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Short Communication

Selectable Marker Recycling: Strategies and Challenges for Efficient Genome Engineering

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DESCRIPTION

Selectable marker recycling is a technique that allows the removal of selectable markers from Genetically Modified Organisms (GMOs) after they have been used for selection [1]. Selectable markers are genes that confer resistance to antibiotics, herbicides, or other agents that can be used to select for the presence of a desired trait in a population of cells or organisms. Selectable markers are essential for efficient genome engineering, as they enable the identification and isolation of cells or organisms that have been successfully modified [2]. However, selectable markers also have some drawbacks, such as potential biosafety risks, public concerns, and regulatory hurdles. Therefore, selectable marker recycling is desirable to eliminate the unwanted selectable markers from GMOs and to reduce the potential negative impacts of their presence. Selectable marker recycling can be achieved by various methods, depending on the type of GMO and the nature of the selectable marker.

Some of the common methods for selectable marker recycling

Cre-loxP system: This system uses a site-specific recombinase enzyme called Cre that recognizes specific DNA sequences called loxP and catalyzes their recombination [3]. By placing the selectable marker gene between two loxP sites in the same orientation, the Cre enzyme can excise the selectable marker gene from the genome, leaving behind a single loxP site. The Cre enzyme can be expressed transiently or inducibly in the GMOs to trigger the removal of the selectable marker gene.

Flp-FRT system: This system is similar to the Cre-loxP system, but uses a different site-specific recombinase enzyme called Flp that recognizes specific DNA sequences called FRT and catalyzes their recombination [4]. By placing the selectable marker gene between two FRT sites in the same orientation, the Flp enzyme can excise the selectable marker gene from the genome, leaving behind a single FRT site. The Flp enzyme can be expressed transiently or inducibly in the GMOs to trigger the removal of the selectable marker gene.

PiggyBac system: This system uses a transposable element called piggyBac that can insert or excise itself from the genome in a precise manner [5]. By placing the selectable marker gene within the piggyBac element, the piggyBac transposase enzyme can excise the entire element from the genome, leaving behind no trace of the selectable marker gene. The piggyBac transposase enzyme can be expressed transiently or inducibly in the GMOs to trigger the removal of the selectable marker gene.

Advantages of selectable marker recycling

Reducing biosafety risks: Selectable markers may pose biosafety risks if they are transferred horizontally to other organisms or if they confer resistance to clinically relevant antibiotics or herbicides [6]. Selectable marker recycling can eliminate these risks by removing the selectable markers from GMOs after they have served their purpose.

Increasing public acceptance: Selectable markers may raise public concerns about the safety and ethics of GMOs, especially if they are derived from bacterial or viral sources. Selectable marker recycling can increase public acceptance by removing these foreign genes from GMOs and making them more natural and acceptable.

Facilitating regulatory approval: Selectable markers may face regulatory hurdles in some countries or regions that have strict regulations on GMOs [7]. Selectable marker recycling can facilitate regulatory approval by removing these potentially problematic genes from GMOs and complying with regulatory standards.

Enabling multiple modifications: Selectable markers may limit the number of modifications that can be introduced into a single GMO, as each modification requires a different selectable marker. Selectable marker recycling can enable multiple modifications by freeing up space and resources in the genome and allowing reuse of selectable markers.

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Difficulties and limitations selectable marker recycling

Low efficiency: Selectable marker recycling may not be 100% efficient, as some cells or organisms may not undergo complete removal of the selectable marker gene due to incomplete expression or activity of the recombinase or transposase enzymes or due to inaccurate DNA repair mechanisms [8]. This may result in residual presence of selectable markers in some GMOs or mosaic patterns of removal in others.

Off-target effects: Selectable marker recycling may cause unintended effects on other parts of the genome due to non-specific recognition or binding of the recombinase or transposase enzymes or due to erroneous DNA repair mechanisms [9]. This may result in unwanted mutations, deletions, insertions, inversions, or rearrangements in other genes or regions that may affect the function or stability of GMOs.

Compatibility issues: Selectable marker recycling may not be compatible with all types of GMOs or selectable markers due to differences in their genomic structure, organization, integration, expression, regulation, or function [10]. This may limit the applicability and versatility of selectable marker recycling for various genome engineering purposes. Selectable marker recycling is a valuable technique that can improve efficient genome engineering by removing unwanted selectable markers from GMOs after they have been used for selection. However, selectable marker recycling also poses some challenges and limitations that need to be addressed and overcome by further research and development.

CONCLUSION

Selectable marker recycling is a technique that offers several advantages for efficient genome engineering while addressing some of the drawbacks associated with selectable markers in GMOs. It allows for the removal of selectable markers, which can reduce biosafety risks, increase public acceptance, facilitate regulatory approval, and enable multiple modifications in a single GMO. However, selectable marker recycling also comes with difficulties and limitations, such as low efficiency, off-target effects, and compatibility issues. Further research and development are necessary to address these challenges and optimize the technique. Overall, selectable marker recycling holds promise as a valuable tool in genome engineering, but continued advancements are needed to enhance its effectiveness and applicability.

REFERENCES

1. Jeong BR, Jang J, Jin E. Genome engineering via gene editing technologies in microalgae. Bioresour. Technol. 2023;4:128701.
2. Sun L, Zheng P, Sun J, Wendisch VF, Wang Y. Genome-scale *CRISPRi* screening: a powerful tool in engineering microbiology. Eng. Microbiol.. 2023;100089.
3. Abdullah M, Greco BM, Laurent JM, Vandeloo M, Marcotte EM, Kachroo AH. Rapid, scalable, combinatorial genome engineering by Marker-less Enrichment and Recombination of Genetically Engineered loci (MERGE). bioRxiv. 2022-06.
4. Wang Y, Liu Y, Zheng P, Sun J, Wang M. Microbial base editing: a powerful emerging technology for microbial genome engineering. Trends Biotechnol. 2021;39(2):165-180.
5. Dębczyński M, Mojsak D, Minarowski Ł, Maciejewska M, Lisowski P, Mróz RM. Genome-engineering technologies for modeling and treatment of cystic fibrosis. Adv Med Sci. 2023;68(1):111-120.
6. Zeng Y, Hong Y, Azi F, Liu Y, Chen Y, Guo C, et al.. Advanced genome-editing technologies enable rapid and large-scale generation of genetic variants for strain engineering and synthetic biology. Curr. Opin. Microbiol. 2022;69:102175.
7. Volke DC, Friis L, Wirth NT, Turlin J, Nikel PI. Synthetic control of plasmid replication enables target-and self-curing of vectors and expedites genome engineering of Pseudomonas putida. Metab. Eng. Commun. 2020;10:e00126.
8. Dong C, Schultz JC, Liu W, Lian J, Huang L, Xu Z, et al. Identification of novel metabolic engineering targets for S-adenosyl-L-methionine production in Saccharomyces cerevisiae *via* genome-scale engineering. Metab. Eng. 2021;66:319-327.
9. Shelake RM, Kadam US, Kumar R, Pramanik D, Singh AK, Kim JY. Engineering drought and salinity tolerance traits in crops through CRISPR-mediated genome editing: Targets, tools, challenges, and perspectives. Plant Commun. 2022;3:100417.
10. Mu X, Zhou H, Zhao W, He D, Zhu W, Nie X, et al. High-performance YbAl3/Bi0. 5Sb1. 5Te3 artificially tilted multilayer thermoelectric devices *via* material genome engineering method. J. Power Sources. 2019;430:193-200.