Inhibition of Clostridium difficile strains by intestinal Lactobacillus species

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Indigenous intestinal microflora (including lactobacilli) has an important role in protection against Clostridium difficile infection. To assess in vitro interaction between lactobacilli and C. difficile, antagonistic activity of 50 intestinal Lactobacillus spp. strains against 23 pathogenic C. difficile strains was determined. Phenotypic properties of C. difficile strains [production of short-chain fatty acids (SCFAs) and toxin A, and antimicrobial susceptibility] and lactobacilli (production of SCFAs and H$_2$O$_2$) were investigated. Five lactobacilli (Lactobacillus paracasei and Lactobacillus plantarum species) were antagonistic to all C. difficile strains, 18 were antagonistic to some C. difficile strains and 27 showed no antagonistic activity. This antagonistic activity was strain-specific and seemed to correlate with H$_2$O$_2$ and lactic acid production. C. difficile strains that were more sensitive to lactobacilli (n = 9) usually produced higher toxin levels and more SCFAs, and were more resistant to antibiotics, than strains that were resistant to lactobacilli (n = 14). Compatibility of C. difficile strain properties (resistance to lactobacilli or antibiotics) with intestinal microecological conditions (e.g. presence of antagonistic lactobacilli, concentration of antibiotics) may determine expression of disease.

The aim of our study was to evaluate the inhibitory activity of various intestinal lactobacilli against different pathogenic C. difficile strains in vitro.

Methods

Twenty-three C. difficile strains that belonged to different genotypes and were isolated from faeces of 21 hospitalized patients with sporadic cases of antibiotic-associated diarrhoea were included. Strains were typed with arbitrarily primed PCR as described by Tang et al. (1995). From two patients, two different strains were isolated simultaneously. Strains of intestinal lactobacilli (n = 50) were isolated from faeces of young, healthy children during our previous studies (Mikelsaar et al., 2002).

In vitro toxin A production by C. difficile strains was detected with the Oxoid toxin A test, according to the manufacturer’s instructions. Strains were considered to be low toxin producers if the test was positive with undiluted or 1:10 diluted sample and high producers if the test was positive in a 1:100 or higher dilution.

MICs of chloramphenicol, clindamycin, rifampicin, tetracycline, ampicillin, erythromycin, metronidazole and vancomycin were detected with E tests, according to the manufacturer’s instructions (AB Biodisk), and interpreted according to the current break-points of the National Committee for Clinical Laboratory Standards.

For determination of production of short-chain fatty acids (SCFAs), C. difficile strains were cultivated in peptone/yeast/glucose broth and lactobacilli in MRS broth for 48 h. In vitro production of SCFAs was measured by GC as a concentration of these compounds, as described by Holdeman & Moore (1972). Production of H$_2$O$_2$ by lactobacilli was detected on tetramethyl benzidine medium, as described by Eschenbach et al. (1989).

Abbreviation: SCFA, short-chain fatty acid.
Antagonistic activity of lactobacilli was detected on agar plates as inhibition of *C. difficile* growth. Wilkins–Chalgren blood agar was inoculated with a 10 μl aliquot of a 48 h culture of lactobacilli in MRS broth by streaking the plates. After 48 h incubation in a 10% CO₂ environment, 1 μl *C. difficile* saline suspension (0.5 on the McFarland turbidity scale) was streaked perpendicularly with a lactobacillus growth streak. Inhibition assays with each *Lactobacillus* sp. and *C. difficile* combination were repeated at least four times on two separate plates. Plates were incubated for 24 h in an anaerobic environment and inhibition zones (mm) of *C. difficile* growth from the *Lactobacillus* sp. streak were measured.

Data were analysed with Jandel SigmaStat 2.0 software by using Fisher, Spearman correlation and Mann–Whitney tests.

**Results and Discussion**

Based on the interaction with LB*+*/C0, we divided the lactobacilli into three groups: (i) those able to inhibit growth of all *C. difficile* strains investigated (LB*+*); (ii) those able to inhibit growth of some (nine of 23) *C. difficile* strains (LB*+*/–); and (iii) those without any antagonistic activity (LB–). Species composition of these groups is shown in Table 1.

Five strains of lactobacilli were able to inhibit growth of all *C. difficile* strains tested. These belonged to *Lactobacillus paracasei* and *Lactobacillus plantarum* [facultatively heterofermentative (FHEL) group]. At the same time, all obligately heterofermentative (OHEL) group species (except one) did not show antagonistic activity against any *C. difficile* strain. However, the antagonistic activity of lactobacilli was not strictly correlated with a particular species of lactobacilli.

Based on the interaction with LB*+*/– group lactobacilli, *C. difficile* strains could be divided into two groups: nine strains were sensitive to all these lactobacilli and 14 *C. difficile* strains were resistant. We found that 11 *C. difficile* strains were high toxin producers, 11 were low toxin producers and one strain did not produce toxin A in vitro. High toxin producers were usually sensitive to LB*+*/– group lactobacilli, in contrast to low toxin producers (*P* < 0.001). All *C. difficile* strains tested were highly sensitive to ampicillin, vancomycin and metronidazole. With other antibiotics, MIC values varied greatly. Strains with higher MICs to chloramphenicol, rifampicin, tetracycline and erythromycin were usually sensitive to the antagonistic activity of LB*+*/– lactobacilli and were also highly toxigenic (*P* < 0.001). Thus, based on these phenotypic properties, *C. difficile* strains could be divided into two typical groups: phenotype A (antibiotic-resistant, more susceptible to antagonistic activity of lactobacilli and highly toxigenic) and phenotype B (sensitive to antibiotics, more resistant to inhibition by lactobacilli and low toxin A producers).

