S1 Materials and Methods

Identification of *Bifidobacterium* strain by PCR-based methods

Nine *Bifidobacterium* strains which have been selected according to their probiotic properties (survival in conditions of gastric acids and bile salt) were classified by molecular-biological methods as described previously [1]. Briefly, DNA was prepared from crude bacterial cell lysates by phenol (pH 7.8) and chloroform: isoamyl alcohol (24 : 1) extraction according to Sambrook and Russell [2]. The purity and concentration of nucleic acids were confirmed by UV spectrophotometry as described previously [3]. The genus *Bifidobacterium* was confirmed by PCR with specific primers Pbi F1/Pbi R2 described by Roy and Sirois [4]. Ten sets of specific primers were used for identification of bifidobacterial species frequently found in human samples: *B. longum* ssp. *longum*, *B. longum* ssp. *infantis*, *B. dentium*, *B. adolescentis*, *B. bifidum*, *B. breve*, *B. catenulatum/pseudocatenulatum*, *B. angulatum*, *B. gallicum* [5] and *B. animalis* [4]. Amplified ribosomal DNA restriction analysis (ARDRA) of genus-specific PCR product using three endonucelases *Bam*HI, *Nci*I (Takara, Shiga, Japan) and *Sau*3AI (Roche Diagnostic, Manheim, Germany) were used for species and subspecies classification as described previously [1, 3]. Four type and two collection strains used as control in ARDRA analysis were obtained from the Czech Collection of Microorganisms (*B. longum* ssp. *longum* CCM 3764, *B. adolescentis* CCM 4987T, *B. animalis* CCM 4988T), the American Type and Culture Collection (*B. longum* ssp. *longum* ATCC 15707T, *B. longum* ssp. *infantis* ATCC 17930), and the Deutsche Sammlung von Mikroorganismen und Zellkulturen (*B. longum* ssp. *infantis* DSM 20088T). The PCR products were visualised using GelRed^{TM} Nucleic Acid Gel Stain (Biotinum, Hayward, CA, USA) and images were obtained by Fluorescent Image Analyser FLA-7000 (Fujifilm Corporation, Tokyo, Japan). The fingerprinting profile was

analysed by the software programme Gel Compare II (2.0 version) and dendrogram were constructed using UPGMA analysis and Pearson correlation coefficient.

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