[8] RVA in Italy. *J Med Virol*. 2015;87(8):1292-1302.
44. Urasawa S, Urasawa T, Wakasugi F, et al. Presumptive seventh serotype of human rotavirus. *Arch Virol*. 1990;113-113(3-4):279-282.
45. Pongsuwanna Y, Guntapong R, Chiwakul M, et al. Detection of a human rotavirus with G12 and P[9] specificity in Thailand. *J Clin Microbiol*. 2002;40(4):1390-1394.
46. Trojnar E, Sachsenröder J, Twardziok S, Reetz J, Otto PH, Johne R. Identification of an avian group A rotavirus containing a novel VP4 gene with a close relationship to those of mammalian rotaviruses. *J Gen Virol*. 2013;94(Pt 1):136-142.
47. Samajdar S, Varghese V, Barman P, et al. Changing pattern of human group A rotaviruses: emergence of G12 as an important pathogen among children in eastern India. *J Clin Virol*. 2006;36(3):183-188.
48. Shinozaki K, Okada M, Nagashima S, Kaiho I, Taniguchi K. Characterization of human rotavirus strains with G12 and P[9] detected in Japan. *J Med Virol*. 2004;73(4):612-616.
49. Le VP, Kim JY, Cho SL, et al. Detection of unusual rotavirus genotypes G8P[8] and G12P[6] in South Korea. *J Med Virol*. 2008;80(1):175-182.
50. Vinh NT, Bay PVB, Tra My PV, et al. The emergence of rotavirus G12 and the prevalence of enteric viruses in hospitalized pediatric diarrheal patients in Southern Vietnam. *Am J Trop Med Hyg*. 2011;85(4):768-775.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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