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Resource Announcements



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SCOPE

Microbiology Resource Announcements (MRA) is an online-only, fully open access journal that publishes articles announcing the availability of any microbiological resource deposited in a repository available to the community. In addition to genome sequences of prokaryotic and eukaryotic microbes and viruses in public databases, as published in Genome Announcements, MRA will consider metagenomics sequences, amplicon sequence collections, metabolomics data, proteome data, culture collections, mutant libraries, plasmids and other genetic constructs, publicly available databases and software, and protocols and workflows. Manuscripts submitted to MRA will be peer reviewed for appropriate content and handled by a board of Senior Editors who will accept manuscripts at their discretion. Microbiology Resource Announcements began as Genome Announcements and was published with this title through 5 July 2018 (Volumes 1-6). The eISSN for Genome Announcements is 2169-8287.

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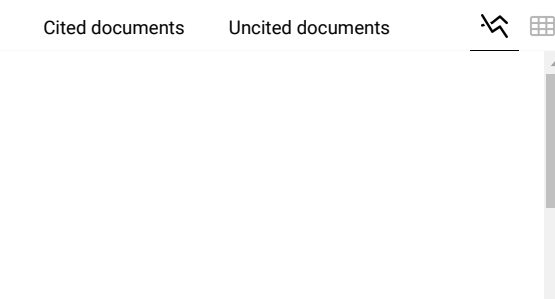
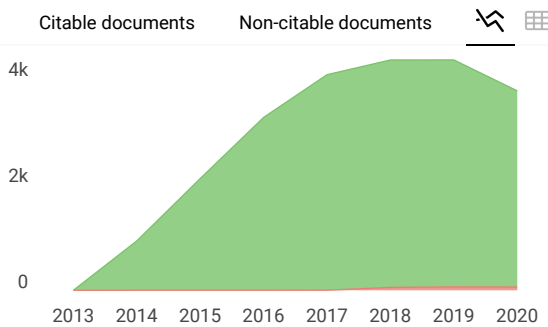
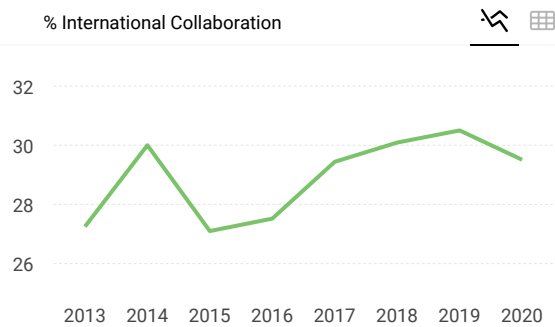
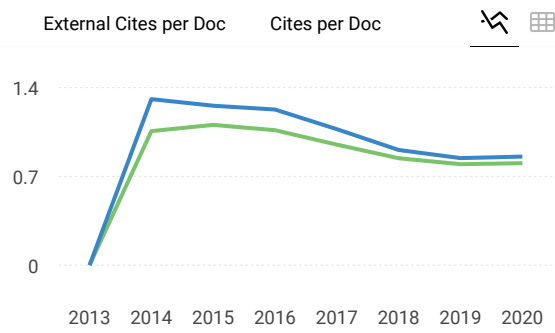
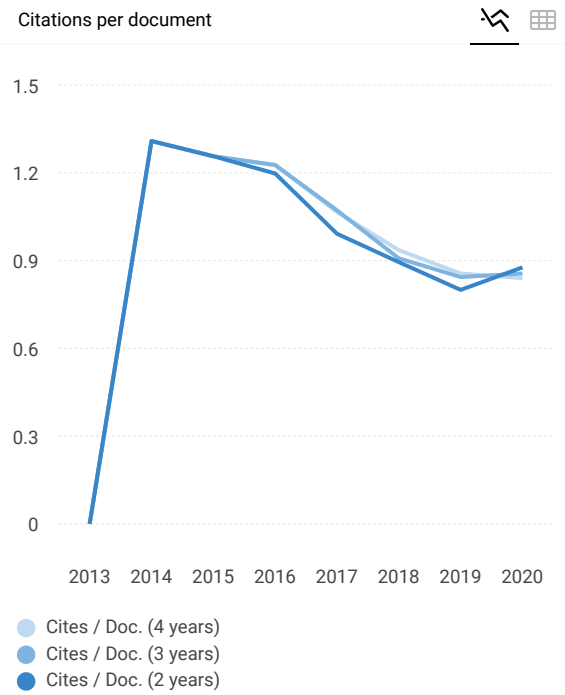
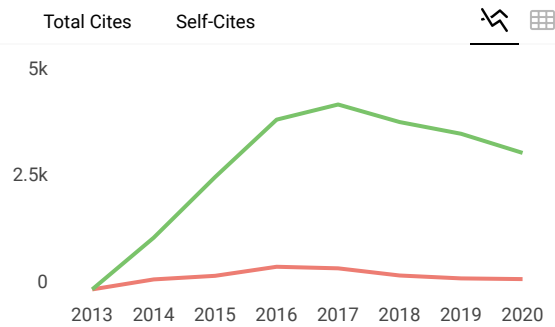
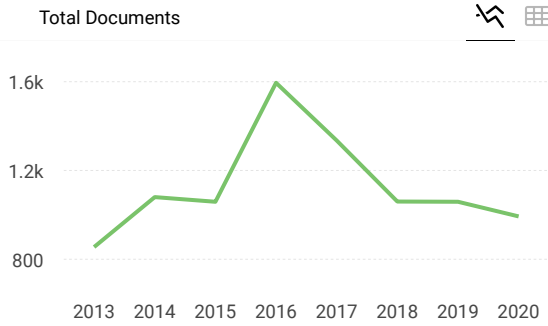
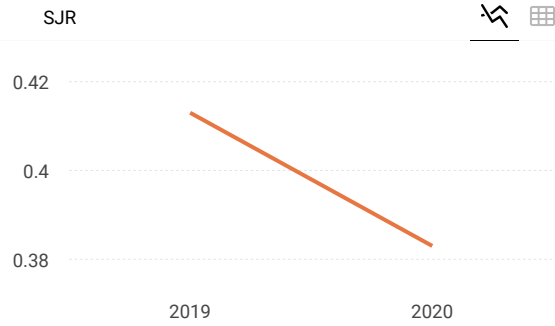
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Genome Sequences

