Review Article

The role of modern biotechnology in the fight against the current and the coming climate change

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 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

Key words : **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 (IPCC, 2014).

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 (Sallema and Mtui, 2008). 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 (Kumar et al., 2015).

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. In addition, more than 70% of the world's available fresh water is used for irrigation (Organization for Economic Cooperation and Development, 2017).

Climate change is predicted to cause widespread distribution and extinction of species (Urban, 2015), and climate-related local extinctions have already occurred in hundreds of species. However, an equal number of species at the edge of the warm zone did not experience local extinction (Wiens, 2016), indicating that either phenotypic plasticity or genetic adaptations may allow some populations to persist in warmer conditions. This shows that it is important to include intraspecies adaptations in the assessment of vulnerability to climate change (Savolainen et al., 2013; Bay et al., 2018). Biotechnology, especially 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 generalis 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 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 reviwe paper is 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.Therole 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 (Falk *et al*., 2001; Frankham, 2005).

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 (Erickson *et al.*, 2004).

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) (Nosil and Rundle, 2012). 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) (Wang and Bradburd, 2014).

Global climate change has become one of the greatest threats to biodiversity (DavisandShaw,2001; Parmesano, 2006). Species may respond to global climate change through local adaptation (Parmesano, 2006), individual migration (Breshear*et al.*, 2008; Lenoir *et al*., 2008), range reduction (Thiller *et al.*, 2005), or a combination of these (Margaret *et al*., 2005).

Local adaptations have been found to be a traditional way for various plant species to respond to climate change (Coop *et al*., 2010; Gonzalez-Martninezetal., 2006; Hancock *et al*., 2011; Savolainen *et al*., 2007).

In addition, projected global warming will have dramatic effects on mountain ecosystems (Kohler *et al.*, 2010), especially alpine plant communities (Gottfried *et al*., 2012). 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 (Bay *et al*., 2017). 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 (Shafer *etal*., 2015). 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 (Pacifici *et al*., 2015). However, such model improvements are limited by the scarcity of observational and experimental studies on local climate adaptation (Hällfors, *et al.*, 2016).

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 (Slatye*etal.*, 2016), but did not affect projections of range size changes at the species level (Valladares *et al*.., 2014). 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 (Ikeda *et al*., 2017).

Recent studies integrate genomic adaptations into ENM projections to identify vulnerable populations that need to adapt to survive future climate change (D'Amen*et al*., 2017;Paul*setal*., 2013). 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 (Fita *et al*., 2015).

3Adaptation 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 (Bray, 1997). 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) (Blum, 2015).

Drought resistance is determined by how effectively and timely the plant senses changing environmental conditions and combining the enviromentalstreesin 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 (Lybbertand Sumner D, 2010) and carbon sequestration (Kleter*etal*. , 2008), less fertilizer (Yan *et al*., 2008), biotic tolerance (Hsieh *et al.*, 2002) and biotic stress (Barrows *et al*., 2014)

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 CO_2, CH_4 and N_2O (Singh *et a*l., 2010) in the soil ecosystem. 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 (Abatenh*et al*., 2018).

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 (Delgado *et al*; 2020).

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 (Du *et al*., 2007; Mohammadi and Sorabi, 2012).

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 (Singh, 2000). 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 (Rajineesh*et al*., 2017).

4.1. The role of cyanobacteria in climate change

Cyanobacteria play an important role in atmospheric nitrogen fixation and carbon fixation and sequestration (Mishra et al; 2019; Schipper *et al*; 2019), 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 (Berla et al., 2013; Nozzi etal.,2013; Case and Atsumi, 2016). These photosynthetic bacteria also improve the activity and diversity of the microbial community through symbiotic associations (Adams et al; 2013) and in addition to EPS, cyanobacteria can secrete several acids, hormones, amino acids and vitamins that promote plant growth and development (Mohan et al; 2019). 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 (Rady et al; 2018) In addition, the ability of cyanobacteria to tolerate different salinities. reduces the fresh water for their cultivation, strengthening their values as NBS (Kirsch et al; 2019) .

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 (Quintana *et al*., 2011). 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 (Quintana*et al*., 2011; Al-Haj *et al*., 2016; Rajneesh *et al.*, 2017).

