Anti-bacterial activity of 17 strains of lactobacilli against elementary bodies of *Chlamydia trachomatis*

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**INTRODUCTION AND PURPOSE**

*Lactobacillus* species dominate the vaginal microbiota of healthy reproductive-age women and protect the genitourinary tract from the attack of several infectious agents. *Chlamydia trachomatis*, a leading cause of sexually transmitted diseases worldwide, can induce severe sequelae, i.e. pelvic inflammatory disease, infertility and ectopic pregnancy. In the present study we investigated the interference of *Lactobacillus crispatus*, *L. gasseri* and *L. vaginalis*, known to be dominant species in the vaginal microbiome, with the infection process of *C. trachomatis*.

**METHODS**

Seventeen *Lactobacillus* strains, isolated from vaginal swabs of healthy pre-menopausal women and cultured in MRS broth were used: in particular, 8 strains of *L. crispatus* (BC1-8), 6 of *L. gasseri* (BC9-14) and 3 of *L. vaginalis* (BC15-17). After turbidimetric determination of cell concentration culture were centrifuged to separate cell pellets (CP) from cell-free supernatants (CFS). All CP and CFS corresponded to 2.5×10⁸, 2.5×10⁹ and 2.5×10⁵ CFU/ml of EBs of CT serotype D. pH were measured in the final volume; EBs diluted in PBS were used as controls. Tubes were incubated for 7, 15 and 60 minutes and then centrifuged. Supernatants were used to infect confluent Hela cells in single tubes containing sterile coverslips. After 48h of incubation at 37°C we evaluated CT infectivity by immunofluorescence. IFUs were counted in 30 randomly chosen 200× microscopic fields and compared with controls. Statistical analyses were performed using GraphPad Prism software, applying Wilcoxon test. ¹H-NMR analysis of metabolic profiles of CFS was conducted on AVANCE spectrometer (Bruker); signals were assigned comparing their chemical shifts and multiplicity with Chenomx software data bank (Chenomx, ver8.02). Statistical analysis of ¹H-NMR data was performed using R computational software, applying Wilcoxon test.

**RESULTS**

Our results demonstrate the ability of different *Lactobacillus* strains of vaginal origin to inactivate *C. trachomatis* EBs through the production of extracellular metabolites in an acidic environment.