

Feature Study

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Advances in the Collection and Utilization of Fresh-Eating Maize Germplasm Resources

Xingzhu Feng ✉

Hainan Institute of Biotechnology, Haikou, 570206, Hainan, China

✉ Corresponding author: xingzhu.feng@hibio.org

Maize Genomics and Genetics, 2025, Vol.16, No.2 doi: [10.5376/mgg.2025.16.0006](https://doi.org/10.5376/mgg.2025.16.0006)

Received: 13 Jan., 2025

Accepted: 27 Feb., 2025

Published: 10 Mar., 2025

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Preferred citation for this article:

Feng X.Z., 2025, Advances in the collection and utilization of fresh-eating maize germplasm resources, Maize Genomics and Genetics, 16(2): 60-69 (doi: [10.5376/mgg.2025.16.0006](https://doi.org/10.5376/mgg.2025.16.0006))

Abstract As the core foundation of fresh corn breeding, germplasm resources play a key role in the selection and industrial application of new varieties. This study summarizes the progress of the collection and utilization of fresh corn germplasm resources, focusing on the development of high-quality traits and the screening methods of stress-resistant resources. The study found that the global fresh corn germplasm resources show rich diversity in quality (such as sweetness and stickiness), resistance (such as drought resistance and salt tolerance) and nutritional traits (such as high zinc and high vitamin A). Modern technologies, including molecular marker-assisted selection, genomic selection and CRISPR/Cas9 gene editing technology, have significantly improved the screening efficiency and breeding accuracy of germplasm resources. In addition, the commercial development of local germplasm resources and the promotion of regionally adaptable new varieties have provided successful cases for market demand-oriented breeding. Future research needs to be further deepened in terms of germplasm resource protection, evaluation standardization, technological innovation and international cooperation to achieve sustainable utilization and industrial application of resources. This study provides a comprehensive reference for the development and utilization of fresh corn germplasm resources and points out the direction for breeding work and agricultural development.

Keywords Fresh-eating maize; Germplasm resources; Collection and conservation; Modern breeding technologies; Commercial applications

1 Introduction

Speaking of corn, it is really a "jack of all trades". In developing countries, it is the main product on the tables of ordinary people and feeds countless people (Nuss and Tanumihardjo, 2010). But you may not know that corn is used for much more than just filling your stomach. It is used to feed livestock and is also indispensable for making biofuels (Ortiz et al., 2010). Interestingly, although developed countries use corn mainly as an industrial raw material, it is still a life-saving food in many places. A study in 2020 pointed out that corn's dual identity makes it particularly important (Palacios-Rojas et al., 2020). To be honest, from farms to factories, to ordinary people's rice bowls, corn is really indispensable. Although there are so many types of crops now, it is rare to find one that can be used as both a food and an economic crop like corn.

Corn farmers are having a hard time now. In the past, corn production was mainly based on yield, but now consumers not only care about yield, but also protein content and vitamin nutrition (Palacios-Rojas et al., 2020). This is the case worldwide, and the requirements for corn quality are getting higher and higher (Langyan et al., 2022). But the problem is that corn production is now more troublesome - droughts are common, and pests and diseases are becoming more and more difficult to deal with (Wattoo et al., 2018). Breeding experts are now in a dilemma: on the one hand, they have to improve nutrition, and on the other hand, they have to make corn more disease-resistant and drought-resistant. Although some research has made breakthroughs (Wang et al., 2022), it will probably take a while to breed a perfect new variety.

To put it bluntly, germplasm resources are a "gene treasure chest". Although there were studies in 2010 that said they were particularly important (Ortiz et al., 2010), we cannot just keep them and not use them. Now with new tools such as CRISPR (Andorf et al., 2019), breeding is indeed much faster. But then again, the drought and

disease resistance genes in old varieties are becoming more and more valuable. Although new technologies such as genomic selection are powerful (Wang et al., 2022), without the old varieties as a foundation, the effect will be discounted. In the final analysis, to solve the future food problem, we still have to dig out these old genes and make good use of them.

This study mainly talks about the fresh corn germplasm resources. Let's talk about collection and preservation first. The technology has indeed made a lot of progress in recent years. Breeding is also very interesting. Various new tools emerge in an endless stream, which are very helpful in improving corn quality and yield. But having said that, although there have been a lot of progress, we still need to think about how to make good use of these resources. Finally, we will also talk about the future development direction. After all, germplasm resources are not wasted if they are just stored. In the final analysis, the key is to make these good resources truly serve breeding.

2 Types and Distribution of Fresh Corn Germplasm Resources

2.1 Types of germplasm resources

There are actually several types of fresh corn, and the ways of eating them are also different. The most special one is sticky corn. After being cooked, the sticky taste is very unique and is particularly popular in China and Southeast Asia (Ruanjaichon et al., 2022). Everyone has eaten ordinary sweet corn, but super sweet corn is even more amazing, with an astonishingly high sugar content (Dong et al., 2019), which is especially popular among sweet lovers. Although they are all fresh corn, the difference is quite obvious - sticky corn wins in taste, while sweet corn and super sweet corn mainly win in sweetness (Dermail et al., 2021). Interestingly, people in different places have different preferences for these corns. Some places like sticky ones, while others like super sweet ones.

