

Framework to Compare Disinfection Characteristics of Various Microorganisms

Frederik Hammes *

Department of Environmental Microbiology, Swiss Federal Institute of Aquatic Science and Technology, Dübendorf 8600, Switzerland

*Corresponding author: Frederik Hammes, Department of Environmental Microbiology, Swiss Federal Institute of Aquatic Science and Technology, Dübendorf 8600, Switzerland, E-mail: hamsfrderik@eawag.ch

Received date: October 04, 2022, Manuscript No. IPJAMB-22-15252; **Editor assigned date:** October 06, 2022, PreQC No. IPJAMB-22-15252 (PQ); **Reviewed date:** October 17, 2022, QC No. IPJAMB-22-15252; **Revised date:** October 27, 2022, Manuscript No. IPJAMB-22-15252 (R); **Published date:** November 04, 2022, DOI: 10.36648/2576-1412.6.11.122

Citation: Hammes F (2022) Framework to Compare Disinfection Characteristics of Various Microorganisms. J Appl Microbiol Biochem Vol.6 No.11: 122.

Description

Chlorine's effectiveness at inactivating bacteria varies depending on the organism and the conditions of the environment. The inconsistencies in the experimental conditions and analytical techniques used in various studies make it difficult to compare various samples and studies, particularly when comparing pure cultures with indigenous bacterial communities. We tried an original 96-well plate FCM exploratory and robotized logical methodology, where bacterial networks and unadulterated societies were suspended in a similar normal water grid preceding chlorination straightforwardly in the plate. We demonstrated that we could accurately compare the results of 32 distinct combinations of chlorine concentration and time also known as chlorine exposure on indigenous aquatic communities and bacterial pure cultures. This made it possible to compare the data from various samples that were subjected to the same experimental conditions. In this review, the 96-well plate computerized FCM approach empowered enormous sets of free chlorination tests to be completed in a brief time frame period. As far as anyone is concerned, this is the biggest dataset of chlorination tests which consumed least time as of not long ago. During chlorination, cellular damage was assessed using SYBR Green I and SG combined with propidium iodide staining. The findings demonstrated that a higher chlorine concentration with a shorter contact time is preferable to the inactivation of bacteria for the same chlorine exposure. Our study offers a promising framework for comparing the disinfection properties of various microorganisms and can be expanded upon to diagnose the effects of antimicrobial products.

Acetoclastic Methanogens via Acetate

Dismutation

It has been demonstrated that bio methane production favors CO₂ reduction through Direct Interspecies Electron Transfer (DIET) between electricigens and methanogens. Furthermore, conductive materials accelerate DIET. Due to a lack of thorough experimental data and poor mechanistic studies, it is not yet clear whether conductive materials can promote other methanogenic pathways. In this study, we hypothesized that in pure cultures of *Methanosarcina* spp., conductive carbon nanotubes independently of electricigens stimulate acetoclastic

methanogenesis and wetland soil that is anaerobic. During the growth phase, we observed a significant increase in the rate of methane production, such as a rise from 0.169 mM to 0.241 mM following the third-day addition of CNTs. Utilizing microbial diversity and electrochemical analysis, CNTs did not improve the electron transfer rate or the abundance of electro microorganisms in anaerobic soils. The CH₃F inhibitor of acetoclastic methanogenesis, stable carbon isotope fractionation, and ¹³C-CH₃COOH labeling were utilized to differentiate methanogenic pathways. In both pure cultures and anaerobic soils, CNTs primarily accelerated acetoclastic methanogenesis rather than CO₂ reduction. In addition, when *Methanosarcina barkeri* and *Methanosarcina mazei* are grown in pure culture and produce more than 0.3 mM methane, the presence of CNTs slightly lessens the effect of CH₃F's inhibition on acetoclastic methanogenesis. Transmission electron microscopy was used to observe CNTs that were very tightly attached to the cell surface. Proteome examination uncovered a feeling of protein blend with about two times the improvement associated with COOH oxidation and electron move. Overall, our findings show that conducting CNTs favor methane production and that acetoclastic methanogens via acetate dismutation, not traditional CO₂ reduction, is the mechanism involved. Biotechnological processes have significantly improved over the past few decades, bringing societies closer to a bio-based economy that is no longer dependent on liquid fossil fuels. Due to its capacity to function as a drop-in fuel for gasoline and its high energy content, biobutanol is regarded as the best sustainable biofuel alternative. Biobutanol production is now on track to become even more environmentally friendly thanks to new developments in resource recovery technology. The research conducted over the past ten years on the production of biobutanol from waste and low-value materials is summarized in this paper. The most common biological pathways for butanol production in ABE fermentation and syngas fermentation are revisited, as are alternative feedstock options. Both single-culture and mixed-culture fermentation are examined in detail, as is the extent to which both methods have advanced to butanol titers that are close to or higher than the butanol's microbial toxicity level. This review delves further into the benefits and drawbacks of each technology, comparing the titers, productivities, and yields of single and mixed microbial cultures to determine the extent to which mixed microbial

cultures can compete with pure cultures. The use of mixed microbial fermentation as the primary platform for the production of butanol and the concentration of future research on this promising technology are clearly supported by feed stocks with low value and waste residue.

Selection and Management in Support Of Agriculture

Cereals dominate global agriculture; maize, wheat, and rice are the crops with the largest growing areas and require high nitrogen inputs from fertilizer application. The amount of nitrogen that must be supplied by humans can be reduced by including legumes in cropping systems. Utilizing cereal-legume mixtures is one strategy for incorporating legumes into cereal systems and meeting the nitrogen requirements of cereals. Symbiotic bacteria in the root nodules allow the legume to primarily utilize biologically fixed nitrogen from the air in such mixtures, reducing competition with the cereal, which relies on inorganic nitrogen from the soil. However, it is challenging to design cereal-legume intercropping systems that are both sustainable and productive. Above-ground and below-ground interactions between cereal and legume species must be taken into account, as must competition for light, water, and nutrients and their mechanisms. Numerous crop characteristics, such as the cereal and legume's distinct capacity for nutrient uptake and differences in rooting systems, canopy structure, height, and leaf

angles, determine the extent to which one species dominates another. Management decisions like row configuration, plant density, fertilization timing and quantity, and sowing dates also influence the degree of interspecific competition on both species. Crop growth models predict the outcomes of production by quantitatively integrating the interactions between intercropped species over time. As a result, they can effectively contribute to the investigation of the overall outcome of all factors that influence intercrop growth, including pedoclimatic conditions, crop and cultivar traits, and management practices. As a result, they are able to advocate for species selection and management in support of agriculture's ecological intensification. To successfully simulate the growth, development, and yield of a wide range of crop species and cultivars in pure cultures in various crop production systems and environments, a number of crop growth models have been developed. Intercropping systems can be simulated by some crop growth models as well. For instance, Denmark and France's pea-barley intercrop systems were simulated using the crop growth models STICS and FASSET, respectively. The model included competition for water due to wheat-maize intercropping. In The Netherlands, the M3 model was used to encourage the nitrogen-limited growth of wheat-fababean strip intercrops. However, crop growth models for cereal-legume intercrops have not been thoroughly parameterized or validated, limiting their use in the creation of the most efficient intercropping systems.