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A Review of Algae Platforms for Enhanced CO_2 Capture and Biofuel via RuBisCO Pathway Analysis

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ABSTRACT

Climate change, driven primarily by greenhouse gas (GHG) emissions, poses a global challenge. Traditional CO_2 mitigation methods are complemented by biological sequestration via photosynthesis, notably facilitated by the enzyme RuBisCO. Algae, particularly green algae (Chlorophyta), are efficient in converting CO_2 into biofuels, contributing to both carbon cycling and renewable energy solutions. This review examines current algae-based platforms for carbon capture and biofuel production, focusing on the RuBisCO pathway in diverse algal species. The study evaluates the genetic diversity and biofuel production potential of various algae, emphasizing the importance of identifying new algal candidates and conducting comprehensive toxicity screenings. Based on the RuBisCO pathway analysis via phylogenetic tree and pairwise protein comparison, genera Edaphochlamys, Pleodorina, Colemanosphaera, Astrephomene, and Volvulina in the Chlorophyta phylum, along with genera Uroglenopsis, Lagynion, Naegeliella, and Poteriospumella in the Chrysophyta phylum, are suggested as potential biofuel production candidates. By expanding the search for genetically diverse algal species and optimizing cultivation conditions, algae can be further developed as a viable platform for biofuel production and CO_2 sequestration. This review underscores the ecological and economic benefits of employing algae in biosequestration and biofuel industries, advocating for continued interdisciplinary research and collaboration to realize algae's full potential in renewable energy technologies.

Background

Climate change presents a significant global challenge, predominantly driven by the emissions of greenhouse gasses (GHGs). Among these, carbon dioxide (CO_2) stands out as the most significant, constituting approximately 79.7% of emissions from critical sectors such as industry, transportation, and domestic energy use (US EPA, 2024). The continuous release of these gasses not only threatens the stability of our global climate but also jeopardizes global biodiversity, necessitating urgent and effective mitigation strategies.

Traditional approaches to mitigate CO_2 emissions encompass a variety of carbon capture and reduction techniques implemented across residential, commercial, and transportation sectors. Concurrently, biological sequestration for CO_2 offers a natural alternative (Hunter. 2017) through photosynthesis, primarily facilitated by the enzyme RuBisCO (Ribulose-1,5-bisphosphate carboxylase/oxygenase). RuBisCO plays a pivotal role in the Calvin cycle, catalyzing the carboxylation of ribulose bisphosphate (RuBP), which is a critical process in carbon fixation across all photosynthetic plants. As indicated its name, RuBisCO possesses both carboxylase and oxygenase activities. The carboxylase function incorporates CO_2 into organic molecules, which is the primary pathway for carbon fixation in the Calvin cycle. The oxygenase function, on the other hand, incorporates O_2 instead of CO_2, leading to the production of 2-phosphoglycolate and 3-phosphoglycerate, and initiating the process of photorespiration (Parker et al. 2008).

$$6CO_2 + 6C_5H_7O_{11}P_2 + 6H_2O \rightarrow 12C_3H_7O_7P$$

Among carbon-fixing organisms, algae have garnered significant attention due to their potential as a sustainable tool for reducing atmospheric CO_2 levels through biosequestration and biofuel production. Green algae (Chlorophyta), in particular, are recognized for their efficiency in converting CO_2 into biofuels such as bioethanol and biodiesel. As illustrated in Figure 1, these processes assimilate inorganic carbon into organic compounds, including starches and sugars, contributing not only to energy solutions but also to carbon cycling within ecosystems (Chandrasekhar et al. 2023; Suganya et al. 2016). Furthermore, algae play an indispensable role in marine biodiversity, providing essential food and shelter within marine ecosystems. Unlike terrestrial plants, algae have a rapid CO_2 absorption rate and a potent oxygen output, which are crucial for mitigating the effects of GHGs and supporting ocean life (Cotas et al. 2023).