 | Announcement | 25 April 2019

Complete Genome Sequences of *Staphylococcus argenteus* TWCC 58113, Which Bears Two Plasmids

Tohru Miyoshi-Akiyama, Takuma Ohnishi, Masayoshi Shinjoh, Hirotohi Ohara, Toshinao Kawai, ... SHOW ALL

<https://doi.org/10.1128/MRA.01582-18>

Staphylococcus argenteus TWCC 58113 was isolated from a specimen from a 12-year-old boy with purulent lymphadenitis. The *S. argenteus* TWCC 58113 genome was completely sequenced.

 | Announcement | 25 April 2019

Genome Sequence of *Staphylococcus pettenkoferi* Strain SMA0010-04 (UGA20), a Clinical Isolate from Siaya County Referral Hospital in Siaya, Kenya

Vincent Otieno, Gary Xie, Qiuying Cheng, Hajnalka Daligault, Karen Davenport, Cheryl Gleasner, ... SHOW ALL

<https://doi.org/10.1128/MRA.01626-18>

Here, we report the sequence of a *Staphylococcus pettenkoferi* clinical isolate, strain SMA0010-04 (UGA20), which contains the PC1 beta-lactamase (*bla_Z*) gene.

 | Announcement | 25 April 2019

Genome Sequences of a *Staphylococcus aureus* Clinical Isolate, Strain SMA0034-04 (UGA22), from Siaya County Referral Hospital in Siaya, Kenya

Gary Xie, Qiuying Cheng, Hajnalka Daligault, Karen Davenport, Cheryl Gleasner, Lindsey Jacobs, ... SHOW ALL

