

breeding programs. Rice Relatives GD fills the gap by providing not only more comprehensive genomic information of rice relatives for the rice community but also specific genes from rice relatives, including stress-related genes, photosynthesis genes and so on. RiceRelativesGD collected and organized published genomic data of rice and its relatives from relevant literatures. Currently, a total of 208 321 specific genes from rice relatives are deposited in RiceRelativesGD (Figure 1).

Conclusion

In conclusion, gene editing technologies, particularly the CRISPR/Cas9 system, hold a greater significance in defining plant research in the recent times. It has truly emerged as the most effective tool for crop improvement owing to its ability to create mutations at desired targets in the genome with greater accuracy, efficiency, and simplicity. A major advantage of this process lies in the fact that the transgenes causing genetic modification can be easily eliminated from the genome through genetic segregation resulting in no differences between the gene-edited plants and those developed through conventional breeding. The development of CRISPR-Cpf1 system and base editing by far holds greater promise for editing rice genome with much more precision and efficiency. Furthermore, genome editing-based epigenetic regulation through the manipulation of DNA methylation and histone modification also holds greater promise in crop improvement as such modifications can be inherited into plant offspring without any change in the genomic sequence. A recent study involving CRISPR/dCas9 fused with DNA methyl transferase 3a (DNMT3a) induced DNA methylation in the target regions of the mammalian cells.

References

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