In this study, we review current algae-based platforms for carbon capture and biofuel production. We collect and compare various algae species in literature currently being utilized, focusing on the bioproducts generated from these algae platforms. To further investigate, we carried out a meta-analysis on the RuBisCO pathway of these algae species, with a particular focus on a crucial gene, the RuBisCO large subunit (*rbcL*), which is pivotal for the RuBisCO enzyme's functionality in diverse algae strains. The aim is to assess the potential of algae as a viable biofuel platform, exploring its efficiency under diverse cultural conditions and environmental impacts. Special attention is given to the evaluation of algal toxicity and its implications. By integrating these aspects, our research not only contributes to the advancement of sustainable energy solutions but also underscores the ecological benefits of employing algae in climate change mitigation strategies. This review with a multifaceted approach provides a comprehensive examination of the current and future roles of algae in both energy production and environmental sustainability.

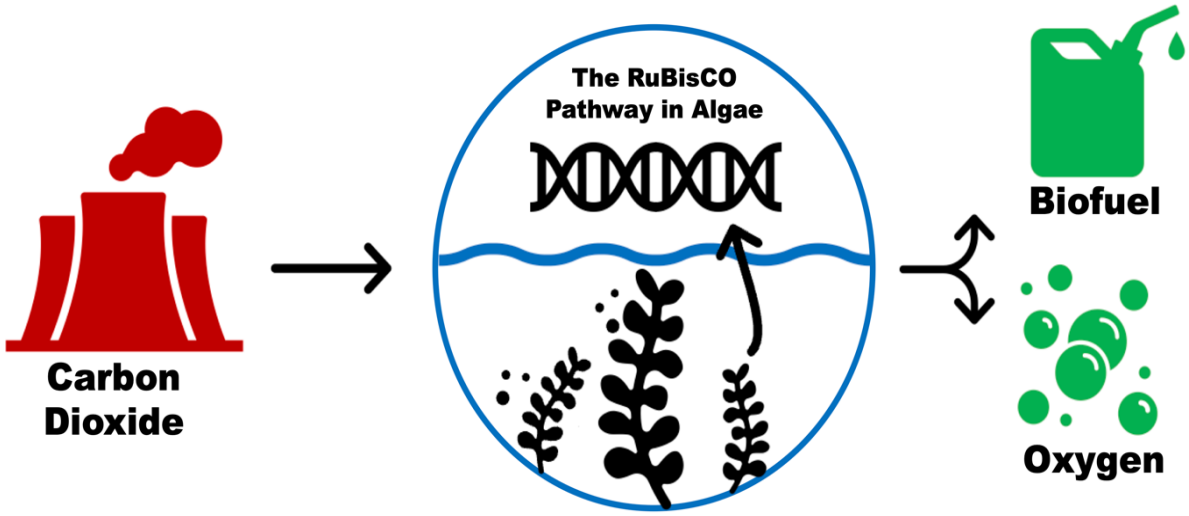

Figure 1. Schematic diagram of algae-based platforms for carbon capture and biofuel production

Algae-Based Platforms for Biofuel Production

Table 1 summarizes the algal species used for biofuel production, including the specific bioproducts pursued through these algal platforms.

Chlorella sp. has been extensively researched for its capability to produce a variety of biofuels, including biodiesel, bioethanol, and biohydrogen. Silva and Bertucco (2017) highlighted the use of nitrogen limitation to induce carbohydrate accumulation in Chlorella sp., resulting in higher yields of fermentable sugars for bio-

ethanol production. The process involved saccharification and fermentation, achieving significant ethanol production efficiency. Bastos (2018) emphasized the high photosynthetic efficiency and adaptability of Chlorella sp. to various water conditions, including wastewater, which makes it a promising candidate for bioethanol production. This method demonstrated yields significantly higher than traditional biomass sources such as corn and sugarcane. Additionally, Sirajunnisa and Surendhiran (2016) detailed the transesterification process for converting lipids from Chlorella sp. into biodiesel, showcasing its high lipid accumulation under nutrient stress conditions. Collectively, these studies underscore the versatility of Chlorella sp. in producing multiple bioproducts, establishing it as a valuable organism in the biofuel industry.