Rapid growth and cultivation in suitable indoor bioreactors and/or non-cultivable soils gives cyanobacteria an advantage over plants (Singh, 2014; Sarma *et al.*, 2016). In addition, cyanobacteria show higher photosynthetic efficiency (~10%) compared to land plants (maximum efficiency ~3-4%) (Lewis and Nocera, 2006; Melis, 2009). 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 (Rajneesh *et al*., 2017). 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 (Rittmann, 2008).

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 (Kaneko et al., 1996). 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 (Ducat *et al.,* 2011; Oliver *et al*., 2016). 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* (Savakis and Hellingwerf, 2014).

In general, a photoautotrophic cyanobacterial body can only produce ~100 mg of biochemicals per liter of cell culture (Gao *et al*., 2016), 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 (Gudmundsson and Nogales, 2015). 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 (Wang *et al*., 2012; Berla *et al.,* 2013; Desai and Atsumi, 2013; Oliver and Atsumi, 2014; Gudmundsson and Nogales, 2015; Markley *et al*., 2015).

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 (Mahanty*et al*., 2017). To this end, biological systems capable of fixing atmospheric nitrogen have been identified (Hegde *et al*., 1999; Vaishampayan *et al*., 2001).

Biological N fixation produces ~2 × 102 Mt N per year (Guerrero *et al.,* 1981). According to Metting (1988), 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 kg N ha−1a−1, but ~10–30 kg N ha−1 per year is fixed by dense cyanobacterial worms (Aiyer *et al.,* 1972; Watanabe *et al.,* 1977). Therefore, cyanobacteria are an important component in naturally available biofertilizers (Vaishampayan *et al., 2001*; Prasanna *et al.,* 2013). Rice production in tropical countries depends mainly on biological N2 fixation by cyanobacteria, which is a natural part of rice fields (Vaishampayan *et al.,* 2001). In these cultivated agricultural systems, ~32 Tg of N are fixed annually by biological N-fixers (Singh *et al.,* 2016), and cyanobacteria add approximately 20–30 kg of N fixed ha−1 to rice fields along with organic matter (Subramanian and Sundaram, 1986; Issa *et al.,* 2014). Cyanobacteria also form symbiotic associations with various photosynthetic and non-photosynthetic organisms such as algae, fungi, diatoms, hornworts, liverworts, mosses, pteridophytesand angiosperms(Rai et al., 2000; Sarma *et al*. 2006).

Cyanobacteria show a higher photosynthetic efficiency ((~10%) compared to land plants (~3-4% maximum efficiency)) (Lewis and Nocera, 2006; Melis., 2009). Cyanobacteria can be genetically manipulated more easily than other algae and thus, act as target chemicals and better than eukaryotic algae in fuel production. The genome size of cyanobacteria is relatively small and the genomes of several genera have been sequenced so far (Rajneesh *et al.,* 2017).

Therefore, cyanobacteria can develop genetic and metabolic technology to produce biomass, which is relatively difficult for eukaryotic algae to do(Rittmann, 2008). This species contains

significant amounts of lipids; especially is located in thylakoids and plasma membranes and shows faster growth and photosynthesis.

The production of biofuels from cyanobacteria through genetic engineering was observed mainly in *synechocystissp.pcc6803 and s.elongatus pcc7942,*whose genomic DNA was completely sequenced (Kaneko *et al.*, 1996). Thus, genetically enhanced cyanobacteria can play a crucial role in reducing oil dependence and carbon dioxide emissions, because carbon dioxide photosynthetically combines directly with biofuels and other valuable secondary metabolic products(Ducat *et al*., 2011; Oliver *et al*., 2016).

