

21. Antimicrobial Resistance Research Center

- 1) Sekizuka T, Kawanishi M, Ohnishi M, Shima A, Kato K, Yamashita A, Matsui M, Suzuki S, Kuroda M. Elucidation of quantitative structural diversity of remarkable rearrangement regions, shufflons, in IncI2 plasmids. *Sci Rep.* 2017, 7(1):928
- 2) Kenri T, Suzuki M, Horino A, Sekizuka T, Kuroda M, Fujii H, Hashimoto T, Nakajima H, Ohya H, Shibayama K. Complete genome sequences of p1 gene type 2b and 2c *Mycoplasma pneumoniae* strains KCH-402 and KCH-405. 2017 *Genome Announc.* 5(24):e00513-17
- 3) Kato K, Hashino M, Ito T, Matsui M, Suzuki S, Kai K, Kitazume M, Sekizuka T, Kuroda M. Rapid and affordable size-selected PacBio single-molecule real-time sequencing template library construction using the bead-bearing DNA extraction method. *J Biol Methods* 2017, 4(3):e79
- 4) Hiki M, Shimizu Y, Kawanishi M, Ozawa M, Abo H, Kojima A, Koike R, Suzuki S, Asai T, Hamamoto S. Evaluation of the relationship between the minimum inhibitory concentration of ceftiofur and third-generation cephalosporins in *Escherichia coli* isolates from food-producing animals. *J Vet Diagn Invest.* 2017 Sep;29(5):716-720
- 5) Pascoe B, Méric G, Yahara K, Wimalarathna H, Murray S, Hitchings MD, Sproston EL, Carrillo CD, Taboada EN, Cooper KK, Huynh S, Cody AJ, Jolley KA, Maiden MCJ, McCarthy ND, Didelot X, Parker CT, Sheppard SK. Local genes for local bacteria: Evidence of allopatry in the genomes of transatlantic *Campylobacter* populations. *Mol Ecol.* 2017 Sep;26(17):4497-4508
- 6) Yu L, Hisatsune J, Hirakawa H, Mizumachi E, Toyoda A, Yahara K, Sugai M. Complete Genome Sequence of Super Biofilm-Elaborating *Staphylococcus aureus* Isolated in Japan. *Genome Announc.* 2017 Oct 12;5(41)
- 7) Miyamoto N*, Yahara K*, Horita R, Yano T, Tashiro N, Morii D, Tsutsui A, Yaita K, Shibayama K, Watanabe H. Integration of DPC and clinical microbiological data in Japan reveals importance of confirming a negative follow-up blood culture in patients with MRSA bacteremia. *J Infect Chemother.* 2017 Oct;23(10):687-691
- 8) Katayama Y, Azechi T, Miyazaki M, Takata T, Sekine M, Matsui H, Hanaki H, Yahara K, Sasano H, Asakura K, Takaku T, Ochiai T, Komatsu N, Chambers HF. Prevalence of Slow-Growth Vancomycin Nonsusceptibility in Methicillin-Resistant *Staphylococcus aureus*. *Antimicrob Agents Chemother.* 2017 Oct 24;61(11)
- 9) Matono T, Morita M, Yahara K, Lee KI, Izumiya H, Kaku M, Ohnishi M. Emergence of Resistance Mutations in *Salmonella enterica* Serovar Typhi Against Fluoroquinolones. *Open Forum Infect Dis.* 2017 Nov 2;4(4)
- 10) Yoshida M, Izumiyama S, Fukano H, Sugiyama K, Suzuki M, Shibayama K, Hoshino Y. Draft genome sequence of *Mycobacterium* sp. shizuoka-1, a novel mycobacterium isolated from ground water of a bathing facility in Shizuoka, Japan. *Genome Announc.* 2017 5(47): e01309-17
- 11) Rimbara E, Mori S, Hyun K, Suzuki M, Shibayama K. Mutations in PBP-encoding genes and efflux pumps play a role in β -lactam resistance of *Helicobacter cinaedi*. *Antimicrob Agents Chemother.* 2018 62(2): e02036-17
- 12) Matsui M, Suzuki M, Suzuki M, Yatsuyanagi J, Watahiki M, Hiraki Y, Kawano F, Tsutsui A, Shibayama K, Suzuki S. Distribution and molecular characterization of *Acinetobacter baumannii* international clone II lineage in Japan. *Antimicrob Agents Chemother.* 2018, 62(2):e2190-17

- 13) Yoshida M, Fukano H, Miyamoto Y, Shibayama K, Suzuki M, Hoshino Y. Complete genome sequence of a type strain of *Mycobacterium abscessus* subsp. *bolletii*, a member of the *Mycobacterium abscessus* complex. Genome Announc. 2018 6(5): e01530-17
- 14) Aoki K, Harada S, Yahara K, Ishii Y, Motooka D, Nakamura S, Akeda Y, Iida T, Tomono K, Iwata S, Moriya K, Tateda K. Molecular Characterization of IMP-1-Producing Enterobacter cloacae Complex Isolates in Tokyo. Antimicrob Agents Chemother. 2018 Feb;23(3)
- 15) Morimoto S, Yahara K. Identification of stress responsive genes by studying specific relationships between mRNA and protein abundance. Heliyon. 2018 Mar 8;4(3):e00558
- 16) Asakura K, Azechi T, Sasano H, Matsui H, Hanaki H, Miyazaki M, Takata T, Sekine M, Takaku T, Ochiai T, Komatsu N, Shibayama K, Katayama Y, Yahara K. Rapid and easy detection of low-level resistance to vancomycin in methicillin-resistant Staphylococcus aureus by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. PLoS One. 2018 Mar 9;13(3):e0194212
- 17) Yaita K, Yahara K, Hamada N, Sakai Y, Iwahashi J, Masunaga K, Watanabe H. Typhoid Vaccination among Japanese Travelers to South Asia and the Factors Associated with Compliance. Intern Med. 2018 Apr 15;57(8):1071-1074
- 18) Yoshida M, Fukano H, Miyamoto Y, Shibayama K, Suzuki M, Hoshino Y. Complete genome sequence of *Mycobacterium marinum* ATCC 927^T using Nanopore and Illumina sequencing data. Genome Announc. 2018 6(20): e00397-18
- 19) Shigemura H, Matsui M, Sekizuka T, Onozuka D, Noda T, Yamashita A, Kuroda M, Suzuki S, Kimura H, Fijimoto S, Oishi K, Sera N, Inoshita Y, Murakami K. Decrease in the prevalence of extended-spectrum cephalosporin-resistant *Salmonella* following cessation of ceftiofur use by the Japanese poultry industry. Int J Food Microbiol. 2018, 274:45-51
- 20) Tsutsui A, Yahara K, Shibayama K. Trends and patterns of national antimicrobial consumption in Japan from 2004 to 2016. J Infect Chemother. 2018 Jun;24(6):414-421