Reported outcomes of ehrlichiosis in solid organ transplant recipients have generally been favorable; for example, 1 case of *E. chaffeensis* infection resolved despite multiorgan involvement (*9*). In a study of 75,077 US blood samples (2007–2013), EME was identified in 69 patients (0.1%), mostly in Minnesota and Wisconsin; 49 were immunocompromised, of which 13 (27%) were on immunosuppressive therapy, including 7 transplant recipients (*10*). All recovered, most after doxycycline treatment.

Clinicians should maintain a high index of suspicion for ehrlichiosis in febrile transplant recipients who have headache, altered mental status, thrombocytopenia, or transaminitis, particularly in those with tick exposure or residence in endemic areas. In this case, transaminitis and severe hyperbilirubinemia with liver allograft dysfunction complicated the diagnosis, underscoring the importance of timely tickborne disease testing. Early recognition and treatment are critical to preventing fatal outcomes.

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Molecular Analysis of Emerging MT27 Macrolide-Resistant *Bordetella pertussis*, Kobe, Japan, 2025

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We report the emergence and spread of multilocus variable-number tandem-repeat analysis type 27 (MT-27) macrolide-resistant *Bordetella pertussis* (MRBP) in Kobe, Japan, in 2025. Whole-genome sequencing revealed that MT27-MRBP did not originate from the widely circulating MT27 macrolide-sensitive *B. pertussis* in Japan but was closely related to MRBP in China.

Table. Clinical features and microbiological profiles of 15 MT27-*Bordetella pertussis* isolates in Kobe, Japan, January 2013–March 2025*

Strain ID	Collection date	Patients		Macrolide susceptibility	Genotyping of virulence-related genes				
		Age/sex	Vaccination (no. doses)		*ptxP*	*ptxA*	*fhaB*	*fim3*	*prn*
KBP0005	2013 Mar 25	1 y/M	DPT (3)	Susceptible	3	1	1	1	2
KBP0006	2015 Apr 21	4 mo/F	NA	Susceptible	3	1	1	1	2
KBP0007	2016 Feb 25	8 mo/M	Unvaccinated	Susceptible	3	1	1	1	2
KBP0009	2019 Sep 24	1 mo/F	Unvaccinated	Susceptible	3	1	1	1	2
KBP0010	2024 Jun 24	1 mo/F	Unvaccinated	Susceptible	3	1	1	1	2
KBP0011	2024 Jun 24	35 y/M	DPT (4)	Susceptible	3	1	1	1	2
KBP0014	2025 Jan 25	8 y/F	DPT-IPV (4)	Susceptible	3	1	1	1	2
KBP0016	2025 Feb 3	10 y/F	DPT-IPV (4)	Resistant	3	1	1	1	150
KBP0017	2025 Feb 12	2 mo/M	DPT-IPV (1)	Resistant	3	1	1	1	150
KBP0018	2025 Feb 13	12 y/M	DPT-IPV (4)	Susceptible	3	1	1	1	2
KBP0019	2025 Feb 18	9 y/F	DPT-IPV (4)	Susceptible	3	1	1	1	2
KBP0020	2025 Feb 20	10 y/F	DPT-IPV (4)	Resistant	3	1	1	1	150
KBP0025	2025 Mar 7	12 y/F	DPT-IPV (4)	Susceptible	3	1	1	1	2
KBP0026	2025 Mar 7	12 y/F	NA	Resistant	3	1	1	1	150
KBP0028	2025 Mar 12	12 y/F	NA	Resistant	3	1	1	1	150

*DPT, diphtheria-pertussis-tetanus; IPV, inactivated polio vaccine; MT, multilocus variable-number tandem-repeat analysis type; NA, not available.

Bordetella pertussis, a gram-negative, pathogenic bacterium of the genus *Bordetella*, is the causative agent of contagious respiratory illness and whooping cough (pertussis). Diphtheria-pertussis-tetanus (DPT) combination vaccines have substantially reduced pertussis-related illness and deaths, especially among infants (*1*). Macrolides represent mostly natural polyketide-class products containing a large macrocyclic lactone ring with potential attachment groups (e.g., deoxy sugars), with antibiotic or antifungal activities. Macrolides are popular pharmaceutical drugs, frequently used for pertussis treatment and prevention. Macrolide-resistant *B. pertussis* (MRBP), characterized by the A2047G mutation in a region critical for macrolide binding to the 23S rRNA gene, has recently emerged and spread worldwide (*2*). In China, the predominant MRBP genetic lineage has shifted in the pertussis toxin promoter region (*ptxP*) allele type from *ptxP1* to *ptxP3*, and the prevalence of the *ptxP3*-carrying multilocus variable-number tandem-repeat analysis type (MT) 28 MRBP strain has increased rapidly (*3*).

