

Genetic Engineering for High Protein Maize

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INTRODUCTION

Maize (*Zea mays L.*) is the world's leading crop and its widely cultivated as cereal grain that was domesticated in Central America. It is one of the most versatile emerging crops having wider adaptability. Maize is known as queen of cereals

because of its highest genetic yield potential. Globally, it is cultivated on more than 160 m ha area across 166 countries having wider diversity of soil, climate, biodiversity and management practices.

HIGH QUALITY PROTEIN MAIZE

✓ High quality protein maize (HQPM), it is an improved variety of maize which is higher in lysine and tryptophan and lower in leucine and isoleucine in an endosperm than those contained in normal maize

✓ QPM is a result of biofortification, a process that uses conventional breeding to improve the nutritional value of crops.

WHAT IS GENETIC ENGINEERING?

Genetic engineering, also known as genetic modification, is biotechnology technique that alters an organism's DNA to create a desired outcome.

Genetic engineering for high protein maize

Genetic engineering is a powerful tool that can be used to improve the nutritional value of crops. Maize is an important staple food for millions of people, and efforts are underway to develop high

protein maize varieties that can help address protein deficiency worldwide.

Gene responsible for modification in high protein maize

- *Opaque-2 (o2) gene*
- *floury2*
- *sugary-2 (su2)*
- *mto140*
- *o16o16*

CASE STUDIES

Wang et al. (2013) studied improved nutritive quality in transgenic maize by simultaneously Overexpression of a Natural Lysine-Rich Protein Gene, *SBgLR*, and an ERF Transcription Factor Gene, *TSRF1*. The study enhanced maize by introducing two genes for increased lysine and salt tolerance, creating transgenic lines with higher protein and lysine levels, improved salt resistance, and better chlorophyll content.

Yue et al. (2014) studied Seed-Specific Expression of a Lysine-Rich Protein Gene, *GhLRP*, from Cotton Significantly Increases the Lysine Content in Maize Seeds. This study

explored using a lysine-rich protein gene (*GhLRP*) from cotton to boost lysine levels in maize seeds. Transgenic maize with *GhLRP* showed a 16.2% to 65.0% increase in lysine content compared to regular maize, with no significant changes in protein, lipid, or starch levels. Agronomic traits of the transgenic maize were normal. *GhLRP* is a promising gene for enhancing lysine content in maize, offering a valuable approach for improving its nutritional value.

Qi et al. (2016) studied High-efficiency CRISPR/Cas9 multiplex gene editing using the

glycine tRNA-processing system-based strategy in maize. The study developed a tRNA-processing system for multiplex CRISPR/Cas9 in maize, using glycine-tRNA to integrate multiple gRNAs under a single U6 promoter. This allows for enhanced targeting efficiency and precision, demonstrating the system's potential for advanced maize genetic research and breeding.

Young *et al.* (2019) CRISPR-Cas9 Editing in Maize: Systematic Evaluation of Off-target

Activity and Its Relevance in Crop Improvement. The study evaluated CRISPR-Cas9 specificity in maize, finding up to 90% accurate on-target editing with no off-target effects from well-designed guide RNAs. Off-target edits occurred only with a promiscuous guide. To reduce off-target activity, guide RNAs should differ by at least three mismatches, especially near the PAM site, ensuring high precision in plant genome editing.

CONCLUSION

- ✓ High protein maize, developed through genetic engineering, offers a promising solution to address global protein deficiency.
- ✓ CRISPR-Cas9 gene editing has emerged as a powerful tool for precise and efficient genetic modification.
- ✓ The examples reported here demonstrate the utility of the tRNA-processing system-based strategy as an efficient multiplex genome editing tool to enhance maize genetic research and breeding.

REFERENCES:

1. Wang, M., Liu, C., Li, S., Zhu, D., Zhao, Q and Yu, J. (2013). Improved nutritive quality and salt resistance in transgenic maize by simultaneously overexpression of a natural lysine-rich protein gene, *SBgLR*, and an ERF transcription factor gene, *TSRF1*. *International Journal of Molecular Sciences*, **14**(5): 9459-9474.
2. Yue, J., Li, C., Zhao, Q., Zhu, D and Yu, J. (2014). Seed-specific expression of a lysine-rich protein gene, GhLRP, from cotton significantly increases the lysine content in maize seeds. *International Journal of Molecular Sciences*, **15**(4): 5350-5365.
3. Qi, W., Zhu, T., Tian, Z., Li, C., Zhang, W. and Song, R. (2016). High-efficiency CRISPR/Cas9 multiplex gene editing using the glycine tRNA-processing system-based strategy in maize. *BMC biotechnology*, **16**(58): 1-8.
4. Young, J., Zastrow-Hayes, G., Deschamps, S., Svitashchev, S., Zaremba, M., Acharya, A and Kumar, S. (2019). CRISPR-Cas9 editing in maize: systematic evaluation of off-target activity and its relevance in crop improvement. *Scientific reports*, **9**(1): 6729.