



The Role of Modern Biotechnology in the Fight against the Current and the Future Climate Change

Adugnaw Admas ^{a*} and Tileye Feyissa ^b

^a Ethiopian Forestry Development, Ethiopia.

^b Addis Ababa University, Ethiopia.

Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

Article Information

DOI: 10.9734/JABB/2024/v27i5822

Open Peer Review History:

This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: <https://www.sdiarticle5.com/review-history/113192>

Review Article

Received: 03/12/2023

Accepted: 07/02/2024

Published: 20/04/2024

ABSTRACT

Climate change causes various negative effects on plants, especially due to rapid changes in temperature, rainfall patterns, floods or droughts, and outbreaks of pests and diseases. Its change is predicted to cause widespread species expansion and extinction. Climate-induced local extinction has already occurred in hundreds of species. However, at the edge of the warm zone, an equal number of species were not exposed to local extinction, indicating that either phenotypic plasticity or genetic adaptations may allow some populations to persist in warmer conditions. This shows the importance of including intraspecific adaptations in climate change vulnerability assessments. In addition, in response to global climate change, the application of gene editing, also known as genome editing or genome engineering, has emerged as a technology to help organisms adapt to global climate change or mitigate climate impacts. Transforming agriculture by developing crops and livestock that can better withstand the effects of climate change is imperative. Gene editing allows precise changes to a plant's genome, speeding up the production of new crop varieties, including those better able to withstand the stress of a changing climate and those that

*Corresponding author: E-mail: adu.biot@gmail.com;

capture and store excess atmospheric carbon dioxide. The precision and efficiency of creating changes has greatly improved with the introduction of CRISPR/Cas systems, although there is certainly more work to be done with other gene editing techniques.

Keywords: Biotechnology; climate change; CRISPER/Cas; drought; gene editing.

1. INTRODUCTION

According to the Intergovernmental Panel on Climate Change (IPCC) group, climate change is the average change or variation in temperature, precipitation and wind patterns over the long term. According to the IPCC report, climate change is largely caused by anthropogenic causes, including human-induced changes in land use, as well as natural forces, such as solar cycles, volcanic eruptions, and continental drift [1].

Most effects of climate change concern soil and water quality, temperature for pests and pathogens, precipitation and weeds. Research data showed that agriculture is responsible for 25% of greenhouse gases and the main sources are methane (48%) and nitrous oxide (52%) from rice fields [2]. Greenhouse gases are both natural and man-made elements that prevent the reflection of radiation in the atmosphere and the warming of the environment. These gases are mainly emitted by industry and other activities, such as carbon dioxide (CO₂), methane (CH₄), nitrous oxide, hydrofluorocarbons (HFC) and sulfur dioxide (SF₆). In the long term, various activities increase their concentration in the atmosphere and lead to global climate change [3].

According to the United States Geological Survey, global warming is one of the aspects of climate change, and according to them, global warming is an increase in the temperature of the earth, which is mainly caused by an increase in the concentration of greenhouse gases in the atmosphere. Due to climate change, arable land is decreasing due to soil erosion, desertification and salinization. Drought threatens agriculture worldwide more than ever before. The Food and Agriculture Organization of the United Nations (FAO) documents that between 2005 and 2015, drought caused USD 29 billion in direct damage to agriculture in developing countries [4]. In addition, more than 70% of the world's available fresh water is used for irrigation [5].

On the other hand, genetic engineering, gives crops a greater advantage in response to stress than traditional breeding. In addition, genetically

modified soybeans, corn and cotton produced for insect resistance and weed tolerance have made very impressive and dramatic progress in pest control and crop improvement worldwide since their first introduction in 1996.

Climate change mitigation strategies in general is immediate goal to reduce the negative impact of environmental problems on land and water bodies. For example, reducing the concentration of greenhouse gases that can be emitted into the atmosphere by limiting the emission of industrial sewage and radioactive substances can be some measures that protect the earth from the effects of climate change. In addition, climate change can be contained through afforestation and other sinks (natural absorbers and adsorbents). Biotechnological methods currently used for mitigation purposes include tissue culture, bioremediation, biosorption, bioleaching, conventional breeding, molecular marker breeding, genetic engineering, and genome editing. Carbon reduction through biofuels, carbon sequestration, use of inorganic fertilizers etc. are other processes.

Hence, the purpose of this review paper is to give highlights the impact of biotechnology on climate change to address pressing environmental challenges through novel approaches that can operate at the scale and efficiency to describe the importance of biotechnology and its intervention in potential disasters resulting from climate change to avoid irreversible damage.

2. THE ROLE OF GENETIC VARIATION FOR ADAPTATION TO CLIMATE CHANGE

Genetic diversity is the most important requirement for all species to survive in the long term and adapt to environmental changes over evolutionary time [6,7].

Genetic structure is very important because it can provide insight into the history of a population, and the current levels and distribution of genetic variation can influence the future success of populations [8].

In some combination of natural selection and random genetic drift, a population separated by geographic distance may diverge due to gene flow and reduced population connectivity (isolation by geographic distance - IBD) [9]. However, population differences can emerge when reproductive isolation develops between neighboring populations in different environments as a result of ecologically based differential selection from isolating environment (IBE) [10].

Global climate change has become one of the greatest threats to biodiversity [11,12]. Species may respond to global climate change through local adaptation [13], individual migration [14,15] range reduction or a combination of these [16].

Local adaptations have been found to be a traditional way for various plant species to respond to climate change [17,18,19,20].

In addition, projected global warming will have dramatic effects on mountain ecosystems [21], especially alpine plant communities [22]. Vulnerability to climate change is most often assessed based on projected distributional changes using ecological niche modeling. This model can predict future changes in the distribution of suitable climatic conditions that characterize the current range of the species [23]. An important limitation of these models, which can lead to incorrect predictions and misplaced conservation efforts, is the neglect of adaptation to internal climate and the resulting differences in population response to climate change [24]. Evidence of contrasting patterns of physiological variation in thermal tolerance between and within species underscores the importance of including within-species variation in ecological niche models (ENM) of climate adaptation [25]. However, such model improvements are limited by the scarcity of observational and experimental studies on local climate adaptation [26].

“To date, studies attempting to incorporate genetic variation into an ecological niche model (ENM) have mostly used a neutral marker to identify phylogeographic structure and create separate models for each genetically distinct population. They led to more pessimistic projections than conventional ENMs, predicting an increased risk of climate change due to the loss of vulnerable populations, but did not affect projections of range size changes at the species level [27,28]. These experiments are limited in scope because neutral markers provide

information about the evolutionary history of species and barriers to gene flow, but not about the ability of individuals to adapt and survive under changing conditions. In addition, range shifts caused by future climate change are expected to result in the genetic homogenization of different species and the disappearance of historical and current population subdivisions [29].

Recent studies integrate genomic adaptations into ENM projections to identify vulnerable populations that need to adapt to survive future climate change [30,31]. However, genetic information related to interspecific variation in climate adaptation has yet to be directly incorporated into ENMs. To overcome these challenges, plant breeders began to produce new crop varieties that increased yield, tolerate abiotic stresses and improved water and nutrient consumption efficiency.

3. ADAPTATION OF AGRICULTURE TO CLIMATE CHANGE THROUGH PLANT BREEDING

In agriculture, drought can generally be defined as a prolonged lack of water that affects plant growth and survival, ultimately reducing crop productivity. In botany, the broadest definition of drought stress is the same as water deficit, which occurs when the rate of evaporation exceeds water consumption” [32]. This can be caused by a lack of water, but also increased salinity or osmotic pressure. From a molecular biology point of view, the first event during drought stress is water loss from the cell or dehydration. Desiccation typically triggers osmotic signals and hormones mainly related to abscisic acid (ABA) [33].