Genera of heterocytic cyanobacteria such as *Nostoc, Anabaena, Nodularia, Scytonema, Cylindrospermum, Mstigocladus, Calothrix, Anabaenopsis, Aulosira, Tolypothrix, Haplosiphon, Campptylonema, Stigonema, Fischerella, Chlopsiofix, Westrogstiarog***(**Vaishampayan, 1993). **Lists of possible cyanobacteria that can be used as biofertilizers in agricultural fields (Vaishampayan *et al*., 2001) are indicated Table 1.**Mixed cultures of free-living forms of cyanobacteria are used to propagate rice fields (Venkataraman, 1972; Roger and Kulasooriya, 1980). The water fern *Azolla* carries *Anabaena azollae* on its fronds, and the cyanobacterium releases ammonium into water when rice fields are inoculated with foam-immobilized strains of *A. atolli* (Kannaiyan *et al.*, 1997). 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 (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 (Pereira *et al*., 2009). In general, 12.5 kg ha−1 cyanobacterial biofertilizers are recommended for quantitative and qualitative improvement of rice production (Dubey and Rai, 1995).

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

Filamentous		Unicellular
Heterocystous	**Non-heterocystous**	
Anabaena, Anabaenopsis, Aulosira, Calothrix, Camptylonema, Chlorogloea, Chlorogloeopsis, Cylindrospermum, Fischerella, Gloeotrichia, Haplosiphon, Mastigocladus, Nodularia, Nostoc, Nostochopsis, Rivularia, Scytonema, Scytonematopsis, Stigonema, Tolypothrix, Westiella, Westiellopsis, Wollea	*Lyngbya, Microcoleus chthonoplastes, Myxosarcina, Oscillatoria, Plectonema Boryanum, Pseudoanabaena, Schizothrix, Trichodesmium*	*Aphanothece, Chroococcidiopsis, Dermocarpa, Gloeocapsa, Myxosarcina, Pleurocapsa, Synechococcus, Xenococcus*

In addition to rice yield, cyanobacterial biofertilization can also improve wheat yield, shoot/root length and dry weight (Spiller and Gunasekaran, 1990; Obreht*et al.*, 1993; Karthikeyan *et al.,* 2009). Soil inoculation with different cyanobacterial strains such as *Nostoc carneum, N.piscinale, Anabaena doliolum and A.torulosa*results in significantly higher acetylene-reducing activity (Prasanna *et al*., 2013).

Moreover, acetylene reducing activity is highest in harvest phase when wheat field is inoculated with *Anabaena-serratia* biofilm along with rock phosphate (Swarnalakshmi*et al*., 2013). Biofertilizers based on cyanobacteria are one third more cost-effective than chemical fertilizers (Prasanna *et al*., 2013). In addition to nitrogen fixation, cyanobacteria also contribute to the mobilization of inorganic phosphates through the secretion of organic acids and extracellular phosphatases (Bose and Nagpal, 1971; Rai and Sharma, 2006). Cyanobacteria solubilize and mobilize insoluble organic phosphatase and improve phosphorus availability to crops (Dorich et al., 1985; Cameron and Julian, 1988). The humus content created after the death and decomposition of cyanobacteria creates strong reducing conditions in the soil, which improve soil structure and fertility (Abdel-Raouf *et al.*, 2012).

Various cyanobacterial strains can produce plant growth hormones and siderophores, and therefore cyanobacteria can affect crop development and productivity (Rodriguez *et al*., 2006; Rastogi and Sinha, 2009). 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 (Brouers*et al.*, 1987; Shi and Hall, 1988; Vaishampayan *et al.*, 2000).

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. .Mycorestoration 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.

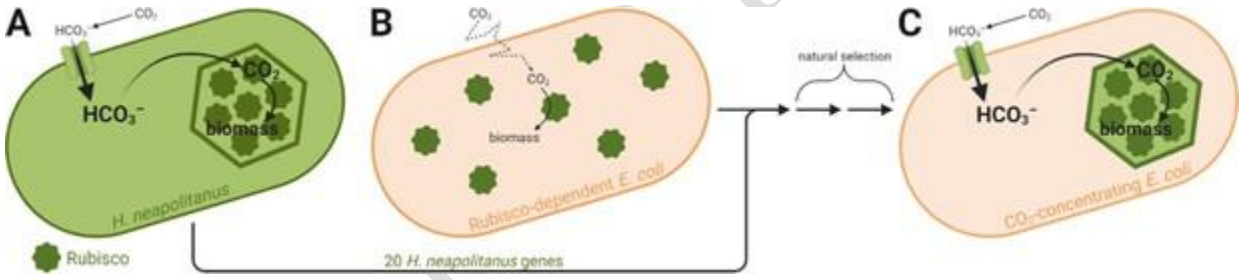
Fungal applications of biotechnology, called mycobiotechnology, are part of a broader trend of using living systems to solve environmental problems and restore degraded ecosystems((Saikia and Jain, 2007) .

