Etymologia: Buruli Ulcer

Tony M. Korman, Paul D.R. Johnson, John Hayman

Author affiliations: Monash University, Melbourne, Victoria, Australia (T.M. Korman); Austin Health, Melbourne (P.D.R. Johnson); University of Melbourne, Melbourne (P.D.R. Johnson, J. Hayman)

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To the Editor: The recent etymologia by Henry in the March 2020 issue of Emerging Infectious Diseases recounts the fascinating origin of the name Buruli ulcer (*1*). Further to the history, in 1948, pathologist Peter MacCallum first described the clinical features for 6 patients from Victoria, Australia, each with an ulcer with undermined edges on an arm or a leg, and the characteristic histopathologic findings, including extensive necrosis and abundant acid-fast bacilli without granuloma formation (*2*). Five of the patients were identified by general practitioners D.G. Alsop, L.E. Clay, and J.R. Searls from the city of Bairnsdale (thus, another eponym "Bairnsdale ulcer") (*3*). Glen Buckle and Jean Tolhurst at the Alfred Hospital in Melbourne established experimental animal infections, and eventually isolated the causative organism (*2*), which they later named *Mycobacterium ulcerans* (*4*). The growth of *M. ulcerans* required prolonged incubation at a temperature of 30°C–33°C (*2*), which was only realized after the inadvertent use of a faulty incubator.

In 1964, Clancey described a "new" mycobacterium causing chronic skin ulcers in Uganda that "resembled" *M. ulcerans* which he named "*Mycobacterium buruli*" (*5*). However, the causative organism of Buruli ulcer was subsequently recognized as *Mycobacterium ulcerans,* which had been originally described in Australia.

About the Author

Dr. Korman is an adjunct clinical professor at Monash University; Director, Monash Infectious Diseases; and Director of Microbiology, Monash Health, Clayton, Australia. He has a wide range of clinical, laboratory, and research interests.

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Address for correspondence: Tony M. Korman, Monash Infectious Diseases, Monash Health Centre, 246 Clayton Rd, Clayton, VIC 3168, Australia; email: tony.korman@monash.edu

Arthritis Caused by MRSA CC398 in Patient without Animal Contact, Japan

Anders R. Larsen, Jesper Larsen

Author affiliation: Statens Serum Institut, Copenhagen, Denmark

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To the Editor: In their recent article, Nakaminami et al. describe a case of human infection caused by Panton-Valentine leucocidin (PVL)–positive livestock-associated methicillin-resistant *Staphylococcus aureus* clonal complex 398 (MRSA CC398) in Japan (*1*). *S. aureus* CC398 includes 2 major MRSA variants with distinct genetic and epidemiologic properties, a highly transmissible and virulent human variant comprising both PVL-positive and PVL-negative strains and a more benign PVL-negative livestock-associated variant (*2*). We have previously shown that, in Denmark, nearly all case-patients colonized or infected with PVL-positive MRSA CC398 strains of the human variant have links to countries in mainland Asia, where the strain is endemic in the community (*3*). Our analysis revealed the existence of 2 phylogenetically distinct lineages (L1 and L2) with unique sequence types (STs), ST398 linked to China and ST1232 linked to Vietnam, Thailand, and Cambodia. Besides being PVL-positive and belonging to ST1232, the isolate described by Nakaminami et al. (*1*) also shared other genetic and phenotypic characteristics with the L2 strains: it carried *spa* type t034 and SCC*mec* type V and was resistant to aminoglycosides (gentamicin), lincosamides (clindamycin),