“Drought resistance is determined by how effectively and timely the plant senses changing environmental conditions and combining the environmental stresses in response to reduced water availability. Plant breeders have identified physiological traits that result from the drought response and facilitate plant adaptation to limited water. Understanding the molecular and physiological mechanisms underlying these traits is important for crop improvement through biotechnology. Biotechnology is a promising way to mitigate the negative effects of climate change by reducing greenhouse gases through biofuels[34] and carbon sequestration [35] less fertilizer [36]), biotic tolerance [37] and biotic stress [38].

4. THE ROLE OF MICROBES IN CLIMATE CHANGE RESILIENCE

Microbes are various organisms found on the surface of the earth. Plants themselves consist of many microbes found in them and in the soil ecosystem. Microbes are known to perform various ecological functions in nature. They regulate the concentration of greenhouse gases and influence the radiative forcing. Microbiota can influence both positive and negative feedbacks on climate tolerance. Several microbial species play important roles in carbon sequestration, carbon minimization and reduction of greenhouse gases such as CO₂, CH₄ and N₂O in the soil ecosystem [39]. Microbes such as bacteria and fungi effectively break down organic matter, which further stimulates global warming in the environment and the flow of carbon dioxide into the atmosphere. Microbial communities influence the biogeochemical cycle, nutrient cycling, carbon and methane cycle status in the atmosphere [40].

Microbial respiration is a key pathway for carbon dioxide efflux that promotes the natural release of carbon dioxide. On the other hand, methanotrophs play an important role as biological sinks that reduce methane emissions to the atmosphere. Microbial respiration is an important carbon dioxide emission pathway that contributes to the natural release of carbon dioxide. The plant microbiome also contributes to global food security by determining yield and climate resilience. Climate change mitigation is a necessary measure that can be achieved through several means. The use of biofertilizers composed of microorganisms such as bacteria and fungi can be an effective alternative to chemical fertilizers, as well as the use of biofuels instead of fossil fuels. Soil contains many microorganisms. Soil microbes play important roles in nutrient cycling, resistance to soil-borne pathogens, and regulation of climate change. Soil contains many microorganisms. Soil microbes participate in the decomposition of soil organic matter, regulate carbon supplies and nutrient cycling, and facilitate plant nutrient assimilation [41].

Modern green technologies such as biofertilizers composed of cyanobacteria, fungi (*arbuscular mycorrhiza*, AMF) and bacteria (plant growth-promoting *rhizobacteria*, PGPR) improve and restore soil fertility and ensure sustainable agricultural production. In addition, these microorganisms can reduce energy requirements

in the form of synthetic fertilizers and have the ability to alleviate stressed agricultural ecosystems and desert lands [42,43].

Sustainable agriculture includes soil, water and pest management, crop selection and soil conservation. This practice of sustainable agriculture combined with biotechnology can increase productivity by creating new transgenic plants, microbes and animals [44]. Cyanobacteria produce a number of valuable compounds such as ethanol, butanol, fatty acids and other organic acids and are promising candidates to continuously satisfy our energy needs. Recent advances in cyanobacterial genetic engineering, cultivation, and culture screening have enabled new ways to exploit the riches of these ancient microorganisms. Gene manipulation techniques are well developed for several cyanobacteria [45].

4.1 The Role of Cyanobacteria in Climate Change

Cyanobacteria play an important role in atmospheric nitrogen fixation and carbon fixation and sequestration [46,47] which are essential for plant nutrition and soil fertility.

Among nitrogen fixer cyanobacteria, *Oscillatoria*, *Nostoc*, *Anabaena*, etc., have a potential role in combating stress conditions in various plant species.

In terms of carbon dioxide capture, one of the most promising organisms is a cyanobacterium. These photosynthetic bacteria also improve the activity and diversity of the microbial community through symbiotic associations [48] and in addition to EPS, cyanobacteria can secrete several acids, hormones, amino acids and vitamins that promote plant growth and development [49]. Compared to the growth of other plants with beneficial bacteria (PGPB), after their death and decomposition, cyanobacteria can increase the water holding capacity and soil biomass. In addition, the ability of cyanobacteria to tolerate different salinities, reduces the fresh water for their cultivation, strengthening their values as NBS [50].

4.1.1 Cyanobacteria as a source of bioenergy

First and second generation biofuels use raw materials such as rapeseed, soybeans, sunflower, wheat, grass, peanuts and sesame. Various energy sources such as ethanol,

propanol, butanol and vegetable oils have been produced from these raw materials. However, energy crops used in the production of first and second generation biofuels compete with conventional food sources for water, nutrients and fertile land. Therefore, the third generation using microalgae has emerged as an alternative to biofuels to avoid competition between food crops and energy crops for available natural resources, and in addition, cyanobacteria are one of the most promising raw materials for the production of third generation biofuels.

Rapid growth and cultivation in suitable indoor bioreactors and/or non-cultivable soils gives cyanobacteria an advantage over plants. In addition, cyanobacteria show higher photosynthetic efficiency (~10%) compared to land plants (maximum efficiency ~3-4%) [51,52]. Blue-green algae are easier to genetically manipulate than other algae and are therefore better candidates for the production of chemicals and fuels compared to eukaryotic algae. The genome size of cyanobacteria is relatively small and the genomes of several genera have been sequenced so far. Therefore, cyanobacteria offer an exceptional opportunity for genetic and metabolic engineering research to improve biomass production, which is relatively difficult to do with eukaryotic algae [53].

Cyanobacteria contain significant amounts of lipids; located mainly in the thylakoids and plasma membranes and have greater growth and photosynthesis. Biofuel improvement of cyanobacteria using genetic engineering has been attempted mainly with *Synechocystis sp. PCC 6803* and *S. elongatus PCC 7942*, whose genomes were completely sequenced and established by molecular techniques [54]. Different fuels such as 2,3-butanediol, acetone-1-butanol, ethylene, ethanol, fatty acids, isobutyraldehyde, isobutanol, 2-methyl-1-butanol and isoprene can be produced in cyanobacteria using genetic engineering. Therefore, genetically engineered cyanobacteria can play a crucial role in reducing oil dependence and CO₂ emissions, since CO₂ is directly photosynthetically linked to biofuels and other valuable secondary metabolites [55,56]. However, the use of cyanobacteria for biofuel production has some limitations. Production of valuable chemicals in photoautotrophic cyanobacteria is always lower than in sugar-using systems such as *S. cerevisiae* and *E. coli* [57].

In general, a photoautotrophic cyanobacterial body can only produce ~100 mg of biochemicals per liter of cell culture [58] which is too little for a commercially viable application. "Theoretical yields for the production of several chemicals under heterotrophic and autotrophic growth conditions were calculated for the cyanobacterial body to explain the limiting factors of the cyanobacterial metabolic network [59]. But the study suggests that the low performance is not due to the topology of the photosynthetic metabolic networks of the cyanobacteria. Therefore, it is important to optimize the natural biological framework to increase the yield of cyanobacteria-derived biochemicals. In recent years, several groups have emphasized the construction, design, and expression of biosynthetic pathways and the development of cyanobacterial metabolic engineering tools that can lead to economic viability by increasing the production of existing and new chemicals and biofuels [60,61,63].

4.1.2 Cyanobacteria as biofertilizer

The production of inorganic nitrogen fertilizers is very expensive because it uses a lot of fossil fuel energy. This required the development of alternative, sustainable and cost-effective bioavailable nitrogen resources that can sustainably meet the nitrogen demand of agriculture [64]. To this end, biological systems capable of fixing atmospheric nitrogen have been identified [65,66].