<https://doi.org/10.1128/MRA.01627-18>

Here, we report the genome sequences of a *Staphylococcus aureus* clinical isolate, strain SMA0034-04 (UGA22), which contains one chromosome and one plasmid. We also reveal that isolate SMA0034-04 (UGA22) contains loci in the genome that encode multiple ...

 | Announcement | 25 April 2019

Draft Genome Sequence of a *bla*_{NDM-1}- and *bla*_{PME-1}-Harboring *Pseudomonas aeruginosa* Clinical Isolate from Pakistan

Sidra Irum, Robert F. Potter, Rubina Kamran, Zeeshan Mustafa, Meghan A. Wallace, ... SHOW ALL

<https://doi.org/10.1128/MRA.00107-19>

We performed Illumina whole-genome sequencing on a carbapenem-resistant *Pseudomonas aeruginosa* strain isolated from a cystic fibrosis patient with chronic airway colonization. The draft genome comprises 6,770,411 bp, including the carbapenemase *bla*_{NDM-1} ...

 | Announcement | 25 April 2019

Complete Genome Sequence of the Coralopyronin A-Producing Myxobacterium *Corallococcus coralloides* B035

Sarah Bouhired, Oliver Rupp, Jochen Blom, Till F. Schäberle, Andrea Schiefer, Stefan Kehraus, ... SHOW ALL

<https://doi.org/10.1128/MRA.00050-19>

Myxobacteria are a source of unique metabolites, including coralopyronin A (CorA), a promising antibiotic agent in preclinical development for the treatment of filariasis. To investigate the production of CorA on the genetic level, we present the ...

 | Announcement | 25 April 2019

Draft Genome Sequences of 64 Type Strains of 50 Species and 25 Subspecies of the Genus *Staphylococcus* Rosenbach 1884

Kevin Cole, Dona Foster, Julie E. Russell, Tanya Golubchik, Martin Llewelyn, Daniel J. Wilson, ... SHOW ALL

<https://doi.org/10.1128/MRA.00062-19>

Members of the genus *Staphylococcus* have been isolated from humans, animals, and the environment. Accurate identification with whole-genome sequencing requires access to data derived from type strains.

 | Announcement | 25 April 2019

Whole-Genome Sequence of an Avian Influenza A/H9N2 Virus Isolated from an Apparently Healthy Chicken at a Live-Poultry Market in Indonesia

Arindita N. Novianti, Krisnodi Rahardjo, Rima R. Prasetya, Aldise M. Nastri, Jezzy R. Dewantari, ... SHOW ALL

<https://doi.org/10.1128/MRA.01671-18>

We isolated an avian influenza A/H9N2 virus from an apparently healthy chicken at a live-poultry market in January 2018. This is the first report of a whole-genome sequence of A/H9N2 virus in Indonesia.

 | Announcement | 25 April 2019

Complete Genome Sequence of Oxidase-Positive *Stenotrophomonas maltophilia* Strain SM7059

Shuo Gao, Zhifeng Zhang, Hui Zhou, Hong Zhu, Han Shen, Wanqing Zhou

<https://doi.org/10.1128/MRA.01576-18>

Stenotrophomonas maltophilia is an opportunistic pathogen which causes an increasing frequency of infections in hospitalized patients. Here, we present the complete genome sequence of *Stenotrophomonas maltophilia* SM7059, an oxidase-positive strain ...

 | Announcement | 25 April 2019

Draft Genome Sequence of the Wood-Staining Ascomycete *Chlorociboria aeruginascens* DSM 107184

Enrico Büttner, Christiane Liers, Anna Maria Gebauer, Jérôme Collemare, ... [SHOW ALL](#)

<https://doi.org/10.1128/MRA.00249-19>

Chlorociboria aeruginascens DSM 107184 is a wood-decomposing ascomycetous fungus known to produce the bluish-green dimeric naphthoquinone derivate xylindein. Here, we present the first draft genome sequence, which contains 588 contigs with a total length ...

 | Announcement | 25 April 2019

Draft Genome Sequence of a “*Candidatus* Phytoplasma asteris”-Related Strain (Aster Yellows, Subgroup 16SrI-B) from South Africa

