Genomics as a means to understand bacterial phylogeny and ecological adaptation: the case of bifidobacteria

Marco Ventura · Carlos Canchaya · Gerald F. Fitzgerald ·
Radhey S. Gupta · Douwe van Sinderen

Published online: 26 June 2007
© Springer Science+Business Media B.V. 2007

**Corrigendum to: Antonie van Leeuwenhoek (2007) 91:351–372
DOI 10.1007/s10482-006-9122-6**

Regrettably, the description of plasmid p4M was not properly referenced in the original publication.

On page 354, it reads “and p4M from *B. pseudocatenulatum* (Sgorbati et al. 1982),” when it should have read “and p4M from *B. pseudocatenulatum* (Gibbs et al. 2006),”

The full reference is published below:

Gibbs MJ, Smeianov VV, Steele JL, Upcroft P, Efimov BA (2006) Two families of rep-like genes that probably originated by interspecies recombination are represented in viral, plasmid, bacterial, and parasitic protozoan genomes. *Mol Biol Evol* 23:1097–1100.

The online version of the original article can be found under doi: [10.1007/s10482-006-9122-6](https://doi.org/10.1007/s10482-006-9122-6).

M. Ventura (✉)
Department of Genetics, Anthropology and Evolution,
University of Parma, Parco Area delle Scienze 11a,
Parma 43100, Italy
e-mail: marco.ventura@unipr.it

C. Canchaya · G. F. Fitzgerald · D. van Sinderen
Alimentary Pharmabiotic Centre and Department of
Microbiology, BioSciences Institute, National University
of Ireland, Cork, Ireland

R. S. Gupta
Department of Biochemistry and Biomedical Sciences,
McMaster University, Hamilton, Canada