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Meta-analysis of Design Breeding Approaches in Rice: Lessons and Future Directions

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Abstract This study reviews the effectiveness of various rice designed breeding methods, including traditional breeding techniques, marker-assisted selection (MAS), and genome editing (CRISPR-Cas), by collecting data from numerous studies and using statistical tools to evaluate the performance of each breeding method from different indicators, including yield improvement, genetic gain, and cost-effectiveness. Comparative analysis showed that molecular breeding methods, although initially costly, have higher efficiency and better adaptability in different agro-ecological zones compared with traditional methods. Challenges such as limited genetic diversity, technical complexity, and economic constraints were identified as major barriers to the widespread adoption of advanced breeding technologies. A case study highlights the successful implementation of designed breeding in a specific region, providing valuable insights for expanding these strategies. This study highlights the need to integrate multi-omics data and use artificial intelligence to optimize breeding precision and efficiency, and proposes recommendations for policy support and investment in advanced breeding technologies to increase rice yields and ensure global food security.

Keywords Rice breeding; Meta-analysis; Conventional breeding; Marker-assisted selection; Genome editing

1 Introduction

More than half of the world's population eats rice every day (Zeng et al., 2017), which is a very important thing to think about. But the situation is a bit complicated now - with more and more people, people are eating better and better, and the current yield alone may not be enough (Ye et al., 2021). The old breeding methods used to be effective, and many high-yield and high-quality rice varieties were cultivated. But the problem now is that the traditional methods are a bit difficult to use in order to ensure drought and salt resistance and nutrition (Ganie et al., 2021; Senguttuvel et al., 2023). Fortunately, many new tricks have been developed in recent years. Combining technologies such as genomic selection and molecular markers has indeed improved breeding efficiency a lot (Xu et al., 2021). Of course, it does not mean that these new technologies are perfect, but at least they make breeding work faster. In the final analysis, in order to maintain yields and cope with various environmental challenges, we may really need to rely on these modern technologies to help more.

Rice breeding has indeed made great progress, but to be honest, we still need to compare the various new methods to see which one is better. Some technologies look fancy, but the actual effect may not be as good as expected. At this time, we have to rely on meta-analysis to help - it can summarize the data of different experiments and help us see which methods are really reliable (Selamat and Nadarajah, 2021). Take the study of drought resistance as an example. Some people have predicted yield by locating key gene sites and combining metabolomics data, and the effect is really good (Xu et al., 2016).

This shows that putting data from different technologies together for analysis may lead to new discoveries. Of course, it is not applicable in all cases. Some methods may not work well under certain conditions. In the final analysis, breeding cannot only look at the results of a single study. Integrate and analyze various experimental data to find out the rules, so that you can be more confident when formulating breeding plans. The biggest advantage of meta-analysis is here. It can help us string together scattered studies and draw more reliable conclusions.

When it comes to rice breeding, various new methods have emerged recently, but which one is the most effective? This time we mainly looked at several key indicators-yield, rice quality, and drought and salt resistance. After looking through a lot of the latest research, we found that some methods are indeed effective, but also exposed some areas that need improvement. Breeding is not as simple as it used to be. Using new technologies such as genomic selection and molecular markers can indeed improve efficiency. But how to combine them for the best effect still needs to be explored. From the current situation, although some strategies have achieved good results, there is still a lot of work to be done to cultivate new varieties that are both high-yielding and resistant to stress. Interestingly, the methods applicable to different regions and different varieties may be different. Some technologies perform well under certain conditions, but may not work well in other environments. This also reminds us that future research may require more flexible methods and cannot expect one solution to solve all problems.

2 Overview of Design Breeding Approaches in Rice

2.1 Conventional breeding techniques

When it comes to the old way of growing rice, farmers are most familiar with picking good seedlings for breeding, or hybridizing different varieties. To put it bluntly, it is to select seeds based on appearance - keep the rice plants that grow well, and do this for generations (Arabzai and Gul, 2021). Another way is to let different varieties of rice "marry" to pass on the advantages of both parents to the next generation. However, these old methods are really time-consuming, and sometimes you will encounter headaches. For example, if you want high-yield characteristics, you will also inherit the problem of poor disease resistance (Bian et al., 2023). Although there are various problems, it must be said that over the years, it is precisely these traditional methods that have cultivated so many good varieties that are both high-yield and disease-resistant. Although new technologies are emerging in an endless stream, these old methods are still the basis, and the research and development of many new varieties cannot be separated from them.

