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ADVANCEMENTS IN GENOMIC TECHNOLOGIES AND THEIR IMPACT ON CROP IMPROVEMENT AND BREEDING METHODS

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Abstract *Recent advances in genome sequencing of essential crop plants allow genotype and phenotype data integration in crop development. Advanced statistical methods identified quantitative trait genes. Genomic prediction has been used successfully in breeding animals and is now also used in breeding plants. Biometric statistics, genome-wide markers, and phenotyping enhance gene discovery. This makes biotechnology agricultural plant solutions possible. Improved fertilizer efficiency requires precise plant phenotyping in multiple habitats and seasons, which was previously expensive. DNA sequencing, genetic engineering, and PCR-based marker-assisted selection have made it cheaper. New methods like next-generation sequencing can target climate-responsive crop development. It examines Oryza sativa L. flower opening and closing molecularly and hybrid breeding success in diverse plant types. It discusses CRISPR/Cas9 for crop trait improvement and metabolic studies for Triticum aestivum L. quality group determination. Genetic analysis should use species-specific techniques, according to the study. A Zea mays L. callus induction and growth study examined how media and growth conditions affect callus development. Another drought-stressed Triticum aestivum L. cultivar gene expression study suggests employing RNA editing to respond to environmental stress. PCR-based markers have helped scientists find important genes in landraces that have changed to survive harsh farming conditions, giving them targets for crop growth.*

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Introduction

Recent progress in sequencing the genomes of major food species has opened up new and exciting ways to combine genotyping and phenotyping to improve crops. For example, more advanced statistical methods have helped determine which genes are responsible for different numeric traits. Genomic prediction has been used successfully to breed animals and is now also used to breed plants (Crossa et al., 2017). When genome-wide markers and phenotyping are used in big breeding nurseries or collections, biometric statistics are crucial for finding new genes. It is now feasible to go back to biotechnological concepts and seek out more targeted solutions in crop plants, all thanks to developments in next-generation sequencing and site-directed mutagenesis (Chu and Agapito-Tenfen, 2022). A major obstacle to enhancing nutrient usage efficiency is the need for precise phenotyping of several plants from different environments and development seasons, despite the aim to link genetics with knowledge of plant nutrition (Rebetzke et al., 2019; Sandhu et al., 2021). It used to be too expensive to make labels for orphan crops. But thanks to progress in DNA sequencing, genetic engineering of important food varieties, PCR-based selection methods, and next-generation sequencing, this is now easier and costs less (Saini et al., 2020; Singh et al., 2022).

Over a few years ago, molecular genetics and biotechnology have largely focused on improving crop varieties for human and animal use and biofuel and aesthetic purposes (Sainger et al., 2017). During this time, this collection of research publications explores new methodologies and discoveries in agricultural plants (Bailey-Serres et al., 2019).

Because of its importance in producing staple foods like bread, pasta, and noodles, wheat has been selectively bred to increase grain output and improve quality. When wheat seeds germinate too early because of weather, it lowers the baking quality a problem known as pre-harvest sprouting (PHS), which is a big obstacle in wheat breeding. Seed dormancy, an important genetic factor, has a big impact on how resistant plants are to growing before harvest (PHS). QTLs on the 21 chromosomes of hexaploid wheat control this trait (Ali et al., 2019). Additionally, the review delves into how gibberellin signalling pathways, abscisic acid, alpha-amylase, and flavonoids contribute to PHS resistance. Additional research is necessary to comprehend PHS resistance completely, despite the significant strides achieved by map-based cloning, transcriptomic, and comparative genomes (Salgotra and Stewart Jr, 2020). Developing crops responding to changing climate conditions is another important part of crop breeding that requires biotechnological and digital breakthroughs. Nonetheless, conventional approaches like mutations have received the lion's share of attention in the current research on genetic tools for agricultural improvement, while climate change has been largely ignored. Spring and winter barley and wheat varieties are cultivated with various spike shapes and end uses; breeding businesses routinely use genomic selection to improve these crops (Salgotra and Stewart Jr, 2020). It is essential to develop these crops for quality qualities like malting for beer and whiskey and baking/pasta quality because they are utilized for both human consumption and animal feed (Brzozowski et al., 2023).