These types of fresh corn really depend on the occasion. Sticky corn is most suitable for traditional eating, and it is particularly fragrant when simply boiled in water - although the yield may not be as good as other varieties. There are many ways to play with sweet corn and super sweet corn. In addition to eating them directly, it is also common to make them into canned and frozen foods (Dang et al., 2023). But what's interesting is that the study found that not only do they taste good, but even their growth characteristics such as plant height and ear position are different from ordinary corn. This brings up a problem: super sweet corn is sweet enough, but its ability to resist diseases and pests may be worse; although sticky corn has a lower yield, it has a high market acceptance. In the final analysis, which one to choose depends on local conditions and consumer preferences.

2.2 Geographic distribution and diversity

The places where fresh corn is grown the most are mainly North America, China and Southeast Asia. North America is particularly interesting, with sweet corn and super sweet corn grown the most, after all, Americans love this, whether they eat it directly or process it into cans. China and Southeast Asia are different, glutinous corn is particularly popular here (Ruanjaichon et al., 2022), which may be related to the local people's love of the sticky taste. But then again, these places actually have a rich variety of corn varieties, including various local varieties and wild species (Dong et al., 2019).

Although there are only a few mainstream varieties now, these "local varieties" have a lot of good things hidden in them, which are particularly useful for breeding goals such as disease resistance and increased yield (Dang et al., 2023). Of course, in each specific place, farmers' considerations for seed selection may be different.

2.3 Potential of wild and landrace varieties

Those who are engaged in corn breeding know that those inconspicuous local varieties and wild species are actually quite valuable. Although they may not look good, they are indeed resistant to drought and disease (Dong et al., 2019), and can grow well in barren land - the current delicate commercial varieties do not have this ability. Studies have found that these old varieties are particularly rich in genetic diversity (Ruanjaichon et al., 2022), and transferring good genes to modern varieties through hybridization can indeed improve stress resistance. In 2023, experiments confirmed the effectiveness of this method (Dang et al., 2023). However, these resources are becoming increasingly scarce. If they are not protected in time, they may not be found in the future.

3 Collection and Conservation of Fresh Corn Germplasm Resources

3.1 Germplasm collection methods

There are many ways to collect corn germplasm resources. The most direct way is to go to the fields to collect, especially those local varieties that farmers keep for themselves (Vidal et al., 2020) (Figure 1). The study shows how to determine the best collection strategy through diversity surveys. However, field collection alone is not enough. It is also important to talk to farmers, so that you can learn a lot of local planting tips and variety characteristics. Of course, the collected seeds must be well preserved, and this is what gene banks do - Nass and others emphasized the value of long-term preservation in 2000 (Nass and Paterniani, 2000). Although technology is advanced now, these basic work is still indispensable. After all, no one knows when the unique genes of an old variety will be needed.

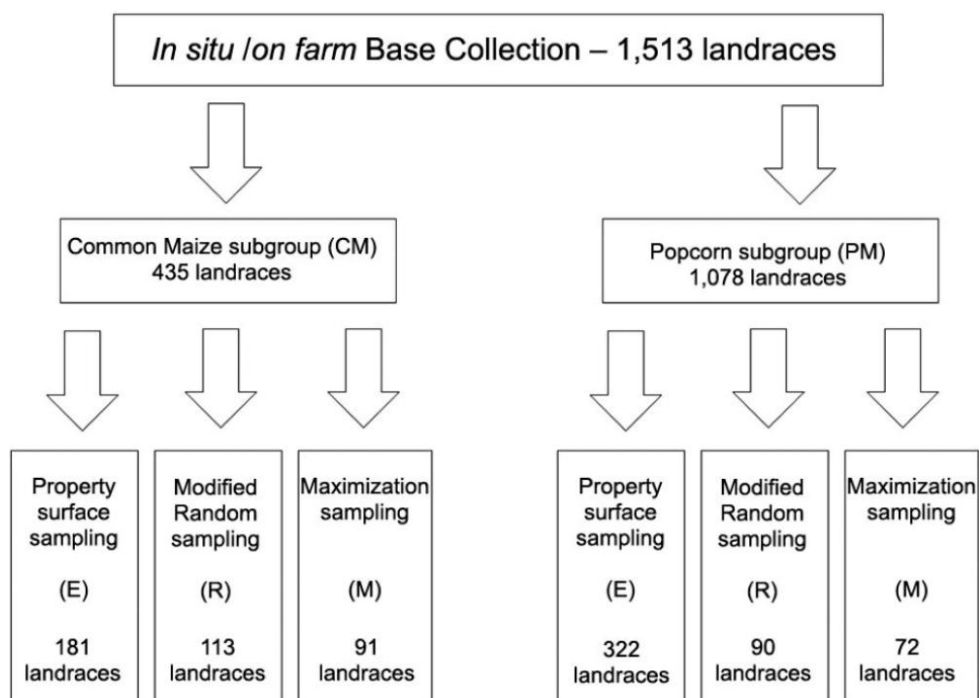


Figure 1 In situ/on farm Base Collection, subgroups and sampling strategies for maize landraces (Adopted from Vidal et al., 2020)