In Japan, pertussis notifications, which decreased during the COVID-19 pandemic, have significantly increased since 2024 (*4*). MRBP was first documented in 2018 during the first isolation of *ptxP1*-MT195-MRBP (*5*). More recently, *ptxP3*-MRBP strains isolated from Tokyo and Okinawa have been described, demonstrating close genetic relation to the China strains (*6*,*7*).

MT27 is a single-locus MT28 variant, and this genotype, carrying the virulence-associated alleles *ptxP3*/*ptxA1*/*prn2*/*fim3-1*, became predominant among macrolide-susceptible *B. pertussis* (MSBP) strains in various countries, including Japan (*8*–*10*). In contrast, to date, just 1 MT27-MRBP strain has been reported in China in 2017 (*8*); no cases have been identified outside of China. In this study, we report 5 MT27-MRBP strains isolated during February–March 2025 from children with pertussis in 1 hospital and 2 private clinics in Kobe, Japan (Table). To investigate the molecular epidemiologic characteristics of these 5 MT27-MRBP isolates, we compared them to Japan MT27-MSBP strains isolated during 2010–2025, including 10 isolates from Kobe, and MRBP strains from China (*3*,*6*–*8*,*10*). This study was approved by the Kobe City Review Board (approval no. SenR3-10).

We collected 9 MT27 strains from patients 2 months through 12 years of age during January–March 2025 (Table). All 5 MT27-MRBP strains harbored the A2047G mutation in the 23S rRNA and exhibited MICs of >256 μg/mL for erythromycin, clarithromycin, and azithromycin. All MT27-MRBP–infected patients recovered without any sequelae. We used the BIGSdb-Pasteur platform (https://bigsdb.pasteur.fr/bordetella) to identify the MT27-MRBP virulence genotype, which yielded identical results for all strains: *ptxP3*/*ptxA1*/*fhaB1*/*fim3–1*/*prn150*. Among the 5 virulence-related genes, we observed a difference in the *prn* allele between the MT27-MSBP and MT27-MRBP strains isolated in Kobe (i.e., *prn2* in MSBP and *prn150* in MRBP) (Table). Of note, *prn150* was identical to the allele in the globally prevalent MT28-MRBP strains (*3*).

To determine genetic relatedness, we performed phylogenetic analyses using whole-genome sequences of 6 MT27-MSBP isolates obtained in Kobe since 2013 (Table) and other publicly available genomes (Appendix Table, https://wwwnc.cdc.gov/EID/article/32/1/25-0890-App1.xlsx). Our single-nucleotide variant–based phylogenetic analysis revealed that the 5 MT27-MRBP strains clustered within the *prn150* lineage, which is genetically closely related to the MRBP strain from