Beatrix Coetzee, Nicoleen Douglas-Smit, Hans J. Maree, Johan T. Burger, Kerstin Krüger, Gerhard Pietersen

<https://doi.org/10.1128/MRA.00148-19>

Here, we report the draft genome sequence of a phytoplasma discovered in grapevine. The genome size is 600,116 nucleotides (nt), with 597 predicted open reading frames.

 | Announcement | 25 April 2019

Draft Genome Sequences of Four *Salmonella enterica* subsp. *enterica* Serovar Gallinarum Strains Isolated from Layer Breeder Flocks in an Outbreak of Fowl

Typhoid in Colombia

Ruy D. Chacón, Quézia Moura, Claudete S. Astolfi-Ferreira, David I. De la Torre, Laura M. C. Guerrero, ... SHOW ALL

<https://doi.org/10.1128/MRA.00122-19>

This report describes the genome sequences of four *Salmonella enterica* subsp. *enterica* serovar Gallinarum (*Salmonella* Gallinarum) strains isolated in Colombia in 2017 from layer breeders of different ages. The layer breeder flocks were presenting with an ...

 | Announcement | 25 April 2019

Complete Genome Sequences of Two Methicillin-Susceptible *Staphylococcus aureus* Clinical Strains Closely Related to Community-Associated Methicillin-Resistant *S. aureus* USA300

Jo-Ann McClure, Kunyan Zhang

<https://doi.org/10.1128/MRA.00356-19>

Predominant community-associated methicillin-resistant *Staphylococcus aureus* strain USA300 is believed to have originated from an ancestral methicillin-susceptible strain, although the details of that evolution remain unknown. To help understand the ...

 | Announcement | 25 April 2019

Draft Genome Sequence of a Medium- and Long-Chain *n*-Alkane-Degrading Bacterium, *Tsukamurella tyrosinosolvans* Strain PS2, with Two Genetic Systems for Alkane Degradation

Valeriya A. Romanova, Eugenia A. Boulygina, Maria N. Siniagina, Maria I. Markelova, ... SHOW ALL

<https://doi.org/10.1128/MRA.00218-19>

Here, we report the genome sequence of *Tsukamurella tyrosinosolvans* strain PS2, which was isolated from hydrocarbon sludge of an organic synthesis factory. This strain was able to utilize a wide range of *n*-alkanes, from C₁₆ to C₃₅, as sole carbon sources.

 | Announcement | 25 April 2019

Genome Sequence of a *Facklamia hominis* Isolate from a Patient with Urosepsis

Heba H. Mostafa, Samantha M. Taffner, Jun Wang, Adel Malek, Dwight J. Hardy, Nicole D. Pecora

<https://doi.org/10.1128/MRA.00100-19>

The genome sequence of a *Facklamia hominis* strain isolated from the urine of a patient with acute cystitis and sepsis is reported. The genome contains *ermB* and *tet(M)* genes, consistent with the isolate's phenotypic resistance

 | Announcement | 25 April 2019

Gene Determinants for Mercury Bioremediation as Revealed by Draft Genome Sequence Analysis of *Stenotrophomonas* sp. Strain MA5

Ashish Pathak, Meenakshi Agarwal, Rajesh Singh Rathore, Ashvini Chauhan

<https://doi.org/10.1128/MRA.00130-19>

A soilborne *Stenotrophomonas* sp. strain (MA5) that is resistant to mercury was isolated. A draft genome sequence-based analysis revealed a suite of gene determinants to resist mercury and other heavy metals, multidrug efflux, stress response, and membrane ...

 | Announcement | 25 April 2019

Complete Genome Sequence of *Salmonella enterica* Serovar Enteritidis Myophage Mooltan

Jacob Chamblee, Chi Zeng, Chandler J. O'Leary, Jason J. Gill, Mei Liu

<https://doi.org/10.1128/MRA.00187-19>

Salmonella enterica serovar Enteritidis is a Gram-negative bacterium and one of the most common foodborne pathogens. Biocontrol using bacteriophage in food products or animals is one possible means by which pathogenic salmonellosis infection could be ...

