Nitrifying bacteria generate Microbial Induced Corrosion (MIC) in recirculating cooling water system of Nitrogenous Fertilizer Industry

Nita J Naik
Manager, Central Laboratory, Krishak Bharati Cooperative Ltd (KRBHICO), Hazira Road, Surat 394515. Gujarat, India. nita.naik@yahoo.co.in

The formation of biofouling due to accumulation of microbes in favourable nutritional environment of recirculating system generates microbiological induced corrosion (MIC) on the surface of heat exchangers and pipelines. The microorganisms may come from make-up water, with mud or in sludge of cooling tower basin and settle with side stream filter’s sand. An active participation of Nitrifying bacteria in nature is a two-step oxidation process of ammonium (NH₄⁺ or ammonia NH₃) to nitrate (NO₃⁻) catalyzed by two ubiquitous bacterial groups. The first reaction is oxidation ammonium to nitrite by ammonium oxidizing bacteria (AOB) represented by Nitrosomonas species.

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\begin{align*}
\text{NH}_4^+ + \text{O}_2 & \rightarrow \text{NO}_2^- + 3\text{H}^+ + 2\text{e}^- \\
\text{NH}_2\text{O} + 2\text{H}^+ + 2\text{e}^- & \rightarrow \text{NH}_4\text{OH} + \text{H}_2\text{O} \\
\text{NH}_2\text{OH} + \text{H}_2\text{O} & \rightarrow \text{NO}_3^- + 3\text{H}^+ + 4\text{e}^- 
\end{align*}
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The second reaction is oxidation nitrite (NO₂⁻) to nitrate by nitrite-oxidizing bacteria (NOB), represented by Nitrobacter, Nitrooccus species [NO₂⁻ + H₂O → NO₃⁻ + 2H⁺ + 2e⁻] so it creates lowering of pH in recirculating system; which ultimately decreases the plant performance efficiency. To overcome these problems, it is essential to isolate the nitrifying organisms using selective medium of Soriano and Walker, Winogradsky’s medium by standard method. The species nitrobroader, nitrosonomas, nitroccocus nitrocytis are commonly found in recirculating system. It can be concluded that these dominating species take part to lowering the pH of recirculating cooling water and generates MIC. So it reduces cross sectional area of heat exchangers and pipeline. The problem of MIC and Biofouling can be controlled by proper periodic application of non-oxidised and oxidised biocide as well as frequent back wash of sand filters.

Keywords: microbial induced corrosion, nitrifying bacteria, recirculating cooling water system.

References

Quantitative analysis of initial adhesion of bacterial vaginosis anaerobes in ME-180 cells

A. Machado¹,², D. Salgueiro¹, M. Harwich¹, K.K. Jefferson² and N. Cerca²

¹IBB - Institute for Biotechnology and Bioengineering, University of Minho, Campus de Gualtar 4710-057, Braga, Portugal
²Department of Microbiology and Immunology, Virginia Commonwealth University, Richmond, VA 23298-0678, USA

Bacterial vaginosis (BV) is the most common vaginal disorder in women of reproductive age [1]. Despite decades of research, the etiology of BV still remains elusive. It is well established that adhesion to host cells or tissues is a necessary early step in the establishment of infection [2]. Since it is often considered a polymicrobial condition, it has been proposed that some bacteria have a preponderant role as early colonizers, while others have an impact later in the development of a multi-species biofilm infection [1]. So, we tested this hypothesis by first quantifying the potential of known anaerobic bacterial species found in BV (Gardnerella vaginalis, Atopobium vaginae, Mobiluncus mulieris, Prevotella bivia and Fusobacteria nucleatum) to compete with a protective lactobacillus (L. crispatus) for initial adhesion to ME-180 cervical epithelial cells. Then, we tested the potential of the two vaginal lactobacilli; L. crispatus, which appears to be protective against BV, and L. iners, which does not protect as effectively against BV, to block these BV-associated anaerobes. And finally, we tested the ability of the BV-associated anaerobes to displace pre-adhered lactobacilli. This work allowed quantification, of the initial adhesion of these BV-associated anaerobes to ME-180 epithelial cells and competition and displacement/blockage assays.

In competition assays, G. vaginalis exhibited the greatest capacity for adherence to ME-180 cells, confirming our previous report [3]. Interestingly, G. vaginalis also maintained its ability to adhere in the presence of L. crispatus better than the other species, and there was only a 10% reduction in adherence with respect to the control. This was statically different from the others BV anaerobes (ANOVA Tukey statistical test values, P < 0.05), as it adhered approximately 4-fold better than A. vaginae or M. mulieris and approximately 2-fold better than P. bivia. Adherence of L. crispatus was not statistically inhibited by any of the BV anaerobes tested.

In order to simulate the introduction of BV-associated bacteria into a healthy vagina colonized by lactobacilli, we performed displacement/blockage assays in the presence of ME-180 cell line. To this end, we first allowed L. crispatus or L. iners to adhere to the epithelial monolayers and subsequently added a BV-associated species to quantify the inhibitory effect of the lactobacilli on secondary colonization. In these displacement/blockage assays, L. crispatus inhibited adherence of G. vaginalis by approximately 43%. Addition of G. vaginalis appeared to cause a slight displacement of adherent L. crispatus but this did not reach statistical significance. L. crispatus also reduced adherence of A. vaginae and M. mulieris by approximately 50%. P. bivia and F. nucleatum appeared to be less susceptible to inhibition by L. crispatus. Interestingly, L. iners, which has been shown in previous studies to be less protective against BV relative to other vaginal lactobacilli [4], had a similar inhibitory effect on adherence by all of the BV-associated species except G. vaginalis. Adherence of G. vaginalis actually increased somewhat in the presence of L. iners, although this increase did not reach statistical significance. None of the BV anaerobes displaced L. iners.

To conclude, L. crispatus and L. iners inhibited adherence of all BV-associated species tested with the exception that L. iners actually enhanced adherence of G. vaginalis. This study supports the possibility that G. vaginalis could be an initial colonizer in BV etiology.

Keywords: Lactobacillus spp.; Gardnerella vaginalis; Bacterial vaginosis; ME-180 epithelial cells

References