By comparing quantitative production of SCFAs, we found that *C. difficile* strains of phenotype A produced significantly higher amounts of isobutyric (mean, 1.84 versus 1.6 mg l⁻¹; *P* < 0.001), butyric (mean, 6.56 versus 5.15 mg l⁻¹; *P* < 0.05), isovaleric (mean, 2.14 versus 1.68 mg l⁻¹; *P* < 0.001) and valeric (mean, 1.85 versus 1.31 mg l⁻¹; *P* < 0.01) acids, compared to phenotype B strains. There was no significant difference in production of acetic or isocaproic acids. All lactobacilli tested produced acetic and lactic acids. We found that LB*+* group strains usually produced more lactic acid (median, 20.9 mg l⁻¹) than LB*+*/– (median, 18.5 mg l⁻¹; *P* < 0.001) and LB– (median, 10 mg l⁻¹; *P* < 0.005) strains. No differences were found in production of acetic acid.

H₂O₂ was produced by 42% of lactobacilli in vitro. We found that LB*+* and LB*+*/– strains were more commonly H₂O₂ producers (14 of 23) than LB– strains (seven of 27; *P* = 0.02). In our study, we found that both in vitro antagonistic activity of lactobacilli against *C. difficile* and susceptibility of *C. difficile* strains to this antagonism was strain-dependent. Previous studies that used only a single indicator *C. difficile* strain to screen several lactobacilli or a single *Lactobacillus* sp. strain against different *C. difficile* strains did not describe this important phenomenon (Bogovič-Matijasˇić et al., 1998; Forestier et al., 2001; Strus et al., 2001).

The important role of in vitro antagonistic activity of lactobacilli against potential pathogens and also the ability

<table>
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<tr>
<th>Lactobacillus group*</th>
<th>Species</th>
<th>No. strains</th>
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<tbody>
<tr>
<td></td>
<td></td>
<td>LB* (n = 5)</td>
</tr>
<tr>
<td>OHOL</td>
<td><em>Lactobacillus acidophilus</em></td>
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<tr>
<td></td>
<td><em>Lactobacillus delbrueckii subsp. delbrueckii</em></td>
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<td><em>Lactobacillus buchneri</em></td>
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<td><em>Lactobacillus brevis</em></td>
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<td><em>Lactobacillus fermentum</em></td>
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<td></td>
<td><em>Lactobacillus coprophilus</em></td>
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</tr>
<tr>
<td>OHEL</td>
<td><em>Lactobacillus paracasei subsp. paracasei</em></td>
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</tr>
<tr>
<td></td>
<td><em>Lactobacillus plantarum</em></td>
<td>3</td>
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*FHEL, Facultatively heterofermentative lactobacilli; OHEL, obligately heterofermentative lactobacilli; OHOL, obligately homofermentative lactobacilli.
to sustain colonization resistance in microecosystems in vivo has been attributed by several investigators to the production of H$_2$O$_2$ and SCFAs (Eschenbach et al., 1989; Brashears et al., 1998; Ouwehand, 1998; Brashears & Durre, 1999; Malakar et al., 1999). Others have found that, in some cases, where lactobacilli show high antagonistic activity against pathogens, these mechanisms are not involved or have only a supportive effect (Su et al., 1987; Coconnier et al., 1997). Bogović-Matijašić et al. (1998) suggested the importance of bacteriocins of lactobacilli in inhibition of C. difficile. Our finding that lactobacilli that were more antagonistic to C. difficile produced H$_2$O$_2$ and high levels of lactic acid more frequently indicates the probable role of these compounds in lactobacilli–C. difficile interactions. However, the role of other mechanisms of antagonism, such as production of bacteriocins, should be investigated and the relevance of in vitro findings should be evaluated by in vivo studies.

In C. difficile strains, we found an inverse relationship between toxicity, resistance to antibiotics and susceptibility to antimicrobial agents that were produced by lactobacilli. Correlation (positive or negative) between virulence and antibiotic resistance has been described in several other species. On one hand, these properties could be selected by the same environmental factors or mediated by related species. On the other hand, expression of resistance may require extra energy and thus reduce virulence and metabolic activity (Martínez & Baquero, 2002). In the case of antibiotic-associated diarrhoea, concentration of antibiotics and the antagonistic effect of indigenous microflora are the main selective factors for C. difficile strains in the intestine. Based on our findings, we suggest that if antibiotic concentration is high and the indigenous microflora is deeply suppressed, antibiotic-resistant (but lactobacilli-sensitive) and more toxigenic strains could have an advantage. In cases of milder alteration of indigenous microflora and lower concentrations of antibiotics, strains of C. difficile that are lactobacilli-resistant and more antibiotic-sensitive, but less toxic, have the advantage to survive and cause infections. If this is true, administration of some antibiotics (e.g. clindamycin) induces more serious C. difficile infection, not only due to deeper alteration of indigenous microflora, but also by selection of more toxigenic C. difficile strains.

We have found a substantial difference in antagonistic activity of intestinal lactobacilli against C. difficile strains with different virulence. Evaluation of the in vivo effect of highly antagonistic strains of lactobacilli and description of the mechanisms involved enable a more complete understanding of the pathogenesis of C. difficile diarrhoea and may introduce new possibilities in an ecological approach to its prophylaxis and therapy.

References