Botryococcus braunii is also a prominent subject of study for biofuel production due to its ability to produce various hydrocarbons and lipids. Research by Kojima and Zhang (1999) focused on optimizing conditions for hydrocarbon production in Botryococcus braunii using bubble column photobioreactors. Their findings indicated that B. braunii adapted to high irradiance showed significant biomass productivity and hydrocarbon content, particularly botryococcenes, which can be converted into fuels like gasoline. This growth-associated hydrocarbon production suggests that maximizing algal growth could enhance yields. In a comprehensive review, Ratledge (2004) discussed the biosynthesis of fatty acids in microorganisms used for single-cell oil (SCO) production, highlighting the substantial lipid accumulation capability of B. braunii. The study emphasized the importance of understanding the biochemical and genetic pathways involved in lipid accumulation to improve yields, positioning B. braunii as a viable candidate for large-scale biofuel production.

The potential of Tetraselmis sp. in biofuel production has been explored extensively, demonstrating its ability to produce various bioproducts. Prabakaran and Karthikeyan (2023) examined the role of Tetraselmis sp. in producing third-generation biofuels, noting its high lipid content and growth rate. The study highlighted the sustainability of cultivating Tetraselmis sp. in various water conditions, including wastewater, making it an eco-friendly option for biofuel production. The researchers identified the prospects and challenges of using Tetraselmis sp. for biodiesel, bioethanol, and biohydrogen production. Furthermore, Hannon et al. (2010) detailed the cultivation and harvesting processes of Tetraselmis sp., focusing on its high oil yield and the efficiency of converting algal lipids into biodiesel through transesterification. Their findings underscore the significance of optimizing cultivation conditions to maximize lipid accumulation, enhancing biodiesel yields.

Dunaliella sp. has garnered attention for its potential in biofuel production, particularly in the form of bioethanol and bio-oil. Lee et al. (2013) investigated the chemo-enzymatic saccharification and subsequent bioethanol fermentation of lipid-extracted residual biomass of Dunaliella tertiolecta. They highlighted that the residual biomass could be efficiently converted to bioethanol without the need for additional pretreatment, achieving a bioethanol yield of 0.14 g ethanol per gram of residual biomass. This approach not only utilizes waste biomass but also improves the economic feasibility of biofuel production from microalgae. Additionally, Shuping et al. (2010) examined the pyrolysis characteristics and kinetics of Dunaliella tertiolecta using a thermogravimetric analyzer. Their study revealed that D. tertiolecta could be thermally decomposed to produce bio-oil, with the process following a single reaction model and an activation energy of approximately 146 kJ/mol. This research provides valuable insights for designing pyrolytic processing systems using D. tertiolecta as feedstock.

Similarly, several other algae species, including Scenedesmus obliquus, Neochloris oleoabundans, Desmodesmus sp., and Chlamydomonas reinhardtii, have been explored to achieve the dual goals of carbon capture and biofuel production.

Table 1. Algae-based platforms for biofuel production, categorized by various algal species