Biological N fixation produces ~2 × 10² Mt N per year. According to Metting study the total nitrogen fixation can be ~90 kg N ha⁻¹ y⁻¹. Symbiotic and free-living eubacteria, including cyanobacteria, are two groups of nitrogen-fixing organisms. "Free-living cyanobacteria fix 10 kgN ha⁻¹ a⁻¹, but ~10–30 kgN ha⁻¹ per year is fixed by dense cyanobacterial worms [67,68]. Therefore, cyanobacteria are an important component in naturally available biofertilizers [69]. "Rice production in tropical countries depends mainly on biological N₂ fixation by cyanobacteria, which is a natural part of rice fields. In these cultivated agricultural systems, ~32 Tg of N are fixed annually by biological N-fixers, and cyanobacteria add approximately 20–30 kg of N fixed ha⁻¹ to rice fields along with organic matter [70]. Cyanobacteria also form symbiotic associations with various photosynthetic and non-photosynthetic organisms such as algae, fungi,

Table 1. List of nitrogen-fixing cyanobacteria important for their application in biofertilizer industry (adapted from Vaishampayan et al., 2001)

Filamentous		Unicellular
Heterocytous	Non- heterocytous	
<i>Anabaena</i> , <i>Anabaenosis</i> , <i>Aulosira</i> , <i>Calothrix</i> , <i>Camptylonema</i> , <i>Chlorogloea</i> , <i>Chlorogloeopsis</i> , <i>Cylindrospermum</i> , <i>Fischerella</i> , <i>Gloeotrichia</i> , <i>Haplosiphon</i> , <i>Mastigocladus</i> , <i>Nodularia</i> , <i>Nostoc</i> , <i>Nostochopsis</i> , <i>Rivularia</i> , <i>Scytonema</i> , <i>Scytonematopsis</i> , <i>Stigonema</i> <i>Tolypothrix</i> , <i>Westiella</i> , <i>Westiellopsis</i> , <i>Wollea</i>	<i>Lyngbya</i> , <i>Microcoleus</i> , <i>Chthonoplates</i> , <i>Myxosarcina</i> , <i>Oscillatoria</i> , <i>Plectonema Boryanum</i> , <i>Pseudoanabaena</i> , <i>Schizothrix</i> , <i>Trichodesmium</i>	<i>Aphanothecece</i> , <i>Chroococciopsis</i> , <i>Dermocarpa</i> , <i>Gloeocapsa</i> , <i>Myxosarcina</i> <i>Pleurocapsa</i> <i>Synechococcus</i> <i>XEnococcus</i>

diatoms, hornworts, liverworts, mosses, pteridophytes and angiosperms [71,72].

Lists of possible cyanobacteria that can be used as biofertilizers in agricultural fields are indicated in Table 1. Mixed cultures of free-living forms of cyanobacteria are used to propagate rice fields [73,74]. Significant increases in grain yield, biomass and nutritive value of rice can be achieved by inoculating *Anabaena doliolum* and *A. fertilissima* in rice fields with or without urea [75] (Dubey and Rai, 1995). Several species of cyanobacteria such as *Anabaena iyengarii* var. *considered*, *A. fertilissima*, *Nostoc community*, *N. ellipsosporum*, *N. linckia* and *Gloeotrichianatans* can contribute to the productivity of rice fields in Chile [76] (Pereira et al., 2009).

In addition to rice yield, cyanobacterial biofertilization can also improve wheat yield, shoot/root length and dry weight [77,78,79]. Soil inoculation with different cyanobacterial strains such as *Nostoc carneum*, *N. piscinale*, *Anabaena doliolum* and *A. torulosum* results in significantly higher acetylene-reducing activity [80].

Moreover, acetylene reducing activity is highest in harvest phase when wheat field is inoculated with *Anabaena-serratia* biofilm along with rock phosphate [81]. Biofertilizers based on cyanobacteria are one third more cost-effective than chemical fertilizers [82]. In addition to nitrogen fixation, cyanobacteria also contribute to the mobilization of inorganic phosphates through the secretion of organic acids and extracellular phosphatases [83]. Cyanobacteria solubilize and

mobilize insoluble organic phosphatase and improve phosphorus availability to crops. The humus content created after the death and decomposition of cyanobacteria creates strong reducing conditions in the soil, which improves soil structure and fertility [84].

Various cyanobacterial strains can produce plant growth hormones and siderophores, and therefore cyanobacteria can affect crop development and productivity [85,86]. EPS secreted by cyanobacteria induces soil aggregation, items that improve soil structure and fertility by increasing accumulation. Together, these findings confirm the importance of cyanobacteria as biofertilizers, and methods have been developed for their cultivation and use in the fertilizer industry [87,88].

4.1.3 The role of myco-biotechnology in climate change

Mycobiotechnology is the use of fungi to create various products. These methods use fungi to restore damaged ecology that endo- and ectomycorrhizal symbiotic fungi with actinomycetes have been used as inoculants to restore degraded forests. Mycoremediation tries to use mushrooms as an aid in the restoration of an ecologically weakened environment. Whether the environment has been damaged by a man-made or natural disaster, saprophytic and mycorrhizal fungi can help it recover. Afforestation would indirectly improve product safety and food security, as forests create a microclimate that can improve availability.

Fungal applications of biotechnology, called mycobotechnology, are part of a broader trend of using living systems to solve environmental problems and restore degraded ecosystems.

Various fungal species are generally distinguished by their biochemical, physiological and metabolic capacities to metabolize or degrade various hazardous or persistent chemicals. Myco-remediation could be one of the ideal strategies to clean the contaminated soil and water. Myco-remediation is economically efficient and ecological sound strategy to counter the escalating crisis of aquatic and terrestrial pollution. The advantages of fungi are mainly due to robust growth, immense hyphal network, production of multipurpose extracellular enzymes, and increased surface area to volume ratio, confrontation capabilities towards complex pollutants, adaptability to fluctuating pH, temperature, and having metal-binding proteins [89].

5. INCREASING THE UPTAKE OF CARBON DIOXIDE OF ORGANISMS BY GENETIC ENGINEERING

Plants, certain bacteria and algae continuously use photosynthesis to convert sunlight, water and atmospheric carbon dioxide (CO₂) into most of our food, furniture and fuel [90]. However, this process has become more complicated over time. Rubisco is an enzyme that transforms CO₂ into organic molecules. In turn, slow uptake of CO₂ limits the expansion of many plants, including crops such as rice and wheat [91]. However, some organisms have developed ways to concentrate carbon dioxide around Rubisco, allowing the enzyme to work faster [92]. Introducing such carbon-concentrating mechanisms to crops can increase yields by 60% while reducing the need for water and fertilizers [93]. The simplest understood mechanism of carbon concentration is the mechanism found in bacteria, predicted in the protein structure of the so-called carboxysome, which contains Rubisco and other enzymes involved in carbon fixation.

This species actively imports carbon in the form of bicarbonate (HCO₃⁻), which diffuses into the carboxysome and is converted to CO₂. The high CO₂ concentration achieved in the carboxysome maximizes Rubisco activity and thus increases total CO₂ absorption (Fig. 1).

A. *Halothiobacillus neapolitanus* has carboxysome-based carbon concentration mechanisms. The cell imports carbon dioxide as bicarbonate (HCO₃⁻), which diffuses into the carboxysome. Previous work succeeded in assembling a carboxysome-like structure in the non-photosynthetic model bacterium *Escherichia coli* [94]. However, these cells required a lot of carbon dioxide to grow, indicating that additional components are needed to concentrate the carbon dioxide. Now in eLife, David Savage, Ron Milo and colleagues, including first author Avi Flamholz, report how they require functional carbon concentration mechanisms in an organism that lacks one [95].

The team based at the University of California at Berkeley, the Weizmann Institute of Science and the Max Planck Institute for Molecular Plant Physiology chose the bacterium *Halothiobacillus neapolitanus* as the genetic donor for their experiment. The carboxysomes of this species are simple and well studied. In particular, Savage and workers previously identified 20 candidate genes likely to be necessary for the correct functioning of these structures [96].