3.2 Germplasm preservation techniques

When it comes to preserving corn germplasm resources, there are quite a few methods. The most commonly used method is freezing in gene banks, and large warehouses like CIMMYT are quite reliable (Guzzon et al., 2021). Interestingly, the basic bank at minus 15 degrees Celsius has a better preservation effect than the active bank at minus 3 degrees Celsius, and the seeds can survive longer. However, it is not enough to just store them, and the vitality of the seeds must be checked regularly, and arrangements must be made when it is time to re-breed. A study in 2021 mentioned that field preservation is also a good method (Stagnati et al., 2021), especially for those local varieties, directly planting them in their place of origin can maintain their characteristics. Of course, each method has its advantages and disadvantages, and the key depends on what specific materials are to be preserved.

3.3 Phenotypic and genetic diversity assessment

The evaluation of corn germplasm resources must be approached from multiple angles. In a study conducted in Italy, by measuring appearance traits such as plant height and ear type, it was found that different local varieties were quite different (Stagnati et al., 2021). However, looking at the appearance alone is not enough, molecular marker analysis can better explain the problem. For example, the national corn inbred seed bank in the United States used SNP markers to detect and found more than 680 000 variant sites (Romay et al., 2013). Although SSR markers were used early, SNPs are more popular now because the data is more detailed. Interestingly, some varieties look similar, but they are very different at the genetic level. Of course, in actual operations, these two methods must be combined to fully evaluate genetic diversity.

3.4 Development and sharing of global germplasm databases

When it comes to germplasm research, there have been great changes in recent years. I remember that in the past, each region managed its own data, but now there is a global database, the situation is much better. Although the system needs to be improved, these databases are indeed very practical, with everything from phenotypic to genotypic data (Andorf et al., 2019). The advancement of sequencing technology is also a key factor, which has greatly improved the quality of data. Of course, there are still some minor problems in the specific operation, but for breeding and conservation work, being able to share these resources has been a great help. After all, making good use of this genetic information is very important for solving food security problems.

4 Progress in Utilizing Fresh Corn Germplasm Resources

4.1 Development and utilization of high-quality traits

Fresh corn breeding now focuses on several key points - it must be sweet enough, sticky, and disease-resistant. Although progress in disease resistance is relatively slow, there have indeed been many breakthroughs in improving sweetness and stickiness. For example, studies have found that the *sh2* gene has a great influence on sweetness (Ruanjaichon et al., 2021), while the *qWx9* locus can effectively distinguish between sticky and non-sticky varieties (Ruanjaichon et al., 2022). GWAS analysis is also very useful, helping us quickly identify key genetic markers (Hou et al., 2024). However, the good results in the laboratory may not be the same when they are actually planted in the field, and they still have to go through a lot of tests and verifications in the middle.

4.2 Utilization of stress-resistant traits

Now, stress resistance has become a top priority in corn breeding. The climate is becoming more and more unstable, and problems such as drought and salinity are becoming more and more common (Cai et al., 2024). CIMMYT has done a good job in this regard. They have promoted a number of stress-resistant varieties in Africa and Asia, and the field test results are quite good (Prasanna et al., 2021). However, when it comes to drought resistance research, Badr's experiment is quite interesting - using PEG to simulate drought, the higher the concentration, the worse the corn grows (Badr et al., 2020) (Figure 2). The study clearly shows this change. Interestingly, some particularly drought-resistant materials were found through screening. Although the number is small, it at least provides a direction for subsequent breeding. Of course, whether these varieties can adapt to the actual planting environment depends on their field performance.