2.2 Marker-assisted selection (MAS)

In rice breeding today, marker-assisted selection (MAS) has indeed brought about a lot of changes. In the past, seed selection was mainly based on appearance, but now we can directly look for the desired characteristics at the genetic level (Ludwików et al., 2015). Simply put, it is to track specific genes through DNA markers, so that seed selection is fast and accurate. Interestingly, this method can "pile" several resistance genes into one variety, allowing rice to resist multiple pests and diseases and harsh environments at the same time (Figure 1) (Haque et al., 2021). But then again, this new technology alone is not enough. Now many places are combining MAS with traditional breeding, and the effect is better (Miah et al., 2015; Steele et al., 2018). For example, disease resistance has been improved, and yield has not fallen, which is a compromise. In fact, MAS is not omnipotent, and it still cannot handle some complex traits. But it is undeniable that since the advent of this technology, breeding efficiency has indeed improved a lot. MAS has been of great help, especially to those regions that are in urgent need of new varieties.

2.3 Genome editing and CRISPR-Cas approaches

If we talk about the most cutting-edge technology in rice breeding now, CRISPR-Cas gene editing is definitely one of them. This thing is like a pair of gene scissors. It can change whatever you want and can accurately add, delete or adjust specific genes (Chen and Zhang, 2024; Ma, 2024). In recent years, researchers have used this technology to create a lot of good things. For example, some new varieties have higher yields, better rice quality, and stronger resistance to diseases and pests (Cui et al., 2019). The most amazing thing is that someone used it to create a thermosensitive sterile line, which is a key material for hybrid rice production (Zhou et al., 2016). But then again, although CRISPR is powerful, it is not omnipotent. It still can't handle some complex traits. But it is undeniable that this technology that can accurately modify genes has indeed brought revolutionary changes to breeding work (Tang et al., 2023). Breeding goals that used to take several years to complete can now be accomplished in a few months.

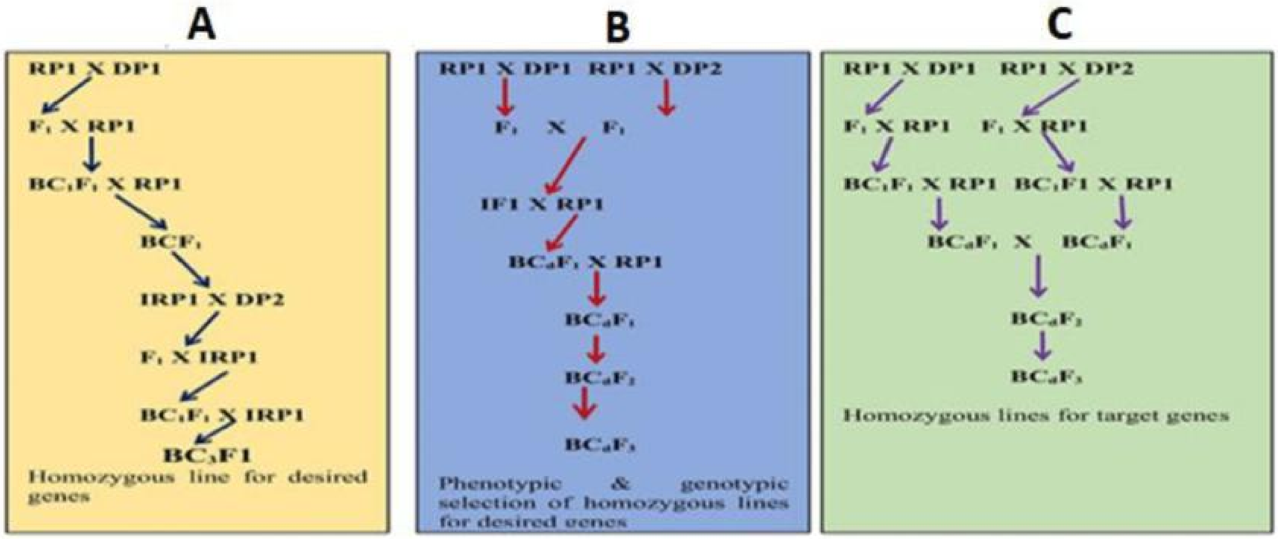

Figure 1 Schematic presentation of different backcrossing techniques for marker-assisted gene pyramiding. RP, recurrent parent; DP, donor parent; BC, backcross; IRP, improved recurrent parent; BCd, double backcross. (A) Stepwise transfer. (B) Simultaneous transfer. (C) Simultaneous and stepwise transfer combined. In order to develop a population of BC_1F_1, the F_1 populations are crossed back to the recurrent parents (RP) (Adopted from Haque et al., 2021)