As a receiving species, Flamholz *et al.*, 2020 chose *E. coli*, which they genetically engineered to rely on Rubisco for growth. Without the carbon concentration mechanism, this strain could not grow in ambient air, but required an additional concentration of carbon dioxide approximately 100 times greater than that in the atmosphere. Hoping to reintroduce a functional carbon concentration mechanism, the team transferred 20 candidate genes to *H. neapolitanus E. coli* strain. It is not surprising that the strain was initially unable to grow in ambient carbon dioxide, as simply adding genes is often not enough to

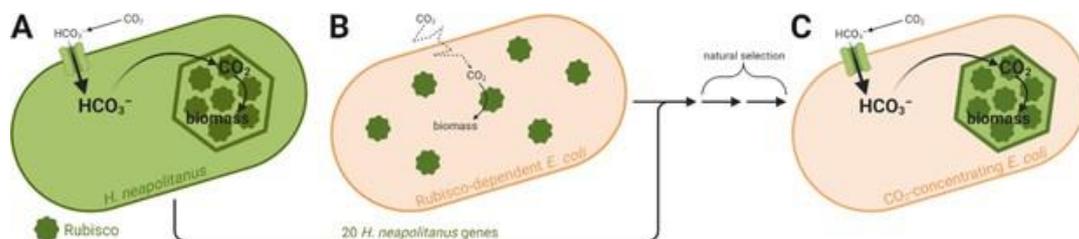


Fig. 1. Engineering a carbon-concentration into *E. coli*

form a complex pathway to a new organism [97]. However, Flamholz et al. could use genetically modified *E. coli* strain - its growth rate is proportional to Rubisco activity. This allowed the team to use a natural process experiment to identify mutations that cause the carbon concentration mechanism to malfunction, thereby increasing Rubisco activity. The experiment revealed a mutant that can grow at ambient CO₂ levels, apparently by regulating the expression level of proteins that cooperate in the carbon concentration process. This result indicated that the carboxysome-based carbon concentration mechanism of *H. neapolitanus* was successfully restored in their *E. coli* strain.

To further support this conclusion, electron microscopy was used to observe carboxysome-like structures in the engineered *E. coli* strain. To ensure the functionality of these constructs, they individually knocked out several genes known to be important for carboxysome function in the original host. These mutations had the same effect on *E. coli* than in *H. neapolitanus* - cells no longer grew at ambient CO₂ levels - confirming that the carboxysome functioned in the engineered strain as it did in the original host. These results of Flamholz et al. 2020 show that the carboxysome-based carbon concentration mechanism is transferable and functional in another organism, providing a blueprint that paves the way for engineered plants with increased carbon absorption and thus higher yields.

6. THE ROLE OF GENE EDITING IN COMBATING CLIMATE CHANGE

Climate change is a major threat to the environment in the long term because it affects agriculture, biodiversity, human society and almost every part of our world. The first cause of climate change is the addition of greenhouse gases caused by humans to the atmosphere. Due to these human-caused emissions, the average temperature of the planet has increased by almost 1 °C since 1850 [98,99]. In response to the challenges of global climate change, gene editing, also known as genome editing, has emerged as a technology to help organisms adapt to global climate change or mitigate the effects of climate change. In agriculture, developing crops and livestock that can better withstand the effects of climate change.

Gene editing can be a method to insert DNA editing at precise genomic locations. These

modifications can result in the deletion or destruction of one or more genes without the permanent addition of foreign DNA. Alternatively, genes from the genome of the organism or other organisms are inserted into precise locations in the genome to correct the trait. Transcription activator-like effector nucleases (TALEN), zinc finger nucleases (ZFN) and CRISPR/Cas systems have been used to achieve precise gene editing [100,101].

The precision and efficiency of creating changes has greatly improved with the introduction of CRISPR/Cas systems, although there is certainly more work to be done with other gene editing techniques. Because gene editing programs make it possible to make precise changes to a plant's genome and accelerate the production of new varieties of organisms, including those that can better withstand the stress of a changing climate and those that capture and store excess atmospheric carbon dioxide.

6.1 Roles of Gene Editing in Abiotic Stress

Future crops must be highly resistant to extreme heat and variable rainfall. In some species, such as rice, genes that confer tolerance to flooding have been identified at specific junctions, and once the genetic basis of tolerance is understood, gene editing can be used to propagate the trait more widely. However, the tolerance of most plants to drought, heat and flooding is due to the influence of several genes [102]. Basic research in species such as sorghum and millet helps us understand how these genes work [103].

6.2 Roles of Gene Editing in Resistance to Pests and Pathogens

Increased abiotic stress makes plants more susceptible to biotic stresses such as pathogens caused by insects, fungi and bacteria [104]. In addition, warmer temperatures increase the abundance of some pathogens and change their geographic distribution. Crop varieties resistant to fungal and bacterial pathogens are usually developed by crossing resistance genes from non-elite varieties or wild relatives to commercial varieties [105].

The hybrids are then crossed with a susceptible parent for several generations to eventually produce disease-resistant elite germplasm. Such breeding programs require significant time - up to

ten years for some species - which is dangerously slow due to rapid climate change. In just one year, gene editing has conferred tolerance to fungal pathogens in wheat [106] and bacterial pathogens in rice [107] by altering genes important for pathogen resistance and response.

6.3 Roles of gene editing for re-domestication

Considerably few plant species provide the food that sustains humanity. During the process of domestication, changes in the expression and activity of a handful of regulatory genes led to a remarkable physical transformation of wild stem cells into the high-yielding modern crops we rely on for food [108,109].

As the climate changes, we benefit from breeding new species that can withstand extreme weather conditions or thrive in marginal areas. Gene editing can greatly accelerate the domestication of these species by changing key regulatory genes to improve their productivity. One candidate for domestication is tef, a cereal crop from Ethiopia and Eritrea. Loss of seeds inhibits productivity.

7. ROLES OF GENETIC ENGINEERING IN CARBON SEQUESTRATION

Plants naturally bind carbon from the atmosphere and fix it in the above and below ground parts of the plant. Unfortunately, this carbon storage is often temporary. When plants die and decompose, carbon is released back into the atmosphere [110]. Gene editing could be used to redirect captured carbon into compounds more resistant to degradation, such as suberin, a carbon-rich compound found in the roots of many plants [111].

In addition, root architecture could be changed to increase underground biomass and thus increase the amount of carbon stored [112]. Even if there is a very small increase in the amount of carbon stored in the soil by larger row crops, millions of tons of carbon can be washed out of the atmosphere [113].

All plants carry out photosynthesis to capture carbon dioxide from the atmosphere, but some plants have developed much more efficient photosynthetic mechanisms. So-called C4 plants, such as corn and sugarcane, are up to 50% more efficient photosynthetically than C3 plants, such as rice and wheat [114].

8. THE ROLE OF SYNTHETIC BIOLOGY IN REDUCING ATMOSPHERIC GREENHOUSE GASES

prospects and challenges of synthetic biology uses the concept of engineering design to engineer, modify, and even resynthesize target organisms at the molecular level, creating new organisms or transforming existing organisms [115]. This process is usually driven by specific biological functions, including mining, designing, building and standardizing biological parts, devices, and genetic circuits, or sometimes complete chemical de novo DNA synthesis, building parts, devices, and circuits with new functions, forming assembled, tested and optimized in networks and platform cells.

Enabling technologies related to synthetic biology generally include DNA sequencing, DNA synthesis, gene editing, genome design, synthesis and assembly, design of biological parts (including new protein design), gene circuit design, computational and biological informatics, data processing and modeling. Using these technologies, it is possible to study functional genes and make cheap and efficient computer simulations of the design, construction and metabolism of these organisms to enable the practical development and application of synthetic biology for various purposes, including climate change mitigation.