Algal name	Bioproduct	References

Chlorella sp.*	Biodiesel	Chisti (2007), He et al. (2008), Alaswad et al. (2015), Günnerken et al. (2015), Mahmood et al. (2023)
	Bioethanol	Silva & Sirajunnisa & Surendhiran (2016), Bertucco (2017), Bastos et al. (2018), Velazquez-Lucio et al. (2018), Cheng et al. (2022),
	biohydrogen	Chen et al. (2013)
Botryococcus braunii*	Hydrocarbons	Kojima & Zhang (1999), Chisti (2007)
	Biodiesel	Ratledge (2004), Chisti (2007)
Tetraselmis sp.*	Biodiesel, Bioethanol	Chisti (2007), Hannon et al. (2010), Xie et al. (2016), Prabakaran & Ravindran (2023)
Dunaliella sp.*	Bioethanol	Hannon et al. (2010), Lee et al. (2013)
	Bio-oil	Shuping et al. (2010)
Scenedesmus obliquus*	Biodiesel, Bioethanol	Prabakaran & Ravindran (2023)
Neochloris oleoabundans*	Biodiesel	Chisti (2007), Li et al. (2014)
Desmodesmus sp. *	Biosorbents	Xie et al. (2016)
Chlamydomonas reinhardtii	Biodiesel	Hannon et al. (2010), Baroukh et al. (2015), Bastos (2018)
Microcystis sp.	Bioethanol	El-Mekkawi et al. (2019)
Spirulina platensis	Bio-oil	Jena & Das (2011)
Saccharomyces cerevisiae	Bioethanol	Choi et al. (2010)
Ankistrodesmus falcatus	Biodiesel	Zbinden et al. (2013)
Nannochloropsis sp.	Biodiesel	Cheng et al. (2014), Parniakov et al. (2015), Chen et al. (2015), Hossain & Mahlia (2019), Neeti & Sharma (2023),
	Bioethanol	Chen et al., (2015), Neeti & Sharma (2023)
	Biogas	Neeti & Sharma (2023)
Laminarin sp.	Bioethanol	Abdallah et al. (2016)
Schizochytrium limacium	Biodiesel	Adeniyi et al. (2018)
Sargassum sp.	Bioethanol	Borines et al. (2013)
Various microalgae	Various biotechnological products, including biofuels	Borowitzka (1992), Cuellar-Bermudez et al. (2015), Ali & Watson (2015), Khan et al. (2018), Srivastava & Mishra (2023)

Methodology for Investigating Genetic Diversity in the RuBisCO Pathway Using Published Algal Genomes

The genetic data for the RuBisCO large subunit (*rbcL*) protein sequence was collected from the National Center for Biotechnology Information (NCBI) GenBank database, including one representative gene from all algal phyla: Bacillariophyta (diatoms), Chlorophyta (green algae), Haptophyta (haptophytes), Euglenophyta (euglenoids), Phaeophyceae (brown algae), Cryptophyta (cryptomonads), Chrysophyta (golden algae), Rhodophyta

(red algae), and Dinophyta (dinoflagellates). The length of the *rbcL* gene is approximately 450-500 amino acids. The representative *rbcL* sequences were then used to perform Basic Local Alignment Search Tool (BLAST) searches to find more diverse genera within the corresponding phylum. To ensure genetic diversity of the collected data, sequences from more than 10 different genera were collected from 9 different phyla. This process resulted in 121 protein sequences as listed in Table 2, which were then aligned using multiple sequence alignment.

Molecular Evolutionary Genetics Analysis (MEGA) software was used to combine all 121 *rbcL* protein sequences. After trimming the combined protein alignments, a phylogenetic tree was generated using the trimmed protein alignments of algae with MEGA. Additionally, a heatmap was generated from the same dataset of 121 combined protein alignments using Python 3, providing a visual representation of the genetic diversity and relationships via pairwise similarity comparison among the algae studied.

Table 2. GenBank accession numbers of RuBisCO protein gene (*rbcL*) from diverse algal species used in this study for meta-analysis