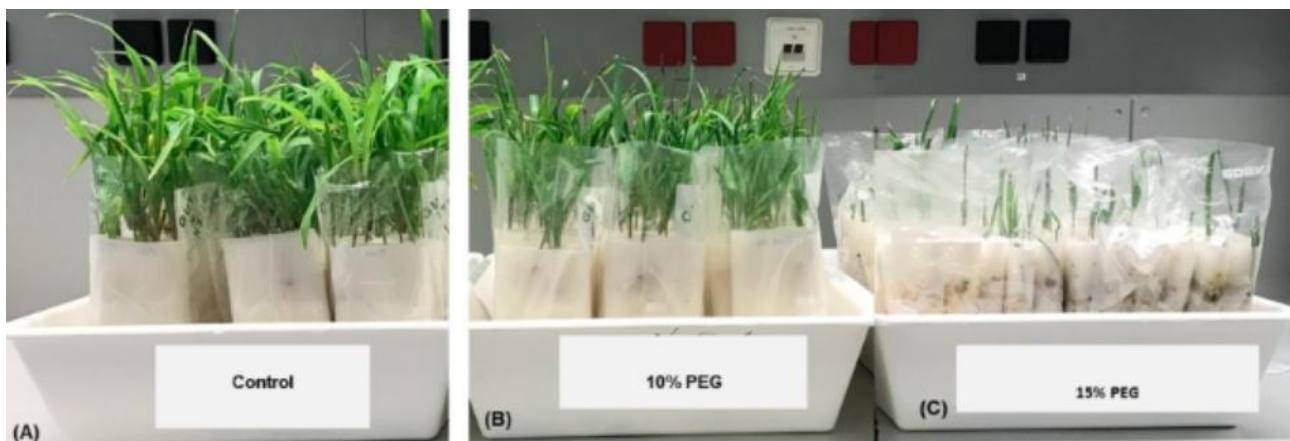


Figure 2 Photographs illustrating the impact of 10% and 15% PEG treatments on 21 days old seedlings of maize accessions (Adopted from Badr et al., 2020)

Image Caption: (A) control, (B) 10% PEG, (C) 15% PEG (Adopted from Badr et al., 2020)

4.3 Development of nutritional traits

When it comes to nutritional improvement of corn, people actually paid more attention to yield issues in the early years (Jompuk et al., 2020). But now the situation has changed a bit, and researchers have begun to focus on improving trace elements such as zinc and vitamin A-although work on reducing the glycemic index is still ongoing. Interestingly, by combining different mutants, such as putting the *shrunken2* (*sh2*), *purple* (*Pr1*) and

opaque2 (*o2*) gene mutations together, it was unexpectedly discovered that not only the sugar content of sweet corn increased, but also the anthocyanin and tryptophan content increased. Of course, the corn cultivated by this new method does perform well in terms of protein quality and has good antioxidant properties, but it may take some time to observe whether it can be actually promoted. In general, these improvements make fresh corn more nutritious, although it is still far from perfect.

4.4 Hybrid breeding and parental line selection

Anyone who is engaged in corn breeding knows that it is not easy to breed high-yield and lodging-resistant varieties. In the past, parents were basically selected based on the experience of old masters, and the results were mixed. Now there are some new methods, such as hybridization with tropical and temperate germplasm (Ndou et al., 2021), and there is no need to worry about lodging even if the seeds are planted densely. But this is not enough. Recently, new technologies such as GS and GWAS have been of great help (Dang et al., 2023), especially in predicting difficult traits such as plant height and ear position, which are much more accurate than before. But in the final analysis, no matter how good the technology is, it must be based on high-quality germplasm resources. Although mixing these methods does improve efficiency, the specific operation still needs to be adjusted according to the actual situation.

5 Application of Modern Technology in the Utilization of Fresh Corn Germplasm Resources

5.1 Marker-assisted selection (MAS)

When it comes to marker-assisted selection (MAS) in corn breeding, the earliest method used was actually traditional phenotypic screening, which was not very efficient. However, with the advent of molecular markers such as SNP, the situation is much better - although there are still some technical difficulties in actual operation. Interestingly, with the popularization of NGS technology, methods such as GBS have been developed (He et al., 2014), which can not only process a large number of samples at the same time, but also is relatively affordable. Of course, this technology is not omnipotent, but it has indeed helped a lot in GWAS and genetic diversity research (He et al., 2014; Kumawat et al., 2020). In general, screening for excellent traits is much faster now than before, but the specific effect depends on the experimental design and material selection.

5.2 Genomic selection (GS)

Corn breeding used to rely mainly on experience, but now with genomic selection (GS) technology, the situation is indeed different. Although there are still problems such as too much data in actual operation, GS can indeed predict breeding value through whole genome markers (Crossa et al., 2017). Interestingly, it not only speeds up the breeding process, but also has a good effect on improving complex traits such as yield and resistance (He and Li, 2020), especially when combined with high-throughput data, even the interaction effect between genotype and environment can be taken into account (Rice and Lipka, 2021). Of course, the most practical use may be to cultivate varieties that adapt to climate change (Budhlakoti et al., 2022), after all, there are more and more extreme weather now. But then again, although GS improves the accuracy of prediction, the effect may still be different for each breeding project.

5.3 Gene editing technologies (CRISPR/Cas9)

When it comes to improving fresh corn, breeding experts are now discussing the CRISPR/Cas9 technology. Although traditional breeding methods have been used for so many years, they do have problems with long cycles and low efficiency. Interestingly, this gene editing tool can directly and precisely modify corn DNA (He and Li, 2020), making it much easier to operate than before, whether it is to improve drought resistance or increase nutritional content. Of course, there are still some technical difficulties in actual application, but it is undeniable that CRISPR/Cas9 does make it faster to cultivate new varieties that are resistant to diseases and adapt to climate change. But then again, it may take time for this new technology to completely replace traditional breeding.