9. CONCLUSION

The long residence time of carbon dioxide in the atmosphere creates an urgent need to include atmospheric carbon reduction in carbon control strategies. Gene editing, genetic engineering and synthetic biology can provide powerful approaches to reduce atmospheric carbon and increase new opportunities. Possibilities include converting carbon dioxide from respiration into stable carbonate, engineering plants with a higher root-to-shoot ratio, creating plants capable of self-fertilization, using genetic engineering to trap carbon dioxide in organisms, editing genetic engineering to invent DNA modifications precisely. genomic locations, and reengineering of biological elements not normally found in nature. However, several important environmental and social challenges must be faced and resolved before such an application can be evaluated, implemented and deployed.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. IPCC. Impacts, Adaptation, and Vulnerability. Intergovernmental Panel on Climate Change (Eds. J Houghton,). Cambridge University Press, Cambridge, UK; 2014.
2. Sallema RE, Mtui GYS. Adaptation technologies and legal instruments to address climate change impacts to coastal and marine resources in Tanzania. *Afr J Environ Sci Technol.* 2008;2(9):239-248.
3. Kumar A, Gupta T, Berzsenyi S, Giangrande A. N-cadherin negatively regulates collective Drosophila glial migration through actin cytoskeleton remodeling. *J. Cell Sci.* 2015;128(5):900--912.
4. FAO. The impact of disasters and crises on agriculture and food security". food and agriculture organization of the united nations; 2018.
5. Organization for Economic Cooperation and Development; 2017.
6. Falk DA, Knapp EE, Guerrant EO. An Introduction to Restoration Genetics. Plant Conservation Alliance, Bureau of Land Management, US Department of Interior, US Environmental Protection Authority. <http://www.ser.org/pdf/SER-restoration-genetics.pdf>. [Google Scholar]; 2001.
7. Frankham R. Stress and Adaptation in Conservation Genetics. *J. Evol. Biol.* 2005;18(4):750–755. DOI:10.1111/j.1420-9101.2005.00885.x
8. Erickson DL, Hamrick JL, Kochert GD. Ecological determinants of genetic diversity in an expanding population of the shrub *Myrica cerifera*. *Molecular Ecology.* 2004;13(6):1655–1664. DOI:10.1111/j.1365-294X.2004.02139.x
9. Nosil P, Rundle HD. *Ecological speciation*. Oxford University Press; 2012.
10. Wang IJ, Bradburd GS. Isolation by environment. – *Mol. Ecol.* 2014;23:5649–5662.
11. Davis MB, Shaw RG. Range shifts and adaptive responses to quaternary climate change. *Science.* 2001;292:673-679.
12. Parmesan C, Martens P. Climate change. In *Biodiversity, Health and the Environment: SCOPE/Diversitas Rapid Assessment Project*, ed. O Sala, L Meyerson, C Parmesan. Washington, DC: Island Press. In press; 2006.
13. Breshears DD, Huxman TE, Adams HD, Zou CB, Davison JE. Vegetation synchronously leans upslope as climate warms. *Proceedings of the National Academy of Sciences.* 2008;105(33):11591–11592. DOI:10.1073/pnas.0806579105
14. Lenoir J, Gegout JC, Marquet PA, De Ruffray P, Brisse H. A significant upward shift in plant species optimum elevation during the 20th century. *Science.* 2008;320(5884):1768–1771. DOI:10.1126/science.1156831
15. Thuiller W, Lavorel S, Araujo MB, Sykes MT, Prentice IC. Climate change threats to plant diversity in Europe. *Proceedings of the National Academy of Sciences.* 2005;102(23):8245–8250. DOI:10.1073/pnas.0409902102
16. Margaret BD, Ruth GS, Julie RE. Evolutionary responses to changing climate. *Ecology.* 2005;86(7):1704–1714. DOI:10.1890/03-0788
17. Coop G, Witonsky D, Di Rienzo A, Pritchard JK. Using environmental correlations to identify loci underlying local adaptation. *Genetics.* 2010;185(4):1411–1423. DOI:10.1534/genetics.110.114819
18. Gonzalez-Martinez SC, Krutovsky KV, Neale DB. Forest-tree population genomics and adaptive evolution. *New Phytologist.* 2006;170(2):227–238. DOI:10.1111/j.1469-8137.2006.01686.x
19. Hancock AM, Brachi B, Faure N, Horton MW, Jarymowycz LB, Sperone FG, Bergelson J. Adaptation to climate across the Arabidopsis thaliana genome. *Science.* 2011;334(6052):83–86.
20. Savolainen O, Pyhäjärvi T, Knürr T. Gene flow and local adaptation in trees. *Annual Review of Ecology, Evolution, and Systematics.* 2007;38(1):595–619. DOI:10.1146/annurev.ecolsys.38.091206.095646
21. Kohler T, Giger M, Hurni H, Ott C, Wiesmann U, Wymann von Dach S, Maselli D. Mountains and climate change: A global concern. *Mountain Research and Development.* 2010;30(1):53–55. DOI:10.1659/MRD-JOURNAL-D-09-00086.1

22. Gottfried M, Pauli H, Futschik A, Akhalkatsi M, Barančok P, Benito Alonso JL, Coldea G, Dick J, Erschbamer B, Fernández Calzado MR, Kazakis G, Krajči J, Larsson P, Mallaun M, Michelsen O, Moiseev D, Moiseev P, Molau U, Merzouki A, Grabherr G. Continent-wide response of mountain vegetation to climate change. *Nature Climate Change*. 2012;2:111–115. DOI:10.1038/nclimate1329
23. Bay RA, Harrigan RJ, Underwood VL, Gibbs HL, Smith TB, Ruegg K. Genomic signals of selection predict climate-driven population declines in a migratory bird. *Science*. 2018 Jan 5;359(6371):83-86. DOI: 10.1126/science.aan4380 PMID: 29302012
24. Shafer AB, Wolf JB, Alves PC, Bergström L, Bruford MW, Brännström I, Colling G, Dalén L, De Meester L, Ekblom R, Fawcett KD, Fior S, Hajibabaei M, Hill JA, Hoazel AR, Höglund J, Jensen EL, Krause J, Kristensen TN, Krützen M, McKay JK, Norman AJ, Ogden R, Österling EM, Ouborg NJ, Piccolo J, Popović D, Primmer CR, Reed FA, Roumet M, Salmona J, Schenekar T, Schwartz MK, Segelbacher G, Senn H, Thaulow J, Valtonen M, Veale A, Vergeer P, Vijay N, Vilà C, Weissensteiner M, Wennerström L, Wheat CW, Zieliński P. Genomics and the challenging translation into conservation practice. *Trends Ecol Evol*. 2015 Feb;30(2):78-87. DOI: 10.1016/j.tree.2014.11.009. Epub 2014 Dec 17 PMID: 25534246
25. Pacifici, Michela, Foden, Wendy, Visconti, Piero, Watson, James, Butchart, Stuart, Kovacs, Kit, Scheffers, Brett, Hole, David, Martin, Tara, Akcakaya, H. Resit, Corlett R, Huntley, Brian, Bickford, David, Carr, Jamie, Hoffmann, Ary, Midgley, Guy, Pearce-Kelly, Paul, Pearson, Richard, Williams, Stephen, Rondinini, Carlo. Assessing species vulnerability to climate change. *Nature Climate Change*. 2015;5:215-224. DOI:10.1038/nclimate2448
26. Hällfors MH, Liao J, Dzurisin J, Grundel R, Hyvärinen M, Towle K, Wu GC, Hellmann JJ. Addressing potential local adaptation in species distribution models: implications for conservation under climate change. *Ecol Appl*. 2016 32. Valladares F, Matesanz S, Guilhaumon F, Araújo MB, Balaguer L, Benito-Garzón M, Cornwell W, Gianoli E, van Kleunen M, Naya DE, Nicotra AB, Poorter H, Zavala MA. The effects of phenotypic plasticity and local adaptation on forecasts of species range shifts under climate change. *Ecol Lett*. 2014 Nov;17(11):1351-64. DOI: 10.1111/ele.12348. Epub 2014 Sep 9 PMID: 25205436
27. Slatyer RA, Nash MA, Hoffmann AA. Scale-dependent thermal tolerance variation in Australian mountain grasshoppers. *Ecography*. 2016;39:572–582.
28. Valladares F, Matesanz S, Guilhaumon F, Araújo MB, Balaguer L, Benito-Garzón M, Cornwell W, Gianoli E, van Kleunen M, Naya DE, Nicotra AB, Poorter H, Zavala MA. The effects of phenotypic plasticity and local adaptation on forecasts of species range shifts under climate change. *Ecol Lett*. 2014 Nov;17(11):1351-64. DOI: 10.1111/ele.12348. Epub 2014 Sep 9. PMID: 25205436. Jun;26(4):1154-69. DOI:10.1890/15-0926. PMID: 27509755.
29. Ikeda DH, Max TL, Allan GJ, Lau MK, Shuster SM, Whitham TG. Genetically informed ecological niche models improve climate change predictions. *Glob Chang Biol*. 2017 Jan;23(1):164-176. DOI: 10.1111/gcb.13470. Epub 2016 Sep 9 PMID: 27543682
30. D'Amen M, Zimmermann NE, Pearman PB. Conservation of phylogeographic lineages under climate change. *Glob EcolBiogeogr*. 2013;22:93–104.
31. Pauls SU, Nowak C, Bálint M, Pfenninger M. The impact of global climate change on genetic diversity within populations and species. *Mol Ecol*. 2013;22:925–946.
32. Bray EA. Plant responses to water deficit. *Trends Plant Sci*. 1997;2(2):48–54. DOI:10.1016/S1360-1385(97)82562-9
33. Blum A. Stress, strain, signaling, and adaptation –not just a matter of definition. *J. Exp. Bot*. 2015;67(3):562–565. DOI:10.1093/jxb/erv497
34. Lybbert T, Sumner D. Agricultural technologies for climate change mitigation and adaptation in developing countries: Policy options for innovation and technology diffusion. ICTSD-IPC Platform on Climate Change; 2010.

