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Development Approaches of Wheat (*Triticum Aestivum*) Cultivars for Achieving Food Security in Afghanistan

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ABSTRACT

Wheat (*Triticum aestivum*) is considered a staple crop that provides most of our energy and nutritional needs while also making up most of our diet in Afghanistan. However, drought stress and climate change are the obstacles to producing enough wheat. High-yielding cultivars resistant to biological and non-biological stresses must be produced using various techniques, including genetic modification and selection. Afghanistan has recently experienced extreme weather variations, which have significantly impacted the evolution of diseases, pests, and the climate. Rapid genetic improvement is required for crop resistance to remain stable in challenging conditions. The major objective of this article is to review wheat breeding methods such as rapid breeding (RB), double haploid (DH), biotechnological improvement (BI), genomic selection (GS), and Genotype-phenotype interaction evaluation (G x E). The traditional development period, which is typically 10–12 years, can be shortened to less than 5 years by integrating the techniques above simultaneously. The precise information on breeding techniques appropriate for Afghanistan's climate and topography is the main focus of this research, and it will be crucial to the wheat breeding program.

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Introduction

Wheat breeding programs that prioritize variety development must first establish inbred breeding lines to generate them for test purposes and variety release. Bulk, pedigree, single-seed descent, and doubling haploids are the main methods of creating new lines (Rajaram et al., 2009). Backcross breeding is generally believed to be an advantageous supplement to these methods. Improvements in population size aim to strengthen the breeding program's overall genetic basis, while selection methods target breeding lines with higher performance or potential.

Similar to line development techniques, many wheat population improvement and selection methodologies have been devised to augment the efficacy of breeding programs and accomplish genetic enhancement(Baenziger, 2016; Rajaram et al., 2009). To