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Draft Genome Sequences of Two *Fusobacterium necrophorum* Strains Isolated from the Uterus of Dairy Cows with Metritis

Amye M. Francis, Soo Jin Jeon, Federico Cunha, KwangCheol Casey Jeong, Kliibs N. Galvão

<https://doi.org/10.1128/MRA.00201-19>

A commensal in the gastrointestinal tract, *Fusobacterium necrophorum* is involved in the pathogenicity of abscesses, foot rot, and metritis in cattle. Here, we present the draft genomes of two *Fusobacterium necrophorum* isolates from the uterus of dairy ...

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Draft Genome Sequence of *Anaerosphaera* sp. Strain GS7-6-2, a Coccal Bacterium Isolated from a Biogas-Related Environment

<https://doi.org/10.1128/MRA.00205-19>

Strain GS7-6-2 was isolated from a mesophilically operated biogas fermenter. The 16S rRNA gene sequence (93.27% identity to *Anaerosphaera aminiphila* WN036^T) indicated that GS7-6-2 represents a putative novel species within the genus *Anaerosphaera* (family ...

 | Announcement | 25 April 2019

Isolation, Whole-Genome Sequencing, and Annotation of *Yimella* sp. RIT 621, a Strain That Produces Antibiotic Compounds against *Escherichia coli* ATCC 25922 and *Bacillus subtilis* BGSC 168

Anutthaman Parthasarathy, Narayan H. Wong, Nicolas D. Burns, Atlantis H. Aziz-Dickerson, ... SHOW ALL

<https://doi.org/10.1128/MRA.00329-19>

Here, we report the isolation, identification, whole-genome sequencing, and annotation of the bacterium *Yimella* sp. strain RIT 621. Concentrated spent medium extract treated with ethyl acetate was found to produce bactericidal compounds against the Gram-...

 | Announcement | 25 April 2019

Complete Genome Sequence of *Klebsiella pneumoniae* Myophage Menlow

Heather N. Newkirk, Lauren Lessor, Jason J. Gill, Mei Liu

<https://doi.org/10.1128/MRA.00192-19>

Klebsiella pneumoniae is an opportunistic pathogen that has become an increasing problem in nosocomial infections. Studying phages that infect *K. pneumoniae* may lead to improvements in phage therapeutics for treating these infections.

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Whole-Genome Sequence of a Serotype 1/2b *Listeria monocytogenes* Strain Isolated from Raw Seafood in Japan

Chihiro Ohshima, Satomi Kanagawa, Satoko Miya, Ayaka Nakamura, Hajime Takahashi, Takashi Kuda, Bon Kimura

<https://doi.org/10.1128/MRA.00206-19>

Listeria monocytogenes is a pathogen typically acquired through the ingestion of foods. It has been specifically reported that the pathogen is widely distributed in raw seafood in Japan.

 | Announcement | 25 April 2019

Two Divergent Isolates of Turnip Yellows Virus from Pea and Rapeseed and First Report of Turnip Yellows Virus-Associated RNA in Germany

Yahya Z. A. Gaafar, Heiko Ziebell

<https://doi.org/10.1128/MRA.00214-19>

Two divergent isolates of turnip yellows virus (TuYV) were identified in pea and rapeseed. The nearly complete genome sequences of the virus isolates share 93.3% nucleotide identity with each other and 89.7% and 92.9% with their closest isolate from South ...

 | Announcement | 25 April 2019

Complete Genome Sequence of *Klebsiella pneumoniae* Myophage Mineola

Justin X. Boeckman, Lauren Lessor, Jason J. Gill, Mei Liu

<https://doi.org/10.1128/MRA.00257-19>

Klebsiella pneumoniae is an important human pathogen due to the wide range of infections it can cause and its emerging drug resistance. Isolation and characterization of phage infecting *K. pneumoniae* could be important for future therapeutic applications.

 | Announcement | 25 April 2019

Complete Genome Sequence of *Spiroplasma alleghenense* PLHS-1^T (ATCC 51752), a Bacterium Isolated from Scorpion Fly (*Panorpa helena*)

Lin Chou (林周), Ting-Yi Lee (庭儀李), Yi-Ming Tsai (乙鳴蔡), Chih-Horng Kuo (志鴻郭)

<https://doi.org/10.1128/MRA.00317-19>

Spiroplasma alleghenense PLHS-1^T (ATCC 51752) was isolated from the gut of a scorpion fly (*Panorpa helena*) collected in West Virginia. The complete genome sequence of this bacterium, which consists of a single 1,336,077-bp circular chromosome, is reported ...