3 Meta-Analysis Methodology

3.1 Data collection and criteria for study inclusion

This research mainly relies on reading various rice breeding literature. To be honest, I was quite picky when looking for information - I only chose those truly useful studies, especially those that talked about specific breeding techniques, genetic resources, and actual results data (Zhang, 2019; Zhang, 2021). I focused on studies using new methods, such as marker-assisted selection and gene editing, and they also had to have data on hard indicators such as yield and quality. Some studies are particularly valuable for reference, such as the study of the HJX74 single-segment replacement line, which was included because of its detailed methods and great contributions. However, not all studies can be used. Although some studies look good, they have to be passed if the data is incomplete. In addition, we also pay special attention to research that can guide practical applications, such as molecular design breeding (Bian et al., 2023). After all, theory alone is not enough, the key lies in whether it can be implemented.

3.2 Statistical methods and analytical tools

The study by Joshi et al. (2023) is quite interesting. They used an analysis method called meta-QTL (MQTL). This method is quite reliable and is particularly suitable for analyzing complex quantitative traits. Why was it chosen? It can narrow the confidence interval and find stable QTL loci under different genetic backgrounds and environmental conditions (Joshi et al., 2023). However, this alone is not enough. They also used tools such as GWAS and haplotype analysis. These methods are quite useful and can clarify the genetic structure and breeding history of rice varieties (Chen et al., 2017; Chen et al., 2023). To be honest, with these advanced analysis tools, it is much easier to find key genetic regions and know their specific contributions to excellent traits. There is also a very practical statistical technique used to calculate the economic benefits of rapid generation advancement (RGA). Through meta-analysis, they comprehensively evaluated the economic value of accelerated breeding methods (Lenaerts et al., 2018). This is very important. After all, breeding not only depends on technology, but also needs to consider cost-effectiveness.

3.3 Evaluation metrics for breeding approaches

This time, the evaluation of breeding methods mainly focuses on several hard indicators. Yield is definitely the primary one, and traits such as grain weight and plant height that directly affect the yield must be examined (Khahani et al., 2021). However, it is not enough to just look at the yield. We also have to see whether these new varieties perform stably under different environments. Interestingly, the new technologies nowadays are really powerful. Gene editing can produce many useful traits, and the efficiency of high-throughput genotyping has also increased a lot. Take the zinc content of rice as an example. Through analysis, it was found that to cultivate nutritious varieties, the key is to find stable and reliable QTL loci. Of course, genetic diversity is also an important indicator (Costa et al., 2020). Although some breeding plans have quick results in the short term, the gene pool is too single, which may not be a good thing in the long run. Therefore, when evaluating, we not only look at the current results, but also consider future sustainability. The accuracy of the experiment must also be checked so that we can find areas that need improvement.

4 Results of the Meta-Analysis

4.1 Effectiveness of conventional breeding approaches

When it comes to rice breeding, the old methods have indeed made great contributions. Over the past few decades, many high-yield, disease-resistant and delicious varieties have been bred through traditional breeding (Guo and Ye, 2014). However, the situation has changed a bit in recent years - the rate of yield improvement has slowed down significantly with the old methods alone. Interestingly, although traditional breeding is very good at improving the taste of rice (Lau et al., 2016), it is indeed time-consuming and labor-intensive, and not as accurate as the new methods. But then again, these old methods are not obsolete now. Many breeding projects are a combination of the old and the new, taking advantage of the strengths and weaknesses. After all, sometimes the most effective methods are these time-tested old methods.

4.2 Impact of marker-assisted selection on yield improvement

Marker-assisted selection (MAS) is a great help in rice breeding nowadays. This technology is easy to use and accurate, and is particularly suitable for improving various traits. Its best feature is to help rice resist pests and diseases, and maintain yield in harsh environments (Ludwików et al., 2015). Interestingly, MAS can "package" several resistance genes into one variety. In this way, rice can resist multiple pests and diseases and bad weather at the same time. Moreover, this technology is quite cost-effective. It not only improves breeding efficiency, but also allows good traits to be inherited stably (Bonnecarrère et al., 2019). Many breeding projects now like to combine MAS with rapid breeding. This combination is more efficient, and it is no wonder that it has become a popular choice in modern breeding. However, although MAS is very powerful, it is not applicable in all situations. It depends on the breeding goals.