5.4 Integration of multi-omics technologies

Now, when studying corn variety improvement, it is not enough to just look at the external characteristics. Researchers have found that combining transcriptomics, metabolomics, and proteomics is more effective (He and

Li, 2020). Although each technology has limitations when used alone, such as transcriptomics can only look at gene expression, and metabolomics mainly analyzes metabolites, but analyzing their data together can provide a more comprehensive understanding of the ins and outs of corn trait formation. Interestingly, this method can not only find key genes, but also discover important metabolic pathways. Of course, the amount of data in actual operation will be very large, but it does help breeders screen out excellent varieties more quickly.

6 Development and Commercial Applications of Fresh Corn Germplasm Resources

6.1 Commercialization of local varieties

In the field of corn breeding, local germplasm resources have always been a treasure trove, although it is indeed difficult to use. Take tropical corn for example. On the surface, it does not match the temperate environment, but experiments have shown that they contain many good genes (Hallauer and Carena, 2014). Now more and more breeding projects are starting to target these local varieties, especially to meet the needs of specific regions. However, it is certainly not enough to rely on university research institutes alone. Thanks to those public-private partnership projects (Byerlee, 2020), old varieties and new technologies have been linked together. But the specific effect depends on the local water, soil and climate. It is not applicable to all places.

6.2 Promotion of ecotype fresh corn

When it comes to corn variety improvement, more and more attention is paid to new varieties that adapt to specific environments. Although traditional varieties perform well under ideal conditions, they cannot withstand extreme weather such as drought and high temperatures. CIMMYT has done a lot of work in this regard (Prasanna et al., 2021). They use tropical corn germplasm with strong stress resistance and modern breeding technology to cultivate a batch of more adaptable varieties. Interestingly, these new varieties have indeed performed well after being promoted in rain-fed areas (Ortiz et al., 2010). They are not only resistant to diseases, but also have relatively stable yields. Of course, some adjustments may need to be made in different regions, but the path of eco-breeding has indeed helped farmers solve many practical problems.

6.3 Market-oriented resource development

The market now has higher and higher requirements for fresh corn. It must not only taste good, but also look good and be easy to process. Although traditional breeding can also improve quality, progress is relatively slow. Interestingly, new methods such as double haploid technology have been used recently (Andorf et al., 2019). Through precise regulation of genomic information, the bred corn has significantly improved taste and processing performance. However, laboratory research alone is not enough. Involving farmers in improvement, as in the Chiapas region of Mexico (Bellon and Risopoulos, 2001), and adjusting according to local actual conditions will have better results. Of course, in specific operations, each place may have to explore a path that suits them.

7 Successful Cases of Fresh Corn Germplasm Development

7.1 Breeding of high-sugar varieties

When it comes to sweet corn breeding, the original intention was to make corn sweeter. Researchers have found that by regulating the starch synthesis pathway, especially by introducing recessive genes such as *sh2* (Revilla et al., 2021), corn can accumulate more sugar. Interestingly, by combining the mutant genes *sh2*, *Pr1* and *o2* (Jompuk et al., 2020), not only the sweetness is improved, but also the protein and anthocyanin content. Of course, there will be many problems in actual operation. For example, Saha et al. (2022) used backcrossing technology to successfully combine the two characteristics of high sugar and stress resistance (Figure 3). Most of the popular sweet corn varieties on the market now come from this, although the taste preferences of consumers in different regions may be different.

7.2 Commercialization of waxy corn

Sticky corn is particularly popular in Asia, especially in China and Southeast Asia, where people often cook and eat it directly (Ruanjaichon et al., 2022). However, to make it taste better, breeders have come up with many ways. For example, hybridizing super sweet corn with sticky corn, so that the improved variety tastes more fragrant. Although traditional breeding methods are time-consuming, now with functional markers such as MassArray,

screening is much more convenient. Of course, people in different places may have different requirements for the taste of sticky corn, but in general, this sticky and sticky corn has become an indispensable delicacy on the local people's tables.



Figure 3 Morphological characteristics of parents and their offspring (Adopted from Saha et al., 2022)
 Image Caption: (A tassel, B silk, and C cob) in parents and improved line (DBT 17-1-1-1-35-1) from *BC2F3* generation of SC11-2×UMI 1230β1+ (Adopted from Saha et al., 2022)

7.3 Application of local germplasm in stress-resistant breeding

In places like Asia and Africa, farmers often have trouble growing corn because of the increasing drought and high temperatures caused by climate change. Although traditional varieties are fine in normal years, they cannot withstand extreme weather. Institutions such as CIMMYT have developed some tropical corn varieties with strong stress resistance (Prasanna et al., 2021), which have shown good results after being promoted in Africa, Asia and Latin America. But having good varieties alone is not enough. Thanks to public-private partnerships, these improved seeds can be delivered to farmers. Of course, the specific problems faced by different regions may be different, but at least there are more ways to deal with climate change.