Phylum	Algal name (Genus, Species, or Strain) with GenBank accession number for the RuBisCO Gene (rbcL) in Parentheses
Bacillariophyta	Ditylum brightwellii (ABF60324), Lithodesmioides polymorpha (YP_010537054), Bellerochea horologicalis (AEB91292), Helicotheca tamesis (YP_010536781), Tenuicylindrus belgicus (YP_010537600), Entomoneis paludosa (ASC55321), Leptocylindrus danicus (YP_009029287), Chaetoceros laevisporus (QXM17834), Extubocellulus spinifer (AVY51305), Achnanthidium sp. (APH82076), Odontella aurita (AEB91306), Thalassiosira tumida (ABF60362), Corethron hystrix (AAT35819)
Chlorophyta	Chlorella vulgaris (QDF82944.1), Botryococcus braunii (YP_009106543.1), Dunaliella salina (YP_005089820.1), Scenedesmus sp. (KAF8054431.1), Desmodesmus abundans (YP_010488918.1), Neochloris aquatica (YP_009238038.1), Tetraselmis sp. (AMP43313.1), Chlamydomonas reinhardtii (NP_958405), Volvulina compacta (QIA46940), Platydorina caudata (WGT92433), Volvox carteri (ACI31253), Astrephomene gubernaculifera (BCA78148), Edaphochlamys debaryana (YP_010580348), Gonium pectorale (YP_007507261), Eudorina sp. NIES-3984 (AXZ97194), Colemanosphaera angeleri (YP_009728191), Pleodorina starrii (YP_007890180), Colemanosphaera charkowiensis (QIA47039), Pandorina morum (QIA46779)
Chrysophyta	Ochromonas sp. CCMP1393 (AIM52760), Chromulina nebulosa (AAF00606), Phaeobotrys solitaria (CAM32962), Kremastochrysopsis austriaca (QFG07011), Chrysocapsa vernalis (AAF00607), Chrysosaccus sp. CCMP368 (ABN46927), Chromophyton cf. rosanoffii (ABN46926), Epipyxis aureus (ABN46916), Uroglenopsis americana (ABN46940), Lagynion cf. ampullaceum (ABN46922), Naegeliella flagellifera (ABN46915), Poteriospumella vasocystis (ABN46945), Rhodomonas salina (YP_001293518), Proteomonas sp. NIES-1005 (BDA98086), Cryptomonas gyropyrenoidosa (YP_010835262), Guillardia theta (NP_050705), Teleaulax amphioxeia (YP_009159196), Storeatula sp. CCMP1868 (ASO75899), Hemiselmis andersenii (BDA99118), Geminigera cryophila (QAA92135), Hanusia phi (QAA92140), Pyrenomonas helgolandii (AAM62090), Urgorri complanatus (APG31611), Baffinella frigidus (QCT05660), Plagioselmis nannoplanctica (APG31613)
Dinophyta	Dinophyceae sp. MRD-151 (BBI28699), Lepidodinium chlorophorum (YP_009139359), Durinskia kwazulunatalensis (BAW35352), Unruhdinium penardii

	(BAF76881), Blixaea quinquecornis (BAE94662), Peridiniopsis cf. kevei (BAF76880), Kryptoperidinium foliaceum (YP_003734573), Karenia brevis (ALP13672), Dinothrix rugata (BAD98975), Peridinium balticum (BAD98976), Karlodinium veneficum (AAQ04823), Dinophysis fortii (BAD42428), Takayama helix (WXH00178)
Euglenophyta	Euglena viridis (YP_007517056), Lepocinclis tripteris (AYQ93413), Trachelomonas grandis (AYB71430), Phacus inflexus (YP_009540868), Cryptoglena skujai (YP_009145389), Trachelomonas volvocina (YP_009145500), Eutreptiella pomquetensis (AST09081), Discoplastis spathirhyncha (YP_009540985), Monomorphina parapyrum (YP_009145456), Colacium vesiculosum (AEW12959), Euglenaformis proxima (YP_009032761), Strombomonas acuminata (AEW12993)
Haptophyta	Diacronema lutheri (YP_007476240), Rebecca salina (BAA08281), Pavlova pinguis (AET10433), Exanthemachrysis gayraliae (BAB20791), Gephyrocapsa oceanica (YP_010393370), Chrysochromulina parva (YP_009459208), Ochrosphaera neapolitana (YP_010930379), Tisochrysis lutea (YP_009550191), Phaeocystis rex (YP_010736018), Emiliania huxleyi (AGB58285), Chrysotila carterae (YP_010596504), Prymnesium parvum (BAB20788), Platychrysis sp. TKB8934 (BAB20789)
Phaeophyceae	Chorda filum (YP_010205199), Dictyopteris prolifera (AAQ92289), Choristocarpus tenellus (YP_011005530), Dictyota dichotoma (AAT09892), Sargassum hemiphyllum var. chinense (QNO36019), Phaeostrophion irregulare (YP_011007033), Pylaiella littoralis (P23651), Dictyotopsis propagulifera (YP_011006187), Zonaria diesingiana (AAQ92297), Diplura sp. DspC (BAG41441), Syringoderma abyssicola (YP_011007603), Ascoseira mirabilis (YP_011044974)
Rhodophyta	Galdieria sulphuraria (P23755), Cyanidioschyzonaceae sp. 2 (UNJ15880), Hildenbrandia sp. NANAE01 (BEV66499), Cyanidiococcus yangmingshanensis (BFG87627), Cyanidium sp. (QQL56290), Chondria littoralis (AHZ13854), Chroothece richteriana (YP_010335713), Rhodomela confervoides (YP_009394101), Cyanidioschyzonaceae sp. 1 (UNJ15487), Laurencia natalensis (ARO52487), Osmundea cf. pinnatifida (ANH79393), Laurencia multiclavata (ARO52491), Chroodactylon ornatum (YP_010336104), Sebdenia monardiana (AAQ55144)