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Whole-Genome Sequence of an Isogenic Haploid Strain, *Saccharomyces cerevisiae* IR-2^{idA30}(*MATa*), Established from the Industrial Diploid Strain IR-2

Kazuhiro E. Fujimori, Yosuke Kobayashi, Taisuke Seike, Takehiko Sahara, Satoru Ohgiya, Yoichi Kamagata

<https://doi.org/10.1128/MRA.00018-19>

We present the draft genome sequence of an isogenic haploid strain, IR-2^{idA30}(*MATa*), established from *Saccharomyces cerevisiae* IR-2. Assembly of long reads and previously obtained contigs from the genome of diploid IR-2 resulted in 50 contigs, and the ...

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Draft Genome Sequence of Thermophilic Halotolerant *Aeribacillus pallidus* TD1, Isolated from Tao Dam Hot Spring, Thailand

Wariya Yamprayoonswat, Satapanawat Sittihan, Watthanachai Jumpathong, Montri Yasawong

<https://doi.org/10.1128/MRA.00204-19>

Aeribacillus pallidus TD1 is a thermophilic bacterium isolated from a hot spring in Thailand. The genome sequence of *A. pallidus* TD1 contains a gene-encoded naphthalene dioxygenase, which is a key enzyme for naphthalene degradation.

 | Announcement | 25 April 2019

Draft Genome Sequence of *Pediococcus pentosaceus* MZF16, a Bacteriocinogenic Probiotic Strain Isolated from Dried Ossban in Tunisia

Mohamed Zommiti, Amine M. Boukerb, Marc G. J. Feuilloley, Mounir Ferchichi, Nathalie Connil

<https://doi.org/10.1128/MRA.00285-19>

Pediococcus pentosaceus strain MZF16 was isolated from dried ossban, a Tunisian dry fermented meat. The MZF16 chromosome consisted of 28 contigs with a total draft genome size of 1,928,373 bp and a G+C content of 37.2%.

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Complete Genome Sequence of *Salmonella enterica* Serovar Heidelberg Myophage Meda

John K. Neff, Yicheng Xie, Jason J. Gill, Mei Liu

<https://doi.org/10.1128/MRA.00253-19>

Salmonella enterica serovar Heidelberg is a multidrug-resistant foodborne pathogen that originated from poultry and cattle. Bacteriophages isolated for this pathogen may be used as biocontrol agents in food products or animals for preventing *Salmonella* ...

 | Announcement | 25 April 2019

Complete Genome Sequence of *Salmonella enterica* Serovar Newport Myophage Melville

Kailun Zhang, Yicheng Xie, Chandler J. O'Leary, Mei Liu, Jason J. Gill

<https://doi.org/10.1128/MRA.00255-19>

Multiple antimicrobial-resistant strains of *Salmonella enterica* serovar Newport have been recorded. Study on phages infecting *S. Newport* may provide new therapeutics or diagnostics for this pathogen.

Omics Data Sets

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Flood Season Microbiota from the Amazon Basin Lakes: Analysis with Metagenome Sequencing

[Célio Dias Santos Júnior](#), [Danyelle Toyama](#), [Tereza Cristina Souza de Oliveira](#), ... [SHOW ALL](#)

<https://doi.org/10.1128/MRA.00229-19>

Despite an apparent geographic separation of the Amazon water bodies, they are an interconnected system. During floods, the microbiota of rivers, lakes, and soil combines.