4.3 Success rates of genome editing techniques

In the rice breeding circle, gene editing technologies such as CRISPR/Cas9 are very popular. Think about it, it used to take several years to change a gene, but now it can be done in a few days (Mehta et al., 2019). Especially for those troublesome things, such as increasing yield and enhancing disease resistance, the effect is particularly obvious. Using CRISPR/Cas9 to enhance rice disease resistance is a piece of cake (Figure 2) (Mishra et al., 2021). What's more, it can produce improved varieties without foreign genes, which makes approval much easier and faster to market (Singh et al., 2022). Recently, some people have mixed genome analysis and multiple editing technologies to improve varieties quickly and accurately (Liu et al., 2022). Although there are still some restrictions now, the prospects of these new technologies are indeed exciting. Maybe in a few years, the breeding method will change again.

5 Comparative Analysis of Breeding Approaches

5.1 Comparative performance of conventional and molecular breeding methods

When it comes to rice breeding, the old methods are indeed indispensable. For decades, farmers and breeders have relied on observing the appearance of plants to select seeds, and have cultivated many high-yield and disease-resistant varieties (Bai et al., 2018). However, this traditional method has a flaw - it is too time-consuming and the selection is not accurate enough. Now the situation is different. New methods such as marker-assisted selection (MAS) and gene editing have improved the accuracy. Take the GW6 gene, for example. The rice improved with it has larger and heavier grains and increased yield (Li et al., 2014). Coupled with technologies such as high-throughput genotyping, breeding new varieties is fast and accurate. Interestingly, the most effective method now is to combine the old and the new. The combination of the precision of molecular technology and the richness of traditional resources has surprisingly good results. Although the new methods are powerful, it is not realistic to completely abandon the old experience. The key is to find a balance.