Genetic Relatedness of Diverse Algae and Its Implication for Biofuel Production

As shown in Table 1, several algal species have been frequently studied for their potential in biofuel production, particularly biodiesel. These include Chlorella vulgaris, Nannochloropsis oceanica, Dunaliella salina, Botryococcus, Desmodesmus, Neochloris, Scenedesmus, and Tetraselmis. The third-generation biofuels derived from these microalgae offer several advantages, including cleaner production processes, more efficient cultivation, enhanced carbon dioxide sequestration, and improved performance metrics.

Chlorella vulgaris is notable for its high heating values and low kinematic viscosity, making it an efficient biodiesel feedstock. The biodiesel blends derived from Chlorella vulgaris improve the performance and emission characteristics of internal combustion engines, significantly reducing emissions of carbon monoxide, hydrocarbons, and soot (Al-Ansari et al., 2023). Additionally, Chlorella vulgaris shows optimal performance when valorized through anaerobic digestion, particularly when cultivated under heterotrophic and sulfur-

limited conditions. These conditions lead to high lipid productivity and the production of suitable fatty acids for biodiesel, along with a high calorific value for efficient energy conversion (Sakarika & Kornaros, 2019).

Nannochloropsis oceanica is another strong candidate for biodiesel production due to its high lipid content, primarily composed of triacylglycerols, which are easily transesterified into biodiesel. Nannochloropsis achieves higher lipid levels under stress conditions, enhancing its suitability for biofuel production (Ma et al., 2016). Similarly, Dunaliella salina is capable of producing competitive lipid levels under high salinity conditions, while simultaneously growing its biomass (Hannon et al., 2010).

Figure 2 shows the phylogenetic and evolutionary relationships of diverse algae inferred by the rbcL gene. The algae species currently widely used, marked with red dots, are locationally limited on the phylogenetic tree. This indicates that the current algal platforms for biofuel production are restricted. This opens the door for utilizing more diverse algae, pending thorough biofuel quality checks and toxicity screenings, which can originate from new algae candidates. As illustrated in Figure 2, it is plausible to assume that closely related RuBisCO protein sequences among robust algal species such as Chlorella, Nannochloropsis, and Dunaliella indicate the potential for other genera within the same Chlorophyta group. For instance, genera such as Edaphochlamys, Pleodorina, Colemanosphaera, Astrephomene, and Volvulina could also be promising candidates for biofuel production due to their genetic similarity to Chlorella vulgaris and the other species mentioned above. Furthermore, algal species in Euglenophyta, such as Lepocinclis and Eutreptiella, can be considered as candidates. However, several Euglenophyta species are recognized for toxin production (Kostygov et al. 2021). Therefore, if any species in Euglenophyta is considered as an algal platform for biofuel production, there should be comprehensive genomic and phenotypic screening for toxicity control over those algal species.

