



## Utilising these Organisms in the Production of Functionalized Molecules through Bacterial Technology

Aftab Alam \*

Department of Environmental Science, University of Bahrain, Zellaq, Bahrain

### ABSTRACT

To achieve sustainable development, traditional resources such as fossil fuels must be replaced by alternative resources. Many bacteria grow faster in marine ecosystems than on land plants. Bacteria are classified into green algae, red algae and brown algae based on their photosynthetic pigments. Brown algae are thought to be a source of bioactive substances such as polyphenols. Additionally, some bacteria absorb about 10 times more carbon dioxide from the atmosphere than land plants. Therefore, they have great potential for use within the environment. Owing to their low lignin content and their applicability to biorefining processes, bacteria have recently established themselves as biomass feedstocks for bioethanol production. Here, we provide an overview of the bioconversion of bacteria to bioactive substances and biofuels using microbial biotechnology, such as genetically modified yeast developed using molecular display technology.

**Keywords:** Bacterial; Phlorotannin; Molecular display; Bioethanol; Xylan; Mannitol; Laminarin; Alginate

### INTRODUCTION

Over the centuries, fossil fuel consumption has increased, resulting in the release of large amounts of carbon dioxide into the atmosphere [1]. Human life also depends on various substances produced through chemical synthesis using large amounts of energy. The demand for energy has increased recently in response to the growth of the world's population and economy [2]. Developing renewable and clean bioenergy sources is therefore critical to paving the way for a sustainable future [3].

### DESCRIPTION

Bioethanol production has been proposed and developed using various agricultural biomass such as maize, sugar cane, sugar beet, potato and wheat. Compared to fossil fuels, bioethanol produces less toxic substances and poses less harmful environmental problems [4]. However, concerns remain that the use of biomass for energy production competes with food use by humans and livestock. Therefore, bacteria have attracted the attention of researchers as an alternative fuel source for bioethanol production. Bacteria can grow faster than land plants and do not require arable land for bacterial growth or fertilization [5]. Additionally, bacteria can thrive in salt water, preventing competition for the fresh water needed to produce crops in the field. Bacteria

<b>Received:</b>	14-June-2023	<b>Manuscript No:</b>	aasrhc-23-17606
<b>Editor assigned:</b>	19-June-2023	<b>PreQC No:</b>	aasrhc-23-17606 (PQ)
<b>Reviewed:</b>	03-July-2023	<b>QC No:</b>	aasrhc-23-17606
<b>Revised:</b>	18-August-2023	<b>Manuscript No:</b>	aasrhc-23-17606 (R)
<b>Published:</b>	15-September	<b>DOI:</b>	10.36648/0976-8610.14.3.115

**Corresponding author:** Aftab Alam, Department of Environmental Science, University of Bahrain, Zellaq, Bahrain; E-mail: alamedu@yahoo.com

**Citation:** Alam A (2023) Utilising these Organisms in the Production of Functionalized Molecules through Bacterial Technology. Adv Appl Sci Res. 14:115.

**Copyright:** © 2023 Alam A. This is an open-access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

are therefore considered to be an ideal resource for third-generation biofuels [6].

Bacteria come in different sizes and colors. They are classified based on photosynthetic pigment, color scheme (red, brown, green, etc.) and habitat. For example, Japan's exclusive economic zone covers approximately 450 million km<sup>2</sup> (1/80<sup>th</sup> of the world's total sea area) and more than 1,000 species of macroalgae live within this limited area [7]. Moreover, they have different chemical compositions and bioactive molecule content.

Polysaccharides represent biomass or bioactive compounds, with brown algae typically containing laminarin and fucoidan, green algae containing urbans and red algae containing large amounts of carrageenan. Brown bacteria also contain alginate, cellulose, hemicellulose, laminarin and mannitol, which are the major carbohydrates and are characterized by high levels of mannitol, laminarin and alginate. Laminarin is composed of  $\beta$ -1,3-linked glucose polymers with  $\beta$ -1,6 cross-linked branches [8]. In brown bacteria, it acts as a long-term storage compound and exhibits seasonal variation of 0%-35% on a dry basis. Brown bacteria also contain mannitol as a carbon storage compound, accounting for up to 20%-30% of dry weight.

### Biological Activity and Bioconversion of Green Bacterial

Green Ulva bacteria species are edible algae that contain health-enhancing and bioactive compounds. The major carbohydrates in Ulva species are urban and glucan, with rhamnose and glucuronic acid averaging 45.0 mol% and 22.5 mol%, respectively. Sea lettuce accounts for 9%-36% of the dry weight of sea lettuce species. Being rich in dietary fiber, it promotes gastrointestinal health and leads to a lower incidence of chronic diseases. Heterologous expression of two marine enzymes, urban lyase PL28 and glucuronyl hydrolase GH105, in *Bacillus licheniformis* efficiently converted the algal polysaccharide urban as a carbon and energy source. In another study on saccharification of urban, a broad-spectrum urban lyase (Cdf7993 protein) from *formosa agariphila* KMM 3901 was identified and studied further [9].

Rhamnose is an important monosaccharide widely distributed in microorganisms and plants. Certain bacterial saponinglycans include rhamnolipids, mycolic acids and extracellular polysaccharides. In the green macroalga Ulva lactuca, L-rhamnose and D-glucose are the major carbohydrates in the Ulva polysaccharide structure. These sugars can be obtained under mild conditions.