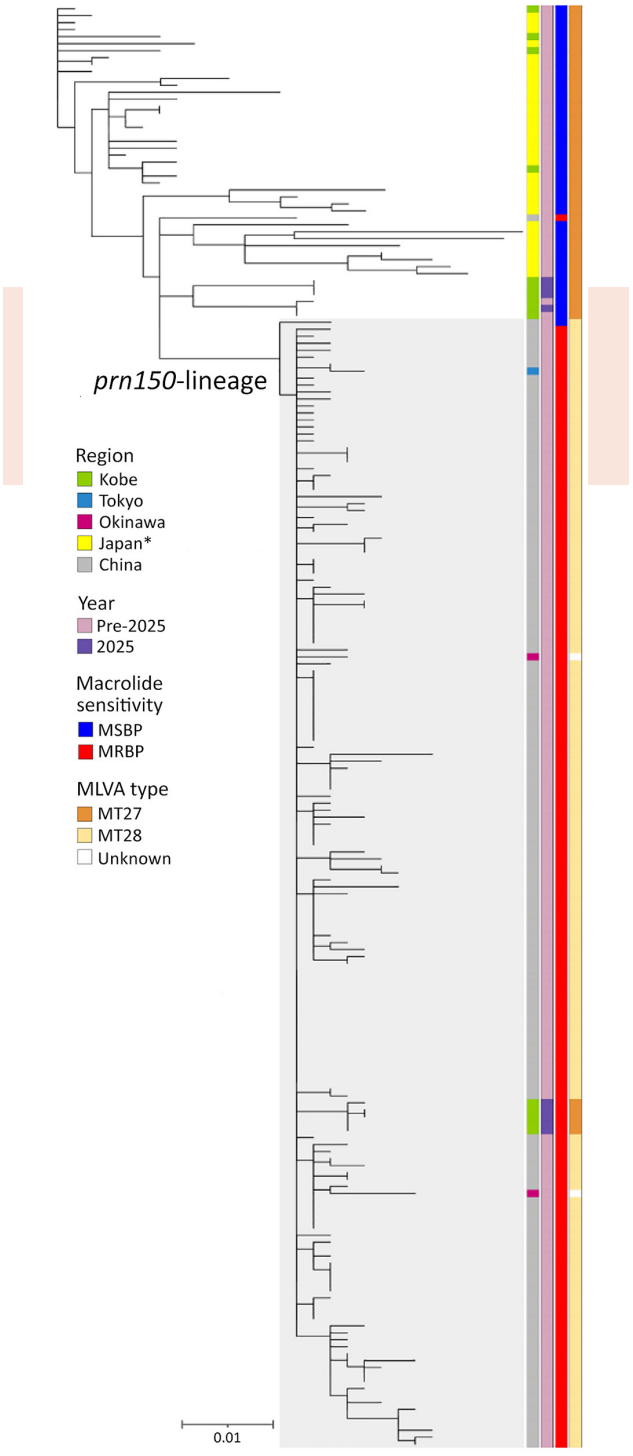

Figure. Phylogenetic tree based on single-nucleotide variants, showing 15 MT27 *Bordetella pertussis* strains isolated in Kobe (green); 37 strains from Japan (yellow), including Tokyo (blue) and Okinawa (magenta); and 155 strains from China (gray) in study of emerging MT27 MRBP, Kobe, Japan, 2025. Scale bar indicates number of substitutions per site. *Excluding regions previously listed. MRBP, macrolide-resistant *B. pertussis*; MSBP, macrolide-sensitive *B. pertussis*; MLVA, multilocus variable-number tandem-repeat analysis; MT, MLVA type.

China and that clonal population (Figure). Furthermore, MT27-MRBP strains in Kobe were genetically distinct from the China MT27-MRBP (GenBank accession no. SRR16306222), as well as from the Japan MRBP strains, BP636 (GenBank accession no. DRR631445) in Tokyo and OkiPb01308 and OkiPb01309 (National Center for Biotechnology Information BioProject accession no. PRJDB20292) in Okinawa (Figure). The identification of genetically divergent strains across 3 geographically separated regions of Japan suggests multiple, epidemiologically independent introductions. In contrast, MT27-MSBP strains KBP0014, KBP0018, KBP0019, and KBP0025, isolated in 2025, belonged to a clade of currently prevalent strains in Japan. Taken together, our results suggest that MT27-MRBP does not originate from the currently circulating MT27-MSBP in Japan but could have been potentially introduced from China. Finally, 5 MT27-MRBP–infected patients resided in 3 different wards with no apparent temporal links, suggesting that this newly emergent strain might be spreading latently in Kobe.

In conclusion, we identified distinct genetic differences between the MT27-MSBP and MT27-MRBP strains collected during January–March 2025 in Kobe. Our study suggests that MT27-MRBP strains closely related to the China MRBP strains have emerged and spread in Kobe, Japan.

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Raw sequencing data for the isolates from Kobe have been deposited in DDBJ/EMBL/GenBank (DRA accession numbers DRR698592–606). GenBank accession numbers for all genome sequences used for phylogenetic analysis are listed in the Appendix Table.

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Donor Screening Failure for *Strongyloides stercoralis* in Solid Organ Transplantation

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We report 2 cases of donor-derived *Strongyloides stercoralis* infection in renal transplant recipients. Despite initial negative serologic testing in donor samples, retrospective testing confirmed transmission. This report underscores the limitations of serologic screening, the need for targeted protocols in endemic-risk populations, and the importance of close posttransplant surveillance.

Strongyloides stercoralis can persist for decades in humans (*1*). In immunocompromised patients, such as transplant recipients, *S. stercoralis* can cause disseminated infection or hyperinfection syndrome (*2*). Mortality exceeds 60% in immunosuppressed persons (*3*), reaching 87% if treatment is not initiated (*4*). We report 2 cases of strongyloidiasis in renal transplant recipients who shared the same donor.

The donor was a 72-year-old man who was born in Ghana and resided in Tenerife, Canary Islands, Spain, for 20 years. He died from subarachnoid hemorrhage after a traumatic brain injury. He had no known immunosuppressive condition, and his eosinophil count was unremarkable. Following National Transplant Organization guidelines on the selection criteria of donors in relation to infectious diseases (*5*), routine donor serologic screening was conducted. Testing for HIV, human T-lymphotropic virus 1 and 2, hepatitis C and B virus, syphilis, cytomegalovirus, Epstein-Barr virus, herpes simplex virus 1 and 2, and toxoplasmosis revealed no noteworthy findings except positive results for cytomegalovirus IgG and hepatitis B core antibody (hepatitis B surface antigen was negative). Because of the donor's geographic origin, Mantoux testing and testing for antibodies against *Coccidioides immitis*, *Histoplasma capsulatum*, *Plasmodium* spp., and *S. stercoralis* were conducted; all results were negative. The additional testing was conducted at an external reference laboratory (Reference Labo-