35. Kleter GA, Harris C, Stephenson G, Unsworth J. Comparison of herbicide regimes and the associated potential environmental effects of glyphosate-resistant crops versus what they replace in Europe. *Pest Manage Sci.* 2008;64(4):479-488.
36. Yan Y, Yang J, Dou Y, Chen M, Ping S, et al. Nitrogen fixation island and rhizosphere competence traits in the genome of root associated *Pseudomonas stutzeri* A1501. *Proc Nat Acad Sci.* 2008;105(21):7564-7569.
37. Hsieh TH, Lee JT, Yang PT, Chiu, LH, Chang YY, et al. Heterogy expression of *Arabidopsis* C-repeat/dehydration response element binding factor I gene confers elevated tolerance to chilling and oxidative stresses in transgenic tomato. *Plant Physiol.* 2002;129:1086-1094.
38. Barrows G, Sexton S, Zilberman D. *Agricultural Biotechnology: The Promise and Prospects of Genetically Modified Crops. J Economic Perspectives.* 2014;28(1):99-120.
39. Singh RB. Biotechnology, biodiversity and sustainable agriculture-a contradiction?" in Regional Conference in Agricultural Biotechnology Proceedings: Biotechnology Research and Policy -Needs and Priorities in the Context of Southeast Asia's Agricultural Activities, ed E. M. T. Mendoza (Bangkok: SEARCA (SEAMEO)/FAO /APSA); 2000.
40. Abatenh E, Gizaw B, Tsegaye Z, Tefera G. Microbial Function on Climate Change - A Review. *Environ Pollut Climate Change.* 2018;2:147.
DOI:10.4172/2573-458X.1000147
41. Abatenh E, Gizaw B, Tsegaye Z, Tefera G (2018) Microbial Function on Climate Change - A Review. *Environ Pollut Climate Change* 2: 147.
DOI:10.4172/2573-458X.100014
42. Abatenh, Endeshaw & Gizaw, Birhanu & Tsegaye, Zerihun & Genene, Tefera. (2018). Microbial Function on Climate Change - A Review. *Environment Pollution and Climate Change.* 02. 10.4172/2573-458X.1000147.
43. Mohammadi K, Sohrabi Y. Bacterial biofertilizers for sustainable crop production: A review. *J. Agric. Biol. Sci.* 2012;7:307–316.
DOI:10.1186/1475-2859-13-66
44. Singh RB. Biotechnology, biodiversity and sustainable agriculture-a contradiction?" in Regional Conference in Agricultural Biotechnology Proceedings: Biotechnology Research and Policy -Needs and Priorities in the Context of Southeast Asia's Agricultural Activities, ed E. M. T. Mendoza (Bangkok: SEARCA (SEAMEO)/FAO /APSA); 2000.
45. Rajneesh, Singh SP, Pathak J, Sinha RP. Cyanobacterial factories for the production of green energy and value-added products: An integrated approach for economic viability. *Renew. Sustain. Energy Rev.* 2017;69:578–595.
DOI: 10.1016/j.rser.2016.11.110
46. Mishra AK, Kaushik MS, Tiwari DN. Nitrogenase and Hydrogenase: Enzymes for Nitrogen Fixation and Hydrogen Production in Cyanobacteria. In *Cyanobacteria*; Mishra, A.K., Tiwari, D.N., Rai, A.N., Eds.; Academic Press: Cambridge, MA, USA, 2019;173–191. ISBN 978-0-12-814667-5
47. Schipper K, Al Muraikhi M, Alghasal GSHS, Saadaoui I, Bounnit T, Rasheed R, Dalgamouni T, Al Jabri HMSJ, Wijffels RH, Barbosa MJ. Potential of novel desert microalgae and cyanobacteria for commercial applications and CO2 sequestration. *J. Appl. Phycol.* 2019;31: 2231–2243.
48. Adams DG, Bergman B, Nierzwicki-Bauer SA, Duggan PS, Rai AN, Schüssler A. Cyanobacterial-Plant Symbioses. In *The Prokaryotes*; Rosenberg E, DeLong EF, Lory S, Stackebrandt E, Thompson F, Eds.; Springer: Berlin/Heidelberg, Germany, 2013;359–400. ISBN 978-3-642-30194-0
49. Mohan A, Kumar B. Plant Growth Promoting Activities of Cyanobacteria Growing In Rhizosphere of Agriculturally Fertile Soil. *J. Biotechnol. Biochem.* 2019;5:28–36.
Rady MM, Taha SS, Kusvuran S. Integrative application of cyanobacteria and antioxidants improves common bean performance under saline conditions. *Sci. Hortic. Amst.* 2018;233:61–69.
50. Kirsch F, Klähn S, Hagemann M. Salt-regulated accumulation of the compatible solutes sucrose and glucosylglycerol in cyanobacteria and its biotechnological potential. *Front. Microbiol.* 2019;10.
51. Lewis NS, Nocera DG. Powering the planet: Chemical challenges in solar energy utilization. *Proc. Natl. Acad. Sci. U.S.A.* 2006;103:15729–15735.