### Component and Bioconversion of Red Bacterial

Carrageenan is the major carbohydrate component of red bacteria such as *Eucheuma denticulatum* and agar is the major component of species such as *Gelidium amansii*. Once the agarose is degraded, enzymatic hydrolysis, acid hydrolysis, acid pre-hydrolysis and subsequent enzymatic hydrolysis yield 3,6-Anhydro- $\alpha$ -L-Galactose (AHG) and D-Galactose (AHG) for subsequent fermentation. Galactose is released. However, carrageenan is difficult to degrade due to the production of

inhibitory compounds such as acetic acid, furfural, 5-HMF and levulinic acid during acid treatment. Therefore, D-galactose from agarose and AHG are suitable target molecules when using red bacteria.

Many marine microorganisms such as *Pseudoalteromonas carrageenovora*, *Soberia galactanivorans*, *Pseudoalteromonas fuliginea* and *Saccharophagus degradans* exhibit agarase activity. Furthermore, the catabolic pathway of AHG in the marine agar-degrading bacterium *Vibrio sp.* I studied well. And the genus *Streptomyces*. As an example of its application in biotransformation, the AHG catabolic pathway was introduced into ethanologenic *E. coli* strains. The genetically engineered strain showed and 1.2-fold higher ethanol production compared to controls [10].

### Microorganisms and their Enzymes

Efficient crushing and saccharification of algal bodies is important for the development of bioconversion methods for algae. Considering these circumstances, it is possible to develop sustainable tools for processing algae using algae-degrading microbes. Previous algal disease outbreaks prompted screening for algal-degrading bacteria [11]. The marine bacterium *Alteromonas elyakovii* KMM 162T was isolated from selectively damaged leaves of the brown macroalga *Laminaria japonica*. Tanaka et al. from the intestine of the abalone *Haliotis gigantean* he isolated four brown algae-degrading gram-negative bacteria, *formosa haliotis* strains. Furthermore, we performed genome analysis of *formosa haliotis* MA1 strain (LMG 28520T) and clarified the decomposition mechanism of algal bodies. As a result, more genes involved in macromolecular degradation were identified than in conventional marine bacteria. Several genes related to hydrocarbon degradation and a gene cluster related to alginate degradation has been identified [12].

## CONCLUSION

The biotransformation of bacteria, mainly brown bacteria, using microbial biotechnology was outlined. The world's land-based natural resources have met expectations for food, energy and valuables. In order to achieve sustainable development, biotechnological methods have been specifically developed and implemented in various processes, including the manufacturing and energy industries. In order to promote the sustainability of these processes, it is important not only to use highly developed technology, but also to choose natural resources. Therefore, using bacterial resources instead of conventional terrestrial resources may be appropriate for these situations. However, further screening of microbes from different regions is required to transform bacteria into desirable precursors. Genetic engineering, such as molecular display technology, will continue to provide green tools for energy production in the future and will be widely used for bacterial utilization.

Bacteria contain several highly demanded compounds. There is a need to discover or develop solutions and technologies applicable to the conservation of bacterial habitats and

marine resources in order to sustain the harmonious use of bacteria in the life cycle.

## REFERENCES

1. Bindari YR, Shrestha S, Shrestha N, Gaire TN (2021) Effects of nutrition on reproduction-a review. *Adv Res Appl Sci.* 4(1):421-429.
2. Vanwonterghem I, Jensen PD, Ho DP, Batstone DJ, Tyson GW (2014) Linking microbial community structure, interactions and function in anaerobic digesters using new molecular techniques. *Curr Opin Biotechnol.* 27(1): 55-64.
3. Leroy F, de Vuyst L (2004) Lactic acid bacteria as functional starter cultures for the food fermentation industry. *Trends Food Sci Technol.* 15(2):67-78.
4. Welman AD, Maddox IS (2003) Exopolysaccharides from lactic acid bacteria: Perspectives and challenges. *Trends Biotechnol.* 21(6):269-274.
5. Okoro V, Azimov U, Munoz J. Recent advances in production of bioenergy carrying molecules, microbial fuels and fuel design-A review. *Fuel.* 316:123330.
6. Cao Y, Fanning S, Proos S, Jordan K, Srikumar S (2017) A review on the applications of next generation sequencing technologies as applied to food-related microbiome studies. *Front Microbiol* 8:1829.
7. Leigh MB, Pellizari VH, Uhlik O, Sutka R, Rodrigues J, et al. (2007) Biphenyl-utilizing bacteria and their functional genes in a pine root zone contaminated with Polychlorinated Biphenyls (PCBs). *The ISME J* 1(2): 134-148.
8. Preston-Mafham J, Boddy L, Randerson PF (2002) Analysis of microbial community functional diversity using sole-carbon-source utilisation profiles-a critique. *FEMS Microbiol Ecol* 42(1):1-4.
9. Torsvik V, Ovreas L (2002) Microbial diversity and function in soil: From genes to ecosystems. *Curr Opin Microbiol.* 5(3):240-245.
10. Smid EJ, Lacroix C (2013) Microbe-microbe interactions in mixed culture food fermentations. *Curr Opin Biotechnol.* 24(2):148-154.
11. Egan S, Thomas T, Kjelleberg S (2008) Unlocking the diversity and biotechnological potential of marine surface associated microbial communities. *Curr Opin Microbiol.* 11(3):219-225.
12. Broadhead R, Craeye L, Callewaert C (2021) The future of functional clothing for an improved skin and textile microbiome relationship. *Microorganisms.* 9(6):1192.