Molecular mechanism of rice flower opening/closing

CMS is a well-known phenomenon that has been researched in over 150 plant species. Hybridology refers to the study of various elements of hybridization (Andrade, 2019). The heterosis effect, visible in superior F1 offspring in terms of productivity, fruit size, and other appealing characteristics, has been a focus of hybrid breeding. Sunflowers can only grow in certain climates, but they have a lot of promise as an oil crop because of how concentrated their oil is and what kinds of fatty acids they contain (Debaeke and Izquierdo, 2021). Growing sunflower hybrids worldwide need to use H. petiolaris PET1 CMS and F1 hybrid seeds with the Rf1 gene (Meena et al., 2022). A recent genomic study called a genome-wide association study (GWAS) correctly located the fertility-restoring gene PET1 to a 7 Mb section on a chromosome. There are 21 possible genes in this area. All but one of them are in the pentatricopeptide gene family (Wani et al., 2020). Other researchers have reported similar findings, such as finding the branching locus that makes flowers last longer in linkage group 10 and the Rf1 gene in linkage group 13 (Wani et al., 2020).

Rice hulls open briefly during the flowering stage to allow fertilization, but then they close again to stop the plant from fertilizing itself (Deyto and Cervancia, 2022). MADS-box genes control this process, and the noh1 rice mutant, found using marker-assisted cloning, is a key player. It was found that the NOH1 gene is on chromosome 1 of rice, within a 60-kb region that has nine other genes (Zhang et al., 2019). Meanwhile, two mutations in faba beans (*Vicia faba L.)* have been discovered to influence the absence of tannins in seeds(Alghamdi and Migdadi, 2020). Because of the crop's potential as a protein source in temperate agroclimatic zones, selection against tannins in faba bean breeding has garnered attention (Mulugeta Kabithiymer, 2020). The recessive zt-1 gene has been successfully connected to molecular markers, allowing it to be used in tannin selection in breeding programs. Identifying essential genes in the mono-lignol biosynthesis pathway has been facilitated by discovering the brown midrib (bmr) phenotype in maize in the 1920s and its subsequent link to enhanced digestibility in cattle (Li et al., 2021). Multiple C3 plants, like rice, barley, and wheat, have been seen to have changes in their photosynthetic processes. Both C4 photosynthetic crops, Cassava and sorghum have also shown similar changes (Bai et al., 2021). With a wealth of knowledge on agronomic performance, genetically modified crops, and cloned mutant genes involved in lignin production, new site-directed mutagenesis techniques are now possible (Ribeiro et al., 2019).

Novel approaches in breeding crops

People sometimes use the words "canola" and "rapeseed" to mean the same thing, but they mean different things. Canola came about because of Canada's rapeseed low acid breeding efforts in the 1970s, which used mutational breeding to improve the plants (Ansari, 2021). Genetic modification has also been used recently to get the same effects. Over the past few years, genetic editing of *Brassica napus L.* has been successful (Ton et al., 2020). The results from studying the model plant Arabidopsis can be used to improve rapeseed. The main goals of improving rapeseed have been to make the seeds contain more oil and change how oil is made (Beszterda and Nogala-Kałucka, 2019). People have been able to do this by breeding and genetically changing single genes. One study by Pandita et al. (2022) showed that adding the soybean transcription factors GmDof4 and GmDof11 to rapeseed can change the FAB2 and FAD2 genes that are involved in making fatty acids, which increases the amount of oleic acid present. The scientists used Agrobacterium to change the "Yangyou" variety, which already had a "double low" trait that they liked (Rasmussen, 2020). It has been found that soybean GmDof11 and GmDof4 target genes in this species. A total of 134 Dof genes have been identified in *B. napus* (Rasmussen, 2020). There is a push to boost rice yields by 2% yearly so that there is enough food for everyone by 2050.

However, this goal may go against cultural beliefs about rice, like how it smells, feels, and tastes. To solve this problem, another study has focused on determining the genes controlling rice grain weight. For example, TGW6 has been shown to boost rice production by 15% when its function is blocked (Kabir and Nonhebel, 2021). CRISPR/Cas9 site-directed mutagenesis has been used to improve maintainer lines and get desirable traits faster in rice hybrid breeding methods based on this knowledge (Romero and Gatica-Arias, 2019). Also, new methods like metabolic analysis of phloem exudates using high-tech equipment like direct injection mass spectrometry have shown promise in telling the difference between different types of wheat and quality groups. Principal component analysis has been used to show that this method works even better (Alghamdi and Migdadi, 2020; Uddin et al., 2019). It's good to have universal standards for model species, but they might not always work well for other species (Piñol et al., 2019). The Cobb et al. (2019) fixed this problem by making a cheaper ddRADseq (restriction site-associated DNA sequencing) that works only on *Eucalyptus dunnii* Maiden. Single nucleotide polymorphism (SNP) arrays are already used in several genotyping systems for Eucalyptus. Cobb et al. (2019) say that their improved protocol can be quickly changed to work with any plant. This method takes advantage of the good things about other protocols while minimizing their flaws using parts of P1 and P2 protocols. ddRADseq technology could be a useful tool for genotyping in the future because it combines traits from RADseq methods, such as finding new markers and lowering ascertainment bias in new germplasm (Tao et al., 2021).