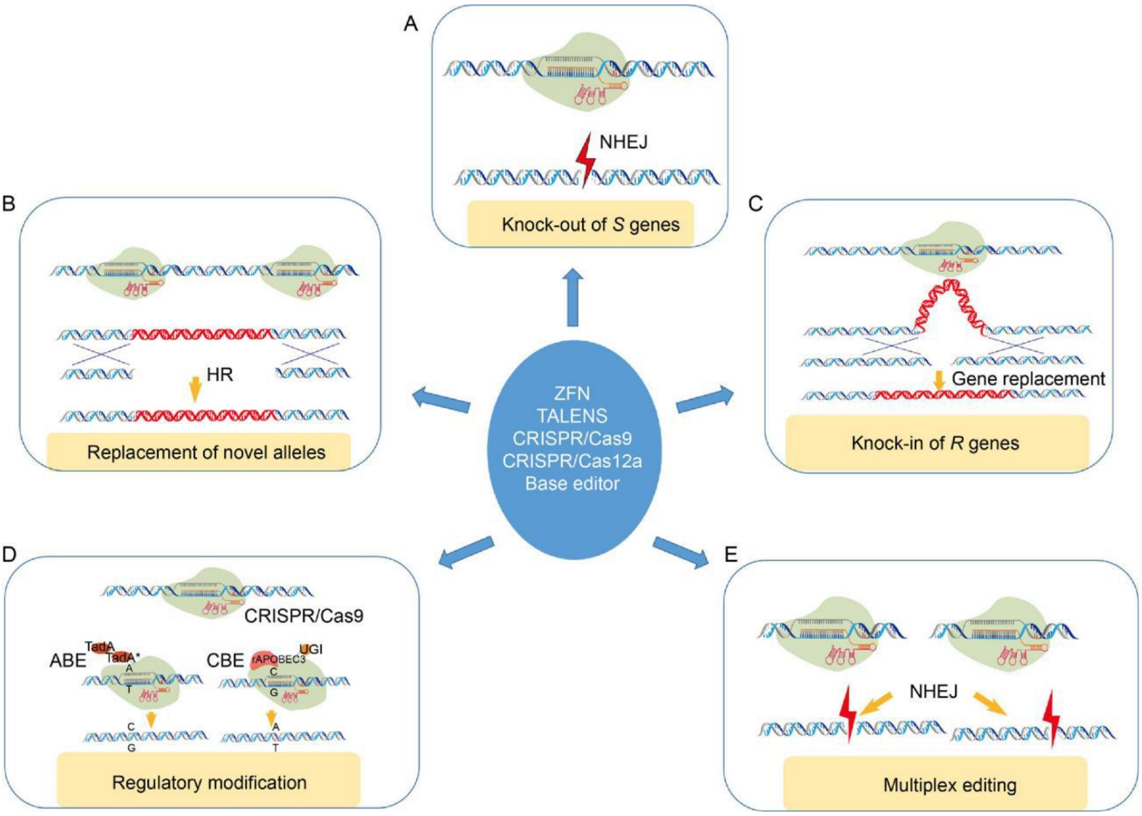

Figure 2 Genome editing strategies towards disease resistance in plants. Multiple genome editing platforms can facilitate disease resistance through knock-out of susceptibility (*S*) genes (A), homology directed replacement of novel alleles (B), knock-in of resistance (*R*) genes (C), regulatory modification of *R/S* gene expression (D) and multiplex editing of resistance and susceptibility factors (E) (Adopted from Mishra et al., 2021)

Note: HR, Homologous recombination; ZFN, Zinc finger nuclease; NHEJ, Non-homologous end joining; ABE, Adenine base editor; CBE, Cytidine base editor; UGI, Uracil DNA glycosylase (Adopted from Mishra et al., 2021)

5.2 Cost-benefit analysis of each breeding approach

When it comes to breeding costs, traditional methods and molecular methods have their own accounts to be calculated. Although the old method requires less equipment investment, it is time-consuming and labor-intensive, and it often takes several years for new varieties to be put on the market (Lenaerts et al., 2018). These days, food crises come and go, and we can't wait that long. Molecular breeding is different. Although it costs a lot of money to buy equipment and train personnel at the beginning, it is fast! For example, the rapid generation advancement (RGA) technology directly cuts the breeding cycle in half. Combined with marker-assisted selection (MAS), it can not only improve efficiency but also ensure stable inheritance of excellent traits (Bonnecarrère et al., 2019). Especially in emergency situations such as pests and diseases, the advantages of molecular breeding are more obvious. But then again, which method to choose depends on the actual situation. Small-scale breeding may still be cost-effective with the old method, but to deal with sudden agricultural crises or pursue high returns, molecular breeding is obviously a wiser choice. After all, the earlier the market is, the earlier the money is.

5.3 Analysis of breeding approaches in different agro-ecological zones

Rice breeding really depends on the local conditions. The soil and climate in different regions are very different, so breeding methods have to change accordingly. Although the old method is slow, the varieties selected through field trials have performed well in many places (Zhang, 2021). However, the environment is changing rapidly now, and the speed of traditional breeding is indeed a bit slow to keep up. At this time, the advantages of molecular breeding are revealed. For example, the HJX74-SSSL platform can accurately assemble genes and cultivate new varieties that are particularly adapted to local conditions (Chen et al., 2023). There is a good example in Northeast China. By analyzing the genome of rice, it is clear which characteristics are suitable for the local cold climate and black soil environment. Interestingly, in some places, varieties cultivated by traditional methods are more stable. So the most reliable approach now may be a combination of the old and the new - both understanding local genetic resources and using molecular technology to speed up. After all, there is no universal solution for breeding.

6 Challenges in Implementing Design Breeding in Rice

6.1 Limitations in genetic resources and diversity

The biggest headache for rice breeding now is that the genetic resources are too single. In recent years, breeders have repeatedly used the same few excellent varieties, resulting in a decreasing genetic diversity of rice (Costa et al., 2020). This is quite troublesome. After all, to improve varieties, new characteristics must be introduced through different genetic backgrounds. There are more problems. Many of the existing germplasm resources have not been thoroughly studied (Li et al., 2014). Sometimes there are good genes, but they are wasted because they are not fully identified. In particular, if you want to find new alleles that can improve stress resistance, the available sources are really limited. It's interesting to say that I used to think that variety improvement was a technical issue, but now I find that genetic resources are the real bottleneck. Without a rich gene pool, even the best breeding technology is difficult to implement.

6.2 Technical challenges in applying advanced breeding techniques

To be honest, it is not easy to use new technologies such as marker-assisted selection (MAS) and gene editing to breed now. First of all, you have to be able to do high-throughput genotyping and accurately determine plant traits. Both of these require money to invest in equipment and train professionals (Li and Zhang, 2013). But many breeding units simply cannot afford it. What is even more troublesome is combining old methods with new technologies. This task looks simple, but it is complicated to do. You have to understand traditional breeding and be proficient in molecular technology. Take finding QTL loci as an example. If you encounter complex traits controlled by multiple genes, it is particularly difficult to verify (Khahani et al., 2021). Sometimes, even if you find the loci, you find that the effect is not ideal when you actually use them in breeding. In fact, the most troublesome thing is that some traits look simple, but behind them are a bunch of genes interacting with each other. In this case, even if you use the most advanced technology, it may not be effective immediately.