Various fungal species are generally distinguished by their biochemical, physiological and metabolic capacities to metabolize or degrade various hazardous or persistent chemicals (Barrech*et al.,* 2018). 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 (Kumar, 2021).

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 (Fischer *et al.,* 2016). However, this process has become more complicated over time. . Rubisco is an

enzyme that transforms CO2 into organic molecules. In turn, slow uptake of CO limits the expansion of many plants, including crops such as rice and wheat (Long *et al.,* 2006). However, some organisms have developed ways to concentrate carbon dioxide around Rubisco, allowing the enzyme to work faster (Hennacy and Jonikas, 2020). Introducing such carbon-concentrating mechanisms to crops can increase yields by 60% while reducing the need for water and fertilizers (McGrath and Long, 2014). 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 (Figure 1)



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

A.*Halothiobacilusneapolitanus* 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 (Bobacci*et al.,* 2012). 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 AviFlamholz, report how they require functional carbon concentration mechanisms in an organism that lacks one (Flamolz*etal.,* 2020).

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 *Halothiobacilusneapolitanus* as the genetic donor for their experiment. The carboxysomes of this species are simple and well studied. In particular, Savgeabd workers previously identified 20 candidate genes likely to be necessary for the correct functioning of these structures (Desmarais *et al.,* 2019).

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 form a complex pathway to a new organism (Antonovsky *et al.,* 2016). However, Flamholzet 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 Flamholzet 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 (IPCC, 2018; Nunez *et al.*, 2019).

In response to the challenges of global climate change, gene editing, also known as genome editinghas 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 invent 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 (Gaj*et al.*, 2016; Khalil, 2020).

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(ku*etal.*,2006).However, the tolerance of most plants to drought, heat and flooding is due to the influence of several genes(Wang etal.,2021) .Basic research in species such as sorghum and millet helps us understand how these genes work(Woldesemayat*etal*.,2017;Tang*etal.*, 2017).

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(Coakley *etal.*,1999).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(Scheben *etal.*,2017).

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 (Wang*etal.*,2014)and bacterial pathogens in rice (Li *etal.*,2012)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(Doebley, 2006;Meyer and Purugganan,2013).

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.

6.4. Improvement of heat tolerance in cattle by genetic modification

In animals, gene editing has also been applied to mitigate abiotic stress caused by global climate change. Recombinetics Inc. subsidiary Acceligen launched an initiative to improve heat tolerance in cattle with the support of Food and Agriculture Research (FFAR) and Semex. Researchers initially focused on reproducing the SLICK phenotype identified in Senepoli cattle through gene editing. Variants of this phenotype in cattle contribute to heat tolerance (Dikmen*et al.,* 2014; Porto-Neto *et al*., 2018). Conventionally bred cattle with SLICK genetics are more heat tolerant as shown by lower vaginal temperature, lower rectal temperature, lower respiratory rate and increased sweating, leading to increased milk production during the summer months (Dikmen*et al.,* 2014). Acceligen aims to reproduce SLICK genetics using gene editing techniques to increase heat tolerance in important cattle breeds (Bellini, 2018).

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(Mulligan *etal.*,2018) .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(Schweitzer *etal.*,2021) .

In addition, root architecture could be changed to increase underground biomass and thus increase the amount of carbon stored (Ogura *etal.*,2019).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(Mulligan*eta*l.,2018).

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(Hibberd *etal*.,2008).

Attempts are being made to engineer C3 plants to carry out C4 photosynthesis(Hibberd *etal*.,2008;. Langdale,2011) .Enabling the C4 trait requires gene editing to alter the genome to produce changes in leaf architecture and metabolism. If successful, rice yields could be greatly increased, and since native C4 plants use less water, engineered C4 plants are likely to be drought tolerant

8.The role of synthetic biology in reducing atmospheric greenhouse gases

prospects and challenges ofsynthetic 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 (zaho, 2019). 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.

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