Developing calluses and growing subcultures were successfully carried out in fully developed eggs and stem sections of *Zea mays L.* Researchers discovered that the changed Linsmaier and Skoog's medium worked well. It had 4 mg/I of 2,4-D and 1 g/I of casamino acids. Specifically, 2,4-D performed better than NAA and IAA when forming calluses and helping them grow. Roots and root-like primordia were plentiful in agar-solidified media and liquid cultures, respectively, when NAA was used as an incubator for the callus. Both kinetin and gibberellic acid did not affect callus induction when added to 2,4-D, and neither stimulated callus growth when subcultured (Bett, 2021). It was discovered that callus growth was about the same on three types of media: B-5 from Gamborg and Eveleigh, Linsmaier and Skoog's, and Schenk and Hildebrandt's. All three media showed 2% sugar, 4 mg/I of 2,4-D, and 1 g/I of casamino acids. Calluses formed more quickly at temperatures lower than 30°C or 35°C, which was interesting. But the growth rate didn't change much when the light conditions changed. Whether it was kept in complete darkness or put through 16-hour rounds of light and dark, it didn't matter. More research showed that glucose and maltose did not affect the growth of calluses in both liquid and agar-solidified cultures. On the other hand, sucrose was the food that helped growth the most (Callaghan, 2020; Degefa, 2019).

Drought stress

Over 60% of food production depends on farming watered by rain, making it vulnerable to weather changes every year (Gomez-Zavaglia et al., 2020). So, genetic progress is needed to make crops that can survive in dry conditions. Resistance to drought is a complicated trait controlled by many genes (Martignago et al., 2020). But, previous research hasn't been very good at connecting molecular data collected in controlled settings with what happens when breeding wheat that can handle drought. To solve this problem, a study found 377 genes differently expressed in "Jimai No.47" wheat cultivars that were both tolerant and responsive to drought in irrigated and drought-stressed fields. There was a lot of signaling transduction and MAP kinase activity in these genes, which shows that they might play a part in how cells respond to stress (Rasmussen, 2020). Also, RNA editing, which changes genes after transcription but happens during transcription, was found to be a possible way for wheat to respond to drought. The study also discovered that changing a single nucleotide in coding sequences could change amino acids. A codon variation from C to T was one of the most common changes. Using cheap and easy SSR markers based on PCR, more research was done on the genetic diversity of Prunus salicina Lindl landraces in the difficult farming climate of the Paraná River Delta in Argentina (Rasmussen, 2020). Using these neutral markers to study population genetics and identify cultivars was possible. In addition, computer analysis of the SSR flanking genome regions found at least 26 genes connected to fruit quality, plant growth, and stress resistance (Singh et al., 2023; Zhang et al., 2023). This means that these genes could be used for breeding.

Conclusion

Genomics has changed crop production by combining data on genotype and phenotype. Quantitative trait genes have been found using advanced statistical methods, and animal genetic prediction tools are used in plant breeding. Utilizing biometric data, genome-wide markers, and phenotyping has made it easier to identify genes and made biotechnology solutions for agricultural plants possible. Cheaper ways to improve fertilizer efficiency include DNA sequencing, genetic engineering, and PCR-based marker-assisted selection. Climate-responsive crop growth is now possible thanks to next-generation sequencing. According to the study, CRISPR/Cas9 can improve the traits of crops, and metabolic studies can determine the quality of crops. Utilizing *Oryza sativa L.*, *Triticum aestivum L.*, and *Zea mays L.* as examples highlights the need for species-specific genetic research. Through PCR-based markers, scientists have also found important genes in landraces that have become suited to harsh farming conditions, which gives farmers guidelines for growing crops. With these genetic advances, crop development has sped up, and farming has a lot of promise.

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