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Whole-Genome Sequence of an Avian Influenza A/H9N2 Virus Isolated from an Apparently Healthy Chicken at a Live-Poultry Market in Indonesia

Arindita N. Novianti,^a Krisnodi Rahardjo,^b Rima R. Prasetya,^b Aldise M. Nastri,^b Jezzy R. Dewantari,^b Adi P. Rahardjo,^a Agnes T. S. Estoepangestie,^a Yohko K. Shimizu,^{b,c} Emmanuel D. Poetranto,^{a,b} Gatot Soegiarto,^b Yasuko Mori,^c Kazufumi Shimizu^{b,c}

^aFaculty of Veterinary Medicine, Airlangga University, Surabaya, Indonesia

^bIndonesia-Japan Collaborative Research Center, Institute of Tropical Disease, Airlangga University, Surabaya, Indonesia

^cCenter for Infectious Diseases, Kobe University Graduate School of Medicine, Kobe, Japan

ABSTRACT We isolated an avian influenza A/H9N2 virus from an apparently healthy chicken at a live-poultry market in January 2018. This is the first report of a whole-genome sequence of A/H9N2 virus in Indonesia. Phylogenetic analyses indicated that intrasubtype reassortment of genome segments is involved in the genesis of the A/H9N2 virus.

Avian influenza A/H9N2 virus was found in domestic poultry and wild birds worldwide and became one of the dominant subtypes of avian influenza virus (1, 2). The virus was isolated also from swine (3). Several cases of human infections were also reported (4, 5). A/H9N2 virus causes respiratory infection and replicates in the reproductive tract in chickens, resulting in decreased egg production (6). In addition, A/H9N2 virus provides some parts of internal genes to a new lethal reassortant in humans (7–9), such as H7H9 virus.

In Indonesia, there were A/H9N2 virus outbreaks in chickens causing decreased egg production from December 2016 to May 2017 (10). In January 2018, we isolated an avian A/H9N2 virus, A/chicken/East Java/Spg147/2018, from an apparently healthy chicken at a live-poultry market. The virus was grown in 10-day-old embryonated chicken eggs for 2 days at 37°C, and the allantoic fluid served as the virus stock. For genome analysis by next-generation sequencing, total RNA was extracted from the virus stock using a QIAamp viral minikit (Qiagen, Tokyo, Japan); linear polyacrylamide was used as a carrier instead of tRNA. An RNA library was prepared using a TruSeq RNA sample preparation kit v2 (Illumina, Japan). The library was loaded in the flow cell of the 300-cycle MiSeq reagent kit v2 (Illumina, USA). The barcoded multiplexed library sequencing (2 × 150 bp) was performed on a MiSeq platform (Illumina). The MiSeq platform generated FASTQ files in which the primer and adapter sequences were trimmed. The files were imported in CLC Genomics Workbench v8.1 (CLC bio, Japan) for analysis; the total number of reads was 929,006, the average read length was 141.5 bp, and the average of the Phred quality scores was Q34.1, 84.4% of which were over Q30 (99.9% accuracy of base calling at a particular sequence position). The total reads were filtered to remove reads with poor quality (those with <Q30, <26 bp long, or containing more than two consecutive ambiguous bases). After filtering, 630,095 reads remained. The filtered reads were mapped to the genomes of 27 reference viruses of influenza type A virus, including all subtypes of hemagglutinin (HA) (H1 to H18) and neuraminidase (NA) (N1 to N11), using the CLC Genomics Workbench. A total of 24,506 reads were mapped to the reference sequences, 78.7% of which were aligned on the genome (or 8 genome segments) of one of the reference viruses, A/chicken/Guangxi/

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Address correspondence to Kazufumi Shimizu, shimizu.kazufumi@gmail.com.