6.3 Economic and policy barriers to adoption

Money and policy are really big problems for rice breeding now. Especially for public breeding institutions and small farmers, seeing the price tag of new technology gives them a headache (Sagare et al., 2020). Technologies such as genetic modification and gene editing are even more troublesome. The approval process alone can take several years. It's interesting to say that although we know that these new technologies can increase yields, they just can't be promoted. On the one hand, it's because the investment is too large, and on the other hand, the policy support is not stable enough (Qian et al., 2016). Today this leader says he wants to develop, but tomorrow he may change his mind. In fact, the most frustrating thing is that some places are in urgent need of new varieties, but they are stuck in the regulatory link and can't move. Funding is also intermittent, which makes breeding plans always intermittent. In my opinion, technology alone is not enough. Without continuous policy and financial support, no matter how good the breeding method is, it can only stay in the laboratory.

7 Case Study

7.1 Background of the selected case study

The history of rice cultivation in Northeast China is quite long, and local farmers have their own set of planting experience. This time we focused on the breeding situation here, mainly to see how they put the design breeding into practice (Chen et al., 2023). NEC's breeding project is quite interesting. They not only use traditional breeding, but also combine a lot of modern molecular technology. After all, the climate in Northeast China is special, with short summers and long winters. Ordinary rice varieties may not grow well here. They just saw this and specially cultivated varieties suitable for local conditions. Speaking of which, the key to the success of this project may be to respect tradition while not rejecting new technologies. The old method is used to maintain the stability of the variety, and the new technology is used to improve efficiency and accuracy. However, the specific operation is definitely not that simple, after all, there are too many things to take into account.

7.2 Key breeding strategies employed and their outcomes

The NEC rice breeding project in Northeast China is quite interesting. They have developed a new method called "designed breeding". Simply put, it is to precisely control the key genes that affect yield (Zhang, 2021). They used the high-quality variety Huajingxian 74 as a basis to build an SSSL gene bank (Figure 3), and added any good genes they wanted. The effect is really good. The new varieties bred are both high-yielding and disease-resistant. For example, the genes for bacterial wilt resistance and insect resistance are packaged together, and they can also withstand waterlogging and salinity (Ludwików et al., 2015). The most rare thing is that these new varieties are not only highly resistant, but also have good yield and quality. They mainly rely on marker-assisted selection and gene stacking technology to achieve this. Although the operation is quite complicated, it does work.

