

Corrigendum to ‘Noncontiguous finished genome sequence and description of *Bartonella mastomydis* sp. nov.’ [New Microbes New Infect 25 (2018) 60–70]

M. Dahmani¹, G. Diatta³, N. Labas¹, A. Diop¹, H. Bassene³, D. Raoult¹, L. Granjon⁴, F. Fenollar² and O. Mediannikov¹

1) Aix-Marseille Université, IRD, AP-HM, MEPHI, 2) Aix-Marseille Université, IRD, AP-HM, SSA, VITROME, Marseille, France, 3) IRD VITROME, Campus Commun UCAD-IRD of Hann, Dakar, Senegal and 4) CBGP, IRD, INRA, CIRAD, Montpellier SupAgro, Université de Montpellier, Montpellier, France

Corresponding author: O. Mediannikov, URMITE, IHU—Méditerranée Infection, 19-21 Boulevard Jean Moulin, 13005 Marseille, France.

E-mail: oleguss1@gmail.com

The publisher wishes to correct the following error which was introduced during the production of this manuscript. The protologue of the *Bartonella mastomydis* contained several misprints and inaccuracies.

The corrected version of the protologue is as follows:

Description of *Bartonella mastomydis* sp. nov. strain 008

Bartonella mastomydis (mas.to/my.dis, N.L. gen. n., from *mastomydis*, ‘of Mastomys,’ isolated from *Mastomys erythroleucus*) is a nonmotile Gram-negative rod. Growth is only obtained at 37°C. Colonies are opaque, grey and 0.5 to 1 mm in diameter on blood-enriched Columbia agar. Cells are rod shaped without flagella or pili. Length and width are 1369.8 ± 423.8 nm and 530.9 ± 105.8 nm respectively. The type strain 008 is sensitive to rifampicin, amoxicillin, amoxicillin/clavulanic acid, oxacillin, nitrofurantoin, doxycycline, linezolid, tobramycin, gentamycin, imipenem, trimethoprim/sulfamethoxazole, fosfomicin and ciprofloxacin and resistant to metronidazole and colistin. The G + C content of the genome is 38.44%. The 16S ribosomal RNA gene sequence and whole-genome shotgun sequence of strain 008 are deposited in GenBank under accession numbers KY555064 and GCA_900185775 respectively. The type strain 008 (CSUR B643, DSM28002) was isolated from the rodent *Mastomys erythroleucus* trapped in the region of Sine-Saloum, Senegal.

The authors would like to apologize for any inconvenience caused.