8 Challenges and Future Directions in Fresh Corn Germplasm Research

8.1 Protection and sustainable utilization of germplasm resources

The protection of corn germplasm resources is now under great pressure. Global warming and land use change have made the problem more difficult - especially for corn in tropical rain-fed areas, where extreme weather such as drought and high temperature will affect yield (Prasanna et al., 2021). Although some highly adaptable varieties have been developed through breeding, this alone is not enough. Interestingly, people like Nass have long reminded (2000) that maintaining genetic diversity is particularly important for future breeding work. Many institutions are now building germplasm banks to preserve seed vitality under optimal storage conditions (Guzzon et al., 2021), but various problems are still encountered in actual operations. Of course, the public-private partnership model has indeed helped a lot, but to completely solve the problem, more efforts may be needed.

8.2 Standardization of germplasm evaluation

The management of corn germplasm resources is not an easy job. Standards vary from place to place, making it very difficult to operate. Although studies in the 1990s provided a good way to maintain genetic diversity (Crossa et al., 1994), the actual implementation was always a little lacking. Recently, standardized phenotyping technology has been developed (Prasanna et al., 2021), making resource evaluation much smoother. However, in order to achieve cross-regional resource sharing (Yang et al., 2011), technical standards alone may not be enough, and the actual conditions in various places must also be taken into account. Unified standards are of course important, but some flexibility must be left in actual operations.

8.3 Multidisciplinary collaboration and innovation

Germplasm resource protection is something that cannot be solved by a single discipline. When fields such as genetics and agronomy come together, new ideas can often be generated - although there are many communication barriers between disciplines in actual operations. For example, breeding with doubled haploid technology, combined with high-throughput phenotyping analysis, has indeed achieved good results (Prasanna et al., 2021). But then again, technology alone is not enough, and cooperation between the government and enterprises is also crucial. After all, they have to build bridges to promote new varieties. Of course, this cross-border cooperation model may have to be adapted to local conditions for each project.

8.4 International cooperation and data sharing

When it comes to corn germplasm resources, global collaboration is becoming increasingly important. Although each country has its own resource bank, international organizations such as NPGS do provide a lot of high-yield germplasm (Kurtz et al., 2016). Interestingly, international agreements such as ITPGRFA make resource exchange much smoother, but there are still various problems in specific implementation. Of course, resource sharing alone is not enough. Collaborative breeding projects such as those mentioned by Ortiz et al. (2010) may be more practical. After all, food security is a global challenge. Although the breeding goals of different countries may be different, data sharing and cooperation can indeed make germplasm resources more valuable (Kurtz et al., 2016).

Acknowledgments

Many thanks to Dr. Huang for their support and assistance in literature review and data analysis.

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.

References

- Andorf C., Beavis W.D., Hufford M., Smith S., Suza W.P., Wang K., Woodhouse M., Yu J., and Lübberstedt T., 2019, Technological advances in maize breeding: past, present and future, *Theoretical and Applied Genetics*, 132(3): 817-849.
<https://doi.org/10.1007/s00122-019-03306-3>
- Badr A., El-Shazly H.H., Tarawneh R.A., and Börner A., 2020, Screening for drought tolerance in maize (*Zea mays* L.) germplasm using germination and seedling traits under simulated drought conditions, *Plants*, 9(5): 565.
<https://doi.org/10.3390/plants9050565>
- Bellon M.R., and Risopoulous J., 2001, Small-scale farmers expand the benefits of improved maize germplasm: a case study from Chiapas, Mexico, *World Development*, 29(5): 799-811.
- Budhlakoti N., Kushwaha A.K., Rai A., Chaturvedi K.K., Kumar A., Pradhan A.K., Kumar U., Kumar R.R., Juliana P., Mishra D.C., and Kumar S., 2022, Genomic selection: a tool for accelerating the efficiency of molecular breeding for development of climate-resilient crops, *Frontiers in Genetics*, 13: 832153.
<https://doi.org/10.3389/fgene.2022.832153>
- Byerlee D., 2020, The globalization of hybrid maize, 1921–70, *Journal of Global History*, 15(1): 101-122.
<https://doi.org/10.1017/s1740022819000354>
- Cai Y.F., Chen B., Hou J.F., Zhao F.C., Wang G.Y., and Cai R.X., 2024, Genetic structure and diversity in *Zea* genus: implications for conservation and breeding, *Maize Genomics and Genetics*, 15(2): 70-79.
- Crossa J., Pérez-Rodríguez P., Cuevas J., Montesinos-López O., Jarquín D., de Los Campos G., Burgueño J., González-Camacho J.M., Pérez-Elizalde S., Beyene Y., Dreisigacker S., Singh R., Zhang X.C., Gowda M., Roorkiwal M., Rutkoski J., and Varshney R.K., 2017, Genomic selection in plant breeding: methods, models, and perspectives, *Trends in Plant Science*, 22(11): 961-975.