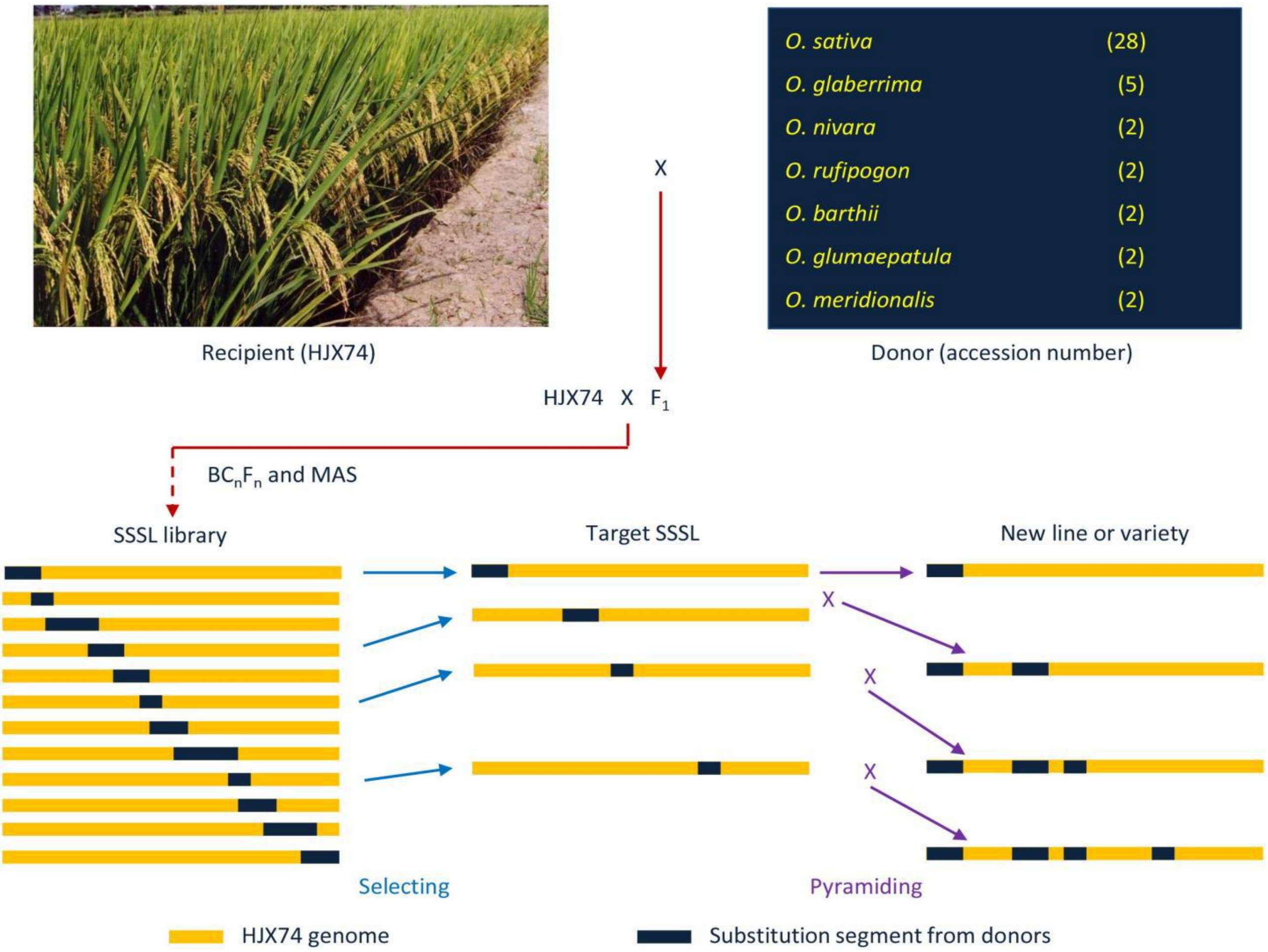

Figure 3 Construction of the HJX74-SSSL library and its application in rice breeding by design. MAS, marker-assisted selection (Adopted from Zhang, 2021)

7.3 Lessons learned and implications for broader application

The NEC breeding project has indeed come up with a lot of ideas, which are quite valuable for breeding work in other places. The smartest thing about them is that they mix old methods with new methods - retaining the resources of traditional breeding and adding modern technologies such as marker-assisted selection (Cui et al., 2019). In this way, it is much faster to breed rice varieties suitable for the local area. Their SSSL gene bank is also very critical. By precisely controlling gene mutations, not only the breeding speed is increased, but the genetic diversity of new varieties can also be well maintained. However, the most eye-catching thing may be the rapid generation advancement technology (RGA). Although the investment is a bit large, it is actually very cost-effective in the end (Bonnecarrère et al., 2019). If the new variety is put on the market one year earlier, farmers can benefit one year earlier. Policymakers should carefully calculate this account. In the final analysis, the success of this project tells us that breeding should not be too rigid. The old experience that should be adhered to should be adhered to, and the new technology that should be used should also be boldly used. The key is to find a balance that is suitable for the local area, after all, the rice planting conditions in each place are not the same.

8 Lessons from the Meta-Analysis

8.1 Key takeaways from the effectiveness of breeding approaches

Speaking of rice breeding, I recently did a comprehensive analysis and found some interesting things. The new idea called "design breeding" is quite promising. To put it simply, it is to select the best genes and combine them together. The SSSL gene bank is particularly suitable for this, and the effect has been verified (Qian et al., 2016). Hybrid super rice is also a highlight. By combining the advantages of different subspecies, the yield and quality have increased. However, the most practical technology may still be molecular technology, such as marker-assisted selection, which is particularly effective in increasing grain weight and yield. Early generation tests have performed well in upland rice breeding, and genetic gain is quite ideal. But to be honest, these methods have their own uses, and the key depends on what specific problems are to be solved. Sometimes the simplest method is the most effective. In breeding, we really can't just pursue new technologies.

8.2 Implications for future breeding strategies in rice

Now, in rice breeding, both old methods and new methods have to be used. From this study, it can be seen that design breeding is indeed effective. The key is to build a good gene bank and select useful traits for combination (Zhang, 2019). Hybrid rice is a good example. The use of scientific methods to design can indeed improve yield and quality. However, this alone is not enough. Technologies such as marker-assisted selection and gene editing must also keep up. After all, they are efficient and can accurately achieve breeding goals. Interestingly, the effect of early generation trials is also very good, which shows that it is important to evaluate breeding methods regularly. Breeding cannot remain unchanged. It must be constantly adjusted to achieve continuous progress. In the final analysis, no method is omnipotent. Traditional technology has its value, and modern methods also have unique advantages. The key is to flexibly match according to specific needs, and be conservative when necessary and innovative when necessary. After all, our goal is clear - to grow better rice.

8.3 Recommendations for optimizing breeding programs

In the matter of breeding, the emphasis is now on "walking on two legs". The old methods cannot be abandoned, and new technologies must keep up. First of all, the gene bank must be larger. SSSL is quite practical and it is much easier to find good genes (Barros et al., 2018). When designing new varieties, you have to use your brain to combine the advantages of different varieties. In actual operation, marker-assisted selection and gene editing are indeed trouble-free, and the selection of traits is fast and accurate. Early generation trials must continue, but attention must be paid to controlling costs. After all, breeding funds are not blown by the wind. It's interesting to say that now we have to deal with population growth and climate change, and the requirements for rice varieties are getting higher and higher. However, as long as these methods are combined well, there is still great hope to breed new varieties with high yield and quality. The key is to be flexible and not stick to one method. Use whatever you need.

9 Future Directions for Rice Breeding

9.1 Integration of multi-omics data for enhanced breeding precision

Rice breeding is becoming more and more interesting now, and all kinds of omics data can be used - genome, transcriptome, proteome, metabolome, none of which can be missing (Mahmood et al., 2022). Thanks to the advancement of second-generation sequencing technology, gene editing and assembly of alleles are now much more accurate. Putting these omics data together for analysis is surprisingly effective. Not only can models be built to predict complex traits, but the breeding accuracy is also greatly improved (Yang et al., 2021). Interestingly, if the phenotypic data of the parents are also included, the prediction of hybrid rice yield-related traits will be more accurate (Xu et al., 2020). But to be honest, it was a headache when I first started doing this. The amount of data is too large and it is very difficult to analyze. But now it seems that multi-omics integration is indeed a major trend in future breeding. Although the operation is a bit complicated, these investments are still worth it in order to breed better rice varieties.

9.2 Leveraging AI and machine learning in rice breeding

Nowadays, there is too much data in rice breeding. However, technologies such as AI and machine learning can come in handy (Cembrowska-Lech et al., 2023). They are best at organizing the messy and massive data clearly and helping to analyze plant traits. It is interesting to say that these technologies can not only process data, but also predict crop performance. For example, when is it likely to get sick, what will happen when encountering bad weather, you can know in advance. In particular, the combination of AI and multi-omics data is much more effective than the old method. Of course, it does not mean that traditional methods are useless. But in the face of such complex breeding needs, AI does provide new ideas. Although it may not be easy to use at the beginning, in the long run, this kind of intelligent predictive breeding should become more and more important. After all, the data will only increase, and manual analysis alone will definitely not be enough.

9.3 Policy recommendations for supporting advanced breeding approaches

Now, for breeding, technology alone is not enough, policy support is the key. The government and research institutions need to invest more money to truly apply those high-end multi-omics technologies and artificial intelligence to breeding (Gong et al., 2022; Chao et al., 2023). It is also very important to build a decent database to bring together all kinds of omics data for convenient use. When it comes to supervision, the current regulations are a bit behind the times. New technologies such as gene editing and genetic modification are developing so fast that relevant policies must be updated in a timely manner (Bao, 2019). Otherwise, it would be a pity if new varieties are cultivated and stuck in the approval process. In fact, enterprises and scientific research institutions can cooperate more. Going it alone is too inefficient, and only by joining forces can the promotion of new technologies be accelerated. In the final analysis, these investments are all for one goal - to ensure that everyone can have enough food and eat sustainably. Although there is still a long way to go, as long as the direction is right, there will always be results if we take it slow.

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Conflict of Interest Disclosure

The authors affirm that this research was conducted without any commercial or financial relationships that could be construed as a potential conflict of interest.

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