- DOI:10.1073/pnas.0603395103
52. Melis A. Solar energy conversion efficiencies in photosynthesis: Minimizing the chlorophyll antennae to maximize efficiency. *Plant Sci.* 2009;177:272–280. DOI:10.1016/j.plantsci.2009.06.005
 53. Rittmann BE. Opportunities for renewable bioenergy using microorganisms. *Biotechnol. Bioeng.* 2008;100:203–212. DOI:10.1002/bit.21875
 54. Kaneko T, Sato S, Kotani H, Tanaka A, Asamizu E, Nakamura Y, et al. Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis sp.* 6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions. *Res.* 1996;3:109–136.
 55. Ducat DC, Way JC, Silver PA. Engineering cyanobacteria to generate high-value products. *Trends Biotechnol.* 2011;29:95–103. DOI:10.1016/j.tibtech.2010.12.003
 56. Oliver NJ, Rabinovitch-Deere CA, Carroll AL, Nozzi NE, Case AE, Kaj Atsumi S. Metabolic technology of blue-green algae for the production of biofuels and chemicals. *Curr. Learn Chem. Biol.* 2016;35:43–50. DOI:10.1016/j.cbpa.2016.08.023
 57. Savakis P, Hellingwerf KJ. Engineered cyanobacteria for direct biofuel production from CO₂. *Curr. Learn Biotechnology.* 2014;33C:8-14. DOI:10.1016/j.copbio.2014.09.007
 58. Gao X, Sun T, Pei G, Chen L, Zhang W. Blue-green algae substrate design for enhanced production of biofuels and chemicals. *Application Microbiol. Biotechnology.* 2016;100:3401–3413. DOI: 10.1007/s00253-016-7374-2
 59. Gudmundsson S, Nogales J. Cyanobacteria as photosynthetic biocatalysts: A systems biology perspective. *Mol. Biosist.* 2015;11:60–70. DOI:10.1039/C4MB00335G
 60. Wang B, Wang J, Zhang W, Kaj Meldrum DR. Applications of synthetic biology in cyanobacteria and algae. *Before. Microbiol.* 3:44 in the morning; 2012. DOI:10.3389/fmicb.2012.00344
 61. Berla BM, Saha R, Immethun CM, Maranas CD, Moon TS, Pakrasi HB. Cyanobacterial synthetic biology: Unique challenges and opportunities. *Before. Microbiol.* 2006;4:246. DOI:10.3389/fmicb.2013.00246
 62. Desai SH, Kaj Atsumi S. Photosynthetic Approaches al Chemical Biotechnology. *Curr. Arvamus. Bioteknologio.* 2013;24:1031-1036. DOI:10.1016/j.copbio.2013.03.015
 63. Mahanty T, Bhattacharjee S, Goswami M, Bhattacharyya P, Das B, Ghosh A. et al. Biofertilizers: a potential approach to sustainable agricultural development. *The neighborhood. To know Contaminate Race. Rev.* 2017;24:3315–3335.
 64. Hegde DM, Dwiwedi BS, Babu S. N.S. (1999). Biofertilizers for cereal production in India: A review. *Indian J. Agriculture. Sci.* 1999;69:73–8.
 65. Vaishampayan A, Sinha RP, Hader DPK, Bhan U, et al. Bioferrous cyanobacteria in recultivated. *Ship. Rev. Fr.* 2001;67:453–516. DOI:10.1007/BF02857893
 66. Metting B. Mikroalgot en agrikultur, in *Micro-Algal Biotechnology*, ed. M.A. Borowitzka and L. J. Borowitzka (Cambridge: Cambridge University Press). 1988;288-304.
 67. Aiyer RS, Sulahudean S, Venkataraman GS. A long-term propagation field experiment with high-yielding rice varieties. *Indian, J. Agric. Theo.* 1972;42:380-383.
 68. Watanabe I, Spinus CR, Berja NSV. Uzo of Azolla-Anabaena complex kiel nitrogensterko by curl. *IRRI Res. Paper Ser.* 1977;11:1-15.
 69. Prasanna R, Sharma E, Sharma P, Kumar A, Kumar R, Gupta V, et al. Soil fertility and potential for inoculated cyanobacteria in rice crops grown under non-flooded conditions. *Paddy Water Environment.* 2013;11:175–183 . DOI:10.1007/s10333-011-0302-2
 70. Subramanian G, Sundaram SS. Evolution of ammonia from the nitrogenfixing cyanobacterium Anabaena. *FEMS Microbiol. Lett.* 1986;37:151–154. DOI:10.1111/j.1574-6968.1986.tb01784.x
 71. Rai AK, Kaj Sharma NK. Phosphate metabolome in the cyanobacterium Anabaena doliolum sub saline. *Curr. Microbiology.* 2006;52:6–12. DOI:10.1007/s00284-005-0043-9
 72. Sarma MK, Kaushik S, Goswami P. Cyanobacteria: Metabolic power to harvest solar energy for bioelectricity and biofuel production. *Biomaso Bioenergio.* 2016;90:187–201. DOI:10.1016/j.biombioe.2016.03.043

73. Venkataraman GS. Algal biofertilizer and rice cultivation. New Delhi: Printers and Publishers of Today and Tomorrow; 1972.
74. Roger PA, Kulasooriya SA. Blue green algae and rice. Manila: International Rice Research Institute; 1980.
Kannaiyan S, Aruna SJ, Kumari SMP, Hall DO. Immobilized cyanobacteria as biofertilizer for rice cultivation. J. Appl. Phycol. 1997;9:167–174.
DOI:10.1023/A:1007962025662
75. Dubey AK, Rai AK. Use of algal biofertilizers (*Aulosira fertilissimatenuis* and *Anabaena doliolum Bhardwaja*) for long-term rice cultivation in North India. Israel J. Plant. To know. 1995;43: 41–51.
DOI: 10.1080/07929978.1995.10676589
76. Pereira I, Rodrigo O, Barrientos L, Moya M, Reyes G, Kramm V. Development of a biofertilizer based on filamentous nitrogen-fixing cyanobacteria for rice cultivation in Chile. J. Apliko de Phycol. 2009;21:135–144.
DOI:10.1007/s10811-008-9342-4
77. Spiller H, Gunasekaran M. An ammonia-secreting mutant strain of the cyanobacterium *Anabaena variabilis* supports wheat growth. Application Microbiol. Biotechnology. 1990;33:477–480.
DOI:10.1007/BF00176670
78. Obreht Z, Kerby NW, Gantar M, Rowell P. Effects of root-associated N₂-fixing cyanobacteria on growth and nitrogen content of wheat (*Triticum vulgare L.*) seedlings. Biol. Fekunda. Grundoj. 1993;15:68–72.
DOI:10.1007/BF00336292
79. Karthikeyan N, Prasanna R, Sood A, Jaiswal P, Nayak S, Kaushik BD. Physiological characterization and electron microscopic studies of wheat rhizosphere-associated cyanobacteria. Leaf Microbiol. 2009;54:43–51.
DOI:10.1007/s12223-009-0007-8
80. Swarnalakshmi K, Prasanna R, Kumar A, Pattnaik S, Chakravarty K, Shivay YS, et al. Evaluation of the effects of novel cyanobacterial biofilmed biofertilizers on wheat soil fertility and plant nutrition. Euros J. Soil Biol. 2013;55:107–116.
DOI:10.1016/j.ejsobi.2012.12.008
81. Bose P, Nagpal USA Tricalcium phosphate solution of cyanobacteria. Curr. Sci. 1971;40:165–1.
Rai AK, Sharma NKK. Phosphate metabolome in the cyanobacterium *Anabaena doliolum* sub saline. Curr. Microbiology. 2006;52:6–12.
DOI: 10.1007/s00284-005-0043-9
82. Dorich RA, Nelson DW, Cage Sommers LE. Estimation of algal available phosphorus in suspended sediments using chemical extraction. J. Environment. Quality. 1985;14:400–405.
DOI:10.2134/jeq1985.00472425001400030018x
83. Cameron HJ, Kaj Julian GR. Utilization of hydroxyapatite by cyanobacteria as a sole source of phosphate and calcium. Plant Earth. 1988;109:123–124.
DOI:10.1007/BF02197589
84. Abdel-Raouf N, Al-Homaidan AA, Ibrahim IB. The importance of algae in agriculture. African J. Biotechnol. 2012;11:11648–11658 .
DOI:10.5897/AJB11.3983
85. Rodriguez AA, Stella AM, Storni MM, Zulpa G, Zaccaro MC. Effects of cyanobacterial extracellular products and gibberellic acid on salinity tolerance of *Oryza sativa L.* Saline Syst. 2006;2:7.
DOI:10.1186/1746-1448-2-7
86. Rastogi RP, Sinha RP. Biotechnological and industrial importance of cyanobacterial secondary metabolites. Biotechnology. Adv. 2009;27:521–539.
DOI:10.1016/j.biotechadv.2009.04.009
87. Brouers M, De Jong H, Shi DJ, Rao KK, Hall DO. Continuous production of ammonia by immobilized cyanobacteria. Program Photosynth. Race. 1987;2:645–647.
DOI:10.1007/978-94-009-3535-8_153
88. Sh DJ, Hall DO. The Azolla-Anabaena association: A historical perspective, symbiosis and energy metabolism. Bot. Rev. 1988;54:253–386.
DOI:10.1007/BF02858416
89. Saikia SP, Vanita Jain. Biological Nitrogen Fixation with Non-Legumes: An Achievable Target or a Dogma? Current Science. 2007;92(3):317–22.
Available:<http://www.jstor.org/stable/24096726>
90. Fischer WW, Hemp J, Johnson JE. Evolution of oxygenic photosynthesis Annual Review of Earth and Planetary Sciences. 2016;44:647–683.
Available:<https://doi.org/10.1146/annurev-earth-060313-05481>

