

CORRIGENDUM

Interactions between gut microbiota, host genetics and diet relevant to development of metabolic syndromes in mice

Chenhong Zhang, Menghui Zhang, Shengyue Wang, Ruijun Han, Youfang Cao, Weiyang Hua, Yuejian Mao, Xiaojun Zhang, Xiaoyan Pang, Chaochun Wei, Guoping Zhao, Yan Chen and Liping Zhao

The ISME Journal (2010) 4, 312–313; doi:10.1038/ismej.2009.144

Correction to: *The ISME Journal* (2010) 4, 232–241; doi:10.1038/ismej.2009.112; published online 29 October 2009

The authors would like to apologize for any inconvenience this may have caused.

Since the publication of this paper, the authors have noticed an error in Figure 4. The correct figure is shown here.

Figure 4 Phylogeny and differential abundance and distribution of phylotypes in the family *Erysipelotrichaceae* among treatment groups. (a) Phylogeny of phylotypes in the family *Erysipelotrichaceae*. One sequence was randomly selected from each operational taxonomic unit (OTU) (97% identify threshold) and was inserted into pre-established phylogenetic trees of full-length 16S rRNA gene sequences in ARB. The tree shown here only includes some reference species of *Firmicutes* and the sequences from this study in the family *Erysipelotrichaceae*. These phylotypes fall into four lineages, M1–M4. The DGGE bands in M1–M4 are also shown. (b) Abundance distribution of M1, M2, M3 and M4 in the four groups of animals.

