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ISSN: 2167-7662
Bioenergetics: Open Access

Commentary

Antiquity Enzyme Enhanced in Photosynthesis through Cas-system

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DESCRIPTION

Photosynthesis is considered to be the most important metabolic process for plant biomass accumulation, but it is well known that it is limited by carbohydrates and various environmental stimuli. Therefore, it is important to understand the regulatory mechanisms of the photosynthetic process and improve crop yield potential. Interestingly, increased evidence supports the hypothesis that polyamines (PAs) regulate photosynthetic capacity. PA is commonly found in photosynthetic equipment and has been reported to be closely associated with plant growth and stress response. Overexpression of genes involved in PA biosynthesis leads to an increase in the Photosynthetic Rate (Pns) of transgenic plants. In addition, Putrescine plays an active role in stimulating photophosphorylation and regulating adenosine triphosphate synthesis, at least to some extent. PA is an important regulator of redox homeostasis and increases photosynthesis by activating antioxidant enzymes and regulating Reactive Oxygen Species (ROS) homeostasis.

For high-yielding, high-quality, climate-resilient, and environmentally friendly agriculture, genome editing is essential. For plant genome editing, the clustered regularly interspaced short palindromic repeats-associated protein (CRISPR-Cas) technique is commonly utilized. Ribulose-1,5-bisphosphate carboxylase/oxygenase (Rubisco), a crucial CO_2-fixing enzyme that governs the rate of photosynthesis in plants, is one of the key targets for improving photosynthesis. Rubisco activity is restricted in the current environment due to its Low Catalytic Rate (kcat), poor affinity for CO_2 (Kc), and specificity for CO_2. It is made up of big (52 kDa) and small (14-15 kDa) subunits that are encoded by a single gene in the chloroplast genome (RbcL) and a multigene family in the nucleus (RbcS). Rubisco has a lower kcat in C3 plants than in C4 plants in general. Researchers recently used the CRISPR-Cas system to disrupt the RbcS multigene family in rice (C3 plant) and replace its RbcS machinery with RbcS from the C4 plant sorghum (*Sorghum bicolor*).

The rice plants that resulted had a photosynthetic rate that was comparable to C4 plants, as well as higher crop output. In the model tetraploid crop tobacco, a CRISPR-Cas9-mediated genome editing technique was used to knock out several rbcS homologs at the same time (*Nicotiana tabacum*). At least 80% of overall rbcS expression in tobacco is accounted for by the three rbcS homologs rbcS S1a, rbcS S1b, and rbcS T1. Three mutant lines were found to have indel mutations, including one with a 670 bp loss in rbcS-T1. In the T1 generation, the Rubisco concentration of three mutant lines was reduced by about 93%, and mutant plants only accumulated 10% of the total biomass of wild-type plants. As a second goal, researchers employed a proof-of-concept technique for co-transforming a non-native rbcS gene into a wild-type tobacco background while creating the triple knockout. Our findings suggest that CRISPR-Cas9 is a promising tool for rbcS family-focused mutagenesis in polyploid species and that it will aid attempts to improve photosynthetic efficiency in plants by expressing superior non-native Rubisco enzymes. Many great genes have been utilized in rice breeding in recent years as a result of continuous innovation in molecular breeding procedures, which is critical for boosting rice yields. The hexokinase gene OsHXK1 was knocked out in the indica rice variety OsHXK1-CRISPR/Cas9 lines in this article using the CRISPR/Cas9 gene-editing approach. The findings showed that using the CRISPR/Cas9 gene-editing technology to knock out OsHXK1 could result in the production of high-photosynthetic efficiency and high-yielding rice cultivars.

CONCLUSION

Rubisco remains the most appealing target for enhancing photosynthetic activity due to its pivotal position as the limiting step in CO_2 absorption under ambient CO_2 and high light circumstances. Modifying Rubisco catalysis in chloroplasts appeared like an impossible task twenty years ago. This changed with the invention of plastome-transformation systems, which allowed Rubisco to increase its engineering capabilities. Understanding the complexities of Rubisco biogenesis in plastids is one of the new challenges that are CRISPR-Cas, as it will allow researchers to expand the number of Rubisco isoforms that can be bioengineered to improve their photosynthetic quality resulting in crop yield.

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Received: 15-Apr-2022, Manuscript No. BEG-22-16975; **Editor assigned:** 20-Apr-2022, PreQC No. BEG-22-16975 (PQ); **Reviewed:** 28-Apr-2022, QC No BEG-22-16975; **Revised:** 10-May-2022, Manuscript No. BEG-22-16975 (R); **Published:** 17-May-2022, DOI: 10.35841/2167-7662.22.10.168

Citation: Boyman M (2022) Antiquity Enzyme Enhanced in Photosynthesis through Cas-system. J Bio Energetics. 10:168.

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