Figure 2. Evolutionary history of 121 RuBisCO (*rbcL*) genes in diverse algal species based on circular phylogenetic tree construction. The red dots represent the algal species utilized in previous algae-based platforms shown in Table 1, indicated with an asterisk (*). The tree was inferred using the Neighbor-Joining algorithm, and the evolutionary distances were computed using the Poisson correction method.

Exploring Untapped Algal Platforms Through RuBisCO Protein Analysis

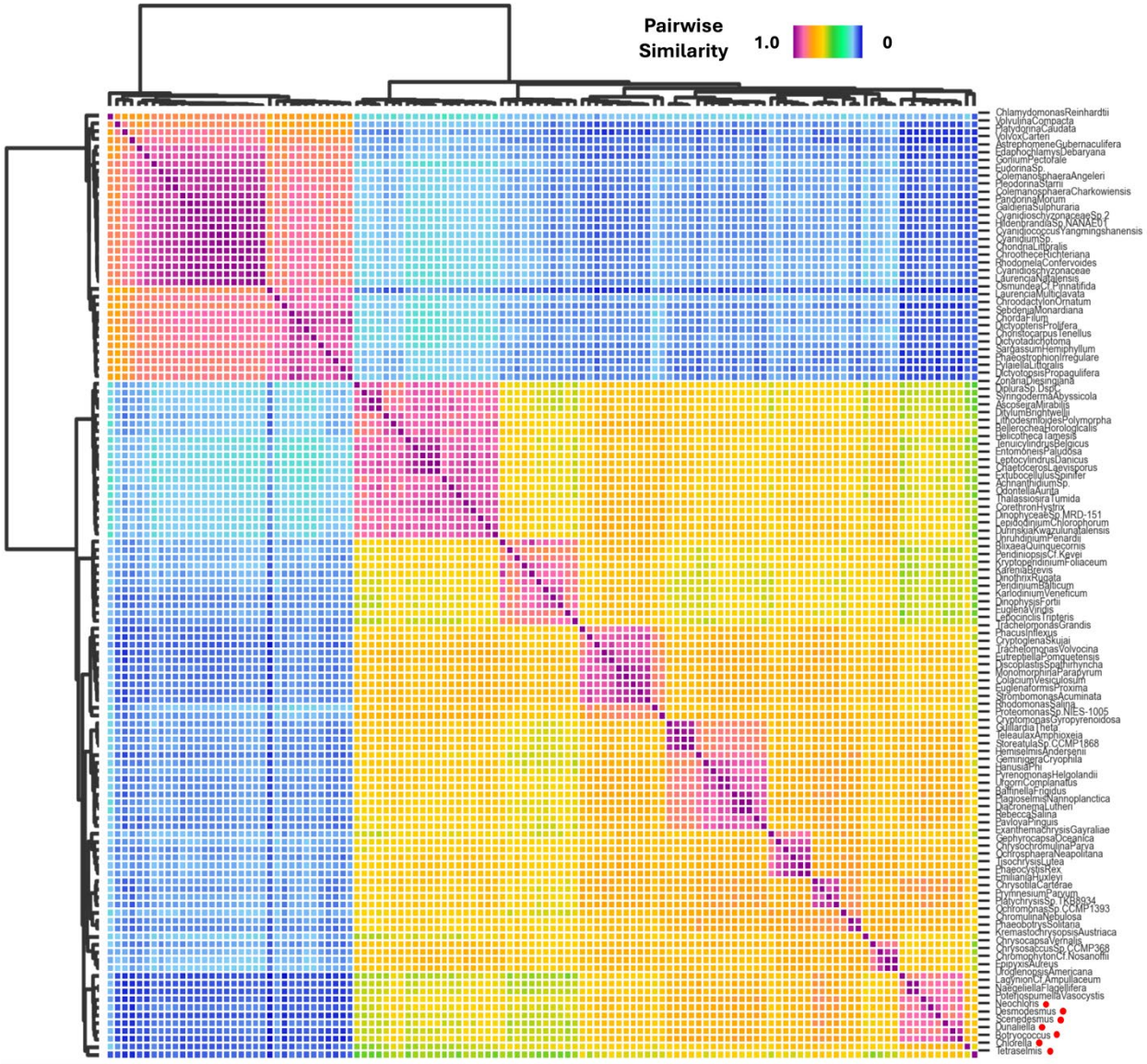

Figure 3. Pairwise genetic similarity comparison is shown in the heatmap using 121 RuBisCO (*rbcL*) genes. The names of algae possessing the *rbcL* gene are listed on the right side of the heatmap. Algal species frequently used in current algal biofuel platforms are marked with red dots next to their names; these are the same species indicated with an asterisk (*) in Table 1. The color key at the top shows the continuous pairwise similarity, with purple representing a similarity of 1 and blue representing a similarity of 0. The diagonal purple line indicates the comparison of the *rbcL* gene within the same algal species.

Figure 3 presents a genetic similarity heatmap of 121 *rbcL* genes collected from NCBI GenBank (Table 2) and analyzed in a phylogenetic tree. This heatmap reveals direct sequence similarities between potential future algal candidates and currently prevalent species used for biofuel production. Notably, Chlorella vulgaris, Nannochloropsis oceanica, Dunaliella salina, Botryococcus, Desmodesmus, Neochloris, Scenedesmus, and Tetraselmis

are highlighted with red dots in the lower right corner of the heatmap. These species show high genetic similarity (80-90%) with Uroglenopsis, Lagynion, Naegeliella, and Poteriospumella, as indicated by the pink and purple squares.

The upper section of the heatmap, from Chlamydomonas to Dictyopteris, comprises approximately one-third of the 121 algae and forms a distinct cluster separate from the rest. This significant division suggests that the currently unused algal groups could be explored for biofuel production. Additionally, the heatmap can guide the selection of diverse algal groups for cultivation, potentially reducing the need for costly sterilization procedures in pure cultures. This is because cultivating diverse algae harmoniously may mitigate the necessity for extensive sterilization, thus lowering the production costs associated with algal biofuel.