- <https://doi.org/10.1016/j.tplants.2017.08.011>
Crossa J., Taba S., Eberhart S.A., Bretting P., and Vencovsky R., 1994, Practical considerations for maintaining germplasm in maize, *Theoretical and Applied Genetics*, 89(1): 89-95.
- <https://doi.org/10.1007/BF00226988>
Dang D.D., Guan Y., Zheng H.J., Zhang X.C., Zhang A., Wang H., Ruan Y.Y., and Qin L., 2023, Genome-wide association study and genomic prediction on plant architecture traits in sweet corn and waxy corn, *Plants*, 12(2): 303.
- <https://doi.org/10.3390/plants12020303>
Dermail A., Fuengtee A., Lertrat K., Suwarno W.B., Lübberstedt T., and Suriham K., 2021, Simultaneous selection of sweet-waxy corn ideotypes appealing to hybrid seed producers, growers, and consumers in Thailand, *Agronomy*, 12(1): 87.
- <https://doi.org/10.3390/agronomy12010087>
Dong L., Qi X.T., Zhu J.J., Liu C.L., Zhang X., Cheng B.J., Mao L., and Xie C.X., 2019, Supersweet and waxy: meeting the diverse demands for specialty maize by genome editing, *Plant Biotechnology Journal*, 17(10): 1853-1855.
- <https://doi.org/10.1111/pbi.13144>
Guzzon F., Gianella M., Juarez J.A.V., Cano C.S., and Costich D.E., 2021, Seed longevity of maize conserved under germplasm bank conditions for up to 60 years, *Annals of Botany*, 127(6): 775-785.
- <https://doi.org/10.1093/aob/mcab009>
Hallauer A., and Carena M.J., 2014, Adaptation of tropical maize germplasm to temperate environments, *Euphytica*, 196: 1-11.
- <https://doi.org/10.1007/s10681-013-1017-9>
He J.F., Zhao X.Q., Laroche A., Lu Z.X., Liu H.K., and Li Z.Q., 2014, Genotyping-by-sequencing (GBS), an ultimate marker-assisted selection (MAS) tool to accelerate plant breeding, *Frontiers in Plant Science*, 5: 584.
- <https://doi.org/10.3389/fpls.2014.00484>
He T.H., and Li C.D., 2020, Harness the power of genomic selection and the potential of germplasm in crop breeding for global food security in the era with rapid climate change, *The Crop Journal*, 8(5): 688-700.
- <https://doi.org/10.1016/j.cj.2020.04.005>
Hou J.F., Zhang J.M., Bao F., Zhang P., Han H.L., Tan H.P., Chen B., and Zhao F.C., 2024, The contribution of exotic varieties to maize genetic improvement, *Molecular Plant Breeding*, 15(4): 198-208.
- [https://doi.org/10.1016/S0305-750X\(01\)00013-4](https://doi.org/10.1016/S0305-750X(01)00013-4)
Jompuk C., Jitlaka C., Jompuk P., and Stamp P., 2020, Combining three grain mutants for improved - quality sweet corn, *Agricultural and Environmental Letters*, 5(1): e20010.
- <https://doi.org/10.1002/ael2.20010>
Kumawat G., Kumawat C.K., Chandra K., Pandey S., Chand S., Mishra U.N., Lenka D., and Sharma R., 2020, Insights into marker assisted selection and its applications in plant breeding, *Plant Breeding-Current and Future Views*, IntechOpen.
- <https://doi.org/10.5772/intechopen.95004>
Kurtz B., Gardner C.A.C., Millard M.J., Nickson T., and Smith S.C., 2016, Global access to maize germplasm provided by the us national plant germplasm system and by US plant breeders, *Crop Science*, 56(3): 931-941.
- <https://doi.org/10.2135/CROPSC12015.07.0439>
Langyan S., Bhardwaj R., Kumari J., Jacob S.R., Bisht I.S., Pandravada S.R., Singh A., Singh P.B., Dar Z.A., Kumar A., and Rana J.C., 2022, Nutritional diversity in native germplasm of maize collected from three different fragile ecosystems of India, *Frontiers in Nutrition*, 9: 812599.
- <https://doi.org/10.3389/fnut.2022.812599>
Nass L., and Paterniani E., 2000, Pre-breeding: a link between genetic resources and maize breeding, *Scientia Agricola*, 57(3): 581-587.
- <https://doi.org/10.1590/S0103-90162000000300035>
Ndou V., Gasura E., Chivenge P., and Derera J., 2021, Grain yield gains and associated traits in tropical × temperate maize germplasm under high and low plant density, *Euphytica*, 217: 186.
- <https://doi.org/10.1007/s10681-021-02918-5>
Nuss E., and Tanumihardjo S., 2010, Maize: a paramount staple crop in the context of global nutrition, *Comprehensive Reviews in Food Science and Food Safety*, 9(4): 417-436.
- <https://doi.org/10.1111/J.1541-4337.2010.00117.X>
Ortiz R., Taba S., Tovar V.H.C., Mezzalama M., Xu Y., Yan J., and Crouch J., 2010, Conserving and enhancing maize genetic resources as global public goods- a perspective from CIMMYT, *Crop Science*, 50(1): 13-28.
- <https://doi.org/10.2135/CROPSC12009.06.0297>
Palacios-Rojas N., McCulley L., Kaepler M., Titcomb T.J., Gunaratna N.S., Lopez-Ridaura S., and Tanumihardjo S.A., 2020, Mining maize diversity and improving its nutritional aspects within agro-food systems, *Comprehensive Reviews in Food Science and Food Safety*, 19(4): 1809-1834.
- <https://doi.org/10.1111/1541-4337.12552>
Prasanna B.M., Cairns J.E., Zaidi P.H., Beyene Y., Makumbi D., Gowda M., Magorokosho C., Zaman-Allah M., Olsen M., Das A., Worku M., Gethi J., Vivek B.S., Nair S.K., Rashid Z., Vinayan M.T., Issa A.B., Vicente F.S., Dhliwayo T., and Zhang X., 2021, Beat the stress: breeding for climate resilience in maize for the tropical rainfed environments, *Theoretical and Applied Genetics*, 134(6): 1729-1752.
- <https://doi.org/10.1007/s00122-021-03773-7>
Revilla P., Anibas C.M., and Tracy W.F., 2021, Sweet corn research around the world 2015–2020, *Agronomy*, 11(3): 534.

