Bacteroides chinchillae sp. nov. and Bacteroides rodentium sp. nov., isolated from chinchilla (Chincilla lanigera) faeces

Author(s) Maki Kitahara¹, Mitsuo Sakamoto¹, Sayaka Tsuchida², Koh Kawasumi², Hiromi Amao², Yoshimi Benno³, Moriya Ohkuma¹

Institution(s) 1. RIKEN BRC-JCM, RIKEN, Wako, Saitama, 351-0198 JAPAN 2. NVLU, Nippon Veterinary and Life Science University, Musashino, Tokyo 180-8602, Japan 3. RIKEN Innovation, RIKEN Innovation Center, wako, Saitama, 351-0198 JAPAN

Abstract:

Chinchillas (Chinchilla lanigera) are nocturnal foragers that live in communal burrows and are native to the rocky slopes of the high Andes. Since the 1950s, chinchillas have become a common animal model in otitis media and other otic diseases. To our knowledge, the bacterial faecal flora of chinchilla has been only studied by Worthington & Fulghum1), and their identification method of isolated strains was based solely on physiological and biochemical characteristics. Strains of Gram-negative anaerobic rods were isolated from chinchilla faeces, and three strains, ST170T, ST180 and ST28T, were investigated taxonomically. Based on the phylogenetic analyses and specific phenotypic characteristics, the three strains belonged to the genus Bacteroides. Phylogenetic analyses of their 16S rRNA gene sequences revealed that the two strains, ST170T and ST180, formed a single cluster and a distinct line of descent, and their sequence similarity was 99.7 %. The highest sequence similarity to ST170T was found with B. massiliensis JCM 13223T (95.1 %), B. dorei JCM 13471T (94.6 %), B. vulgatus JCM 5826T (94.4 %). Strain ST28T also formed a distinct line of descent, and the highest sequence similarity to ST28T was found with B. uniformis JCM 5828T (98.1 %). A low DNA-DNA hybridization value (1 %) between ST28T and B. uniformis JCM 5828T clearly indicated that they were different species. Analysis of the hsp60 gene sequences also supported these relationships. Based on the phenotypic and phylogenetic characteristics, two novel species Bacteroides chichillae sp. nov. and Bacteroides rodentium sp. nov., are proposed. The G+C content of the type strains was 45.2 mol% for B. chinchillae, and 41.0 mol% for B. rodentium. The type strains of B. chinchillae and B. rodentium are ST170 T (= JCM 16497T = CCUG 59335T) and ST28 T (= JCM 16496T = CCUG 59334T), respectively2). 1) Worthington, J. M. & Fulghum, R. S. (1988). Cecal and fecal bacterial flora of the Mongolian gerbil and the chinchilla. Appl Environ Microbiol 54, 1210-1215, 2) Kitahara, M. et al. Bacteroides chinchillae sp. nov. and Bacteroides rodentium sp. nov., isolated from chinchilla (Chinchilla lanigera) faeces. Int J Syst Evol Microbiol first published on May 21, 2010 as doi: 10.1099/ijs.0.024026-0

Key words: Bacteroides chinchillae sp. nov., Bacteroides rodentium sp. nov., chinchilla (Chincilla lanigera), faeces