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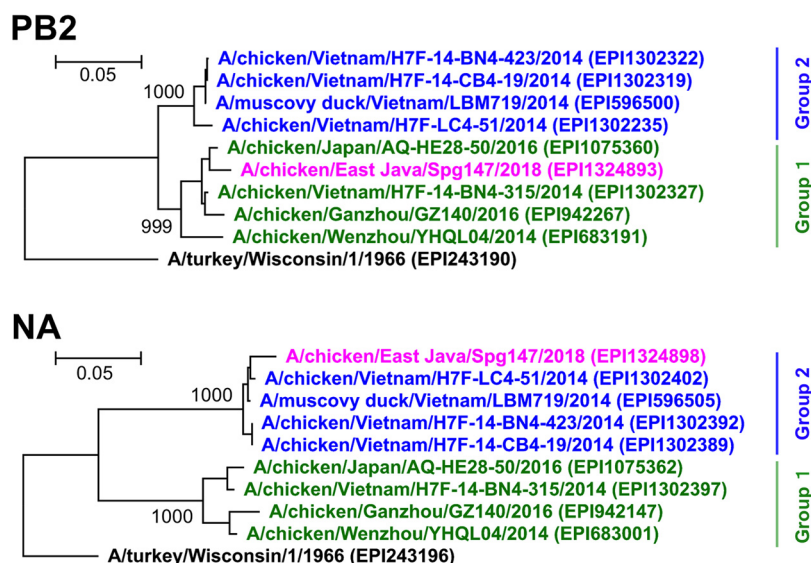


FIG 1 Phylogenetic analysis of PB2 and NA genome segments of A/H9N2 viruses. The phylogenetic trees were generated using coding sequences of PB2 and NA segments in the genetic information processing software Genetyx v14 (Genetyx Co., Tokyo, Japan), using the neighbor-joining method with 1,000 bootstrap replicates and the Kimura 2-parameter model. The tree was rooted from the A/turkey/Wisconsin/1/1966 virus. The viruses included were selected because either the PB2 or NA sequence was highly identical to that of our H9N2 isolate, A/chicken/East Java/Spg147/2018 (pink) by BLAST analysis in the GISAID EpiFlu database; the accession numbers are in parentheses following the virus names. The eight selected viruses formed two distinct groups in both the PB2 and NA phylogenies, which were named group 1 (green) and group 2 (blue), and the members in each group were same between the two phylogenies. PB2 of our isolate belonged to group 1, while NA belonged to group 2, indicating that intrasubtype reassortment of genome segments is involved in the genesis of the A/H9N2 virus.

LS/2013 (H9N2). Tentative complete 8-segment genome sequences were constructed from the assembled consensus and common sequences of type A influenza viruses at the 5' end (12 nucleotides [nt]) and 3' end (13 nt) of the genome segments. The filtered reads were mapped again to the tentative complete genome sequence, and 24,146 reads were aligned to the 8 segments. The Q scores of the mapped reads ranged from 34 to 39, with an average of 37.7. The assembled consensus sequences covered 99.8% of the tentative complete genome (13,605 nt), and the mean depth of coverage was 211. The genome comprised eight segments, polymerase basic 2 (PB2) (2,341 nt), polymerase basic 1 (PB1) (2,341 nt), polymerase acidic (PA) (2,233 nt), HA (1,742 nt), nucleoprotein (NP) (1,565 nt), NA (1,466 nt), matrix protein (M) (1,027 nt), and non-structural protein (NS) (890 nt). The consensus sequences lacked 0 to 6 nt at the 5' and 3' ends of the 8 segments within the common end sequences.

The amino acid sequence at the HA cleavage site is PSRSSR ↓ GLF, which is characteristic of low-pathogenic avian influenza viruses (11). The PB2 protein had an E at position 627 and a D at position 701, which is characteristic of viruses of avian origin. However, the receptor binding site of HA had L222 and G224 (H5 numbering), which suggests that it has the ability to bind with a sialic acid-2,6-NeuAcGal linkage and might have the potential to infect humans (12).

BLAST and phylogenetic analyses revealed that the PB2 and NA segments of this virus were derived from different groups of H9N2 virus (Fig. 1), indicating that intra-subtype reassortment of genome segments is involved in the genesis of the A/H9N2 virus.

Data availability. The genome sequence of A/chicken/East Java/Spg147/2018 (H9N2) has been deposited in the Global Initiative on Sharing All Influenza Data (GISAID) EpiFlu database (13) under the accession numbers EPI1324893 to EPI1324900. The raw reads of the FASTQ format will be provided by the corresponding author as requested.

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