91. Long SP, Zhu X, Naidu S, LOrt DR. Can improvement in photosynthesis increase crop yields? *Plant, Cell and Environment*. 2006;29:315–330. Available: <https://doi.org/10.1111/j.1365-3040.2005.01493.x>
92. Hennacy JH, Jonikas MC. Prospects for engineering biophysical CO₂ concentrating mechanisms into land plants to enhance yields *Annual Review of Plant Biology*. 2020;71:461–485. Available: <https://doi.org/10.1146/annurev-arplant-081519-040100>
93. McGrath J, Mlong SP. Can the cyanobacterial carbon-concentrating mechanism increase photosynthesis in crop species? A theoretical analysis *Plant Physiology*. 2014;164:2247–2261.
94. Bonacci W, Teng PKA, fonso BN, iederholtmeyer H, Grob P, Silver PA, Savage DF. Modularity of a carbon-fixing protein organelle *PNAS*. 2012;109:478–483. Available: <https://doi.org/10.1073/pnas.1108557109>
95. Flamholz AI, Dugan EB, Iikstad C, Gleizer S, Ben-Nissan RA, Mram S, Antonovsky N, Ravishankar S, Noor E, Bar-Even A, Milo R, Savage DF. Functional reconstitution of a bacterial CO₂ concentrating mechanism in *Escherichia coli* *eLife*. 2020;9:e59882. Available: <https://doi.org/10.7554/eLife.59882>
96. Desmarais JJ, Flamholz AI, Blikstad CD, ugan EJ, Laughlin TG, Oltrogge LM, Chen AW, Wetmore K, Diamond S, Wang JY, Savage DF. DABs are inorganic carbon pumps found throughout prokaryotic phyla *Nature Microbiology*. 2019;4:2204–2215. Available: <https://doi.org/10.1038/s41564-019-0520-8>
97. Antonovsky N, Gleizer S, Noor E, Zohar Y, Herz E, Barenholz U, Zelcbuch L, Amram S, Wides A, Tepper N, Davidi D, Bar-On Y, Bareia T, Wernick D, GShani I, Malitsky Jona G, Bar-Even A, Milo R. Sugar synthesis from CO₂ in *Escherichia coli* *Cell*. 2016;166:115–125.
98. IPCC. “Summary for policymakers,” in *Global Warming of 1.5°C. An IPCC Special Report on the Impacts of Global Warming of 1.5°C Above Pre-industrial Levels and Related Global Greenhouse Gas Emission Pathways, in the Context of Strengthening the Global Response to the Threat of Climate Change, Sustainable Development, and Efforts to Eradicate Poverty*, eds V. Masson-Delmotte P, Zhai HO, Pörtner D, Roberts J, Skea PR. Shukla, et al. (Geneva: World Meteorological Organization); 2018
99. Nunez S, Arets E, Alkemade R, Verwer C, Leemans R. Assessing the impacts of climate change on biodiversity: is below 2 °C enough? *Clim. Change*. 2019;154:351–365. DOI: 10.1007/s10584-019-02420-x.
100. Gaj T, Sirk SJ, Shui S, Liu J. Genome-editing technologies: principles and applications. *Cold Spring Harb. Perspect. Biol.* 2016;8:a023754. DOI:10.1101
101. Khalil AM. The genome editing revolution: Review. *J. Genet. Eng. Biotechnol.* 2020;18:68. DOI:10.1186/s43141-020-00078-y
102. Wang J, Li C, Li L, Reynolds M, Mao X, Jing R. Exploitation of Drought Tolerance-Related Genes for Crop Improvement. *International Journal of Molecular Sciences*. 2021;22.
103. Woldesemayat AA, Van Heusden P, Ndimba BK, Christoffels A. An integrated and comparative approach towards identification, characterization and functional annotation of candidate genes for drought tolerance in sorghum (*Sorghum bicolor* (L.) Moench). *BMC Genetics*. 2017;18:119. Available: <https://doi.org/10.1186/s12863-017-0584-5>
104. Coakley SM, Scherm H, Chakraborty S. Climate change and plant disease management. *Annu. Rev. Phytopathol.* 1999;37:399–426. Available: <https://doi.org/10.1146/annurev.phytopathol.37.1.399>
105. Scheben A, Wolter F, Batley J, Puchta H, Edwards D. Towards CRISPR/Cas crops – bringing together genomics and genome editing. *New Phytologist*. 2017;216:682–698. Available: <https://doi.org/10.1111/nph.14702>
106. Wang Y, Cheng X, Shan Q, Zhang Y, Liu J, Gao C, Qiu JL. Simultaneous editing of three homoeoalleles in hexaploid bread wheat confers heritable resistance to powdery mildew. *Nature Biotechnology*. 2014;32:947–951. Available: <https://doi.org/10.1038/nbt.2969>

107. Li T, Liu B, Spalding MH, Weeks DP, Yang B. High-efficiency TALEN-based gene editing produces disease-resistant rice. *Nature Biotechnology*. 2012;30:390–392. Available:<https://doi.org/10.1038/nbt.2199>
108. Doebley JF, Gaut BS, Smith BD. The molecular genetics of crop domestication. *Cell*. 2006;127:1309-1321. Available:<https://doi.org/10.1016/j.cell.2006.12.006>
109. Meyer RS, Purugganan MD. Evolution of crop species: Genetics of domestication and diversification. *Nature Reviews Genetics*. 2013;14:840–852. Available:<https://doi.org/10.1038/nrg3605>
110. Mulligan J, Ellison G, Gasper R, Rudee A. Carbon Removal in Forests and Farms in the United States. Working Paper. Washington, DC: World Resources Institute; 2018. Available:<https://www.wri.org/publication/land-carbon-removal-us>
111. Schweitzer H, Aalto NJ, Busch W, Chat Chan DT, Chiesa M, et al. Innovating carbon-capture biotechnologies through ecosystem-inspired solutions. *One Earth*. 2021;4:49–59. Available:<https://doi.org/10.1016/j.oneear.2020.12.006>
112. Ogura T, Goeschl C, Filiault D, Mirea M, Slovak R, et al. Root System Depth in Arabidopsis Is Shaped by EXOCYST70A3 via the Dynamic Modulation of; 2019.
113. Mulligan J, Ellison G, Gasper R, Rudee A. Carbon Removal in Forests and Farms in the United States. Working Paper. Washington, DC: World Resources Institute. Auxin Transport. *Cell*. 2018;178: 400-412.e16. Available:<https://www.wri.org/publication/land-carbon-removal-us> Available:<https://doi.org/10.1016/j.cell.2019.06.021>
114. Hibberd JM, Sheehy JE, Langdale JA. Using C4 photosynthesis to increase the yield of rice—rationale and feasibility. *Current Opinion in Plant Biology*. 2008;11:228–231. Available:<https://doi.org/10.1016/j.pbi.2007.11.002>
115. Zhang W, Zhang T, Wu S, Wu AL, Xin F, Dong W, et al. Guidance for engineering of synthetic methylotrophy based on methanol metabolism in methylotrophy. *RSC Adv*. 2017;7:4083–4091. DOI:10.1039/C6RA27038G

© Copyright (2024): Author(s). The licensee is the journal publisher. This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/4.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Peer-review history:

The peer review history for this paper can be accessed here:
<https://www.sdiarticle5.com/review-history/113192>