Examining diverse algae for their growth kinetics, as commonly studied with Chlorella vulgaris, can provide valuable insights. The growth kinetics of algae are highly dependent on cultivation environments, as demonstrated by Dunaliella salina thriving under hypersaline conditions (Hannon et al., 2010). Expanding the search for algal candidates for biofuel production to include more diverse groups, and conducting growth kinetics tests under various conditions, can help identify optimal growth and bioproduct yield. This approach will enhance carbon capture, enabling biosequestration into value-added products and reducing reliance on fossil fuels.

Conclusion and Future Remarks

This review highlights the significant potential of algae-based platforms for enhanced CO_2 capture and biofuel production, focusing on the RuBisCO pathway. The analysis of 121 *rbcL* genes from diverse algae species reveals promising candidates beyond the commonly used ones, such as Chlorella vulgaris, Nannochloropsis oceanica, and Dunaliella salina. The phylogenetic tree and genetic similarity heatmap indicate that closely related species, including Edaphochlamys, Pleodorina, Colemanosphaera, Astrephomene, Volvulina, Uroglenopsis, Lagynion, Naegeliella, and Poteriospumella, possess highly homologous RuBisCO proteins with prevalent biofuel-producing algae. This opens avenues for exploring these and other untapped species for biofuel production.

Future research should focus on comprehensive genomic and phenotypic screenings to ensure the safety and efficiency of new algal candidates, particularly those from toxin-producing groups like Euglenophyta. Additionally, examining the growth kinetics of diverse algae under varying environmental conditions will be crucial in identifying optimal cultivation practices for maximum biofuel yield and CO_2 sequestration.

In conclusion, algae-based platforms present a viable and sustainable solution for CO_2 capture and biofuel production. By expanding the genetic diversity and optimizing cultivation conditions, we can significantly enhance the role of algae in mitigating climate change and advancing renewable energy technologies. Continued interdisciplinary research and collaboration will be essential in realizing the full potential of algae in biosequestration and biofuel industries.

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