<https://doi.org/10.3390/AGRONOMY11030534>

Rice B.R., and Lipka A.E., 2021, Diversifying maize genomic selection models, *Molecular Breeding*, 41(5): 33.

<https://doi.org/10.1007/s11032-021-01221-4>

Romay M.C., Millard M.J., Glaubitz J.C., Peiffer J.A., Swarts K.L., Casstevens T.M., Elshire R.J., Acharya C.B., Mitchell S.E., Flint-Garcia S.A., McMullen M.D., Holland J.B., Buckler E.S., and Gardner C.A., 2013, Comprehensive genotyping of the USA national maize inbred seed bank, *Genome Biology*, 14: R55.

<https://doi.org/10.1186/gb-2013-14-6-r55>

Ruanjaichon V., Khammona K., Thunnon B., Suriharn K., Kerd Sri C., Aesomnuk W., Yongsuwan A., Chaomueang N., Thammapichai P., Arikrit S., Wanchana S., and Toojinda T., 2021, Identification of gene associated with sweetness in corn (*Zea mays* L.) by genome-wide association study (GWAS) and development of a functional SNP marker for predicting sweet corn, *Plants*, 10(6): 1239.

<https://doi.org/10.3390/plants10061239>

Ruanjaichon V., Yin K., Thunnon B., Khammona K., Suriharn K., Simla S., Kerd Sri C., Aesomnuk W., Yongsuwan A., Chaomueang N., Oo N.N., Unartngam J., Arikrit S., Wanchana S., and Toojinda T., 2022, Genome-wide association study (GWAS) reveals an snp associated with waxy trait and development of a functional marker for predicting waxy maize (*Zea mays* L. var. *ceratina*), *Agronomy*, 12(10): 2289.

<https://doi.org/10.3390/agronomy12102289>

Saha I., Rathinavel K., Manoharan B., Adhimoolam K., Sampathrajan V., Rajasekaran R., Muthurajan R., and Natesan S., 2022, The resurrection of sweet corn inbred SC11-2 using marker aided breeding for β -carotene, 6: 1004450.

<https://doi.org/10.3389/fsufs.2022.1004450>

Stagnati L., Soffritti G., Martino M., Lanubile A., Desiderio F., Ravasio A., Marocco A., Rossi G., and Busconi M., 2021, Morphological and genetic characterization of local maize accessions from emilia romagna region, Italy, *Sustainability*, 14(1): 91.

<https://doi.org/10.3390/su14010091>

Vidal R., Silva N., and Ogliari J., 2020, Old tools as new support for on farm conservation of different types of maize, *Scientia Agricola*, 77(1): e20180091.

<https://doi.org/10.1590/1678-992X-2018-0091>

Wang Y.H., Tang Q.L., Pu L., Zhang H.W., and Li X.H., 2022, CRISPR-Cas technology opens a new era for the creation of novel maize germplasms, *Frontiers in Plant Science*, 13: 1049803.

<https://doi.org/10.3389/fpls.2022.1049803>

Wattoo F.M., Rana R.M., Fiaz S., Zafar S.A., Noor M.A., Hassan H.M., Bhatti M.H., Rehman S.U., Anis G.B., and Amir R.M., 2018, Identification of drought tolerant maize genotypes and seedling based morpho-physiological selection indices for crop improvement, *Sains Malaysiana*, 47(2): 295-302.

Yang P.Z., Zhong G.X., Xie H., Chen S.F., Su L.S., Liu H.L., and Zhang X., 2011, Research on background and utilization of germplasm resources in maize, *Agricultural Science and Technology*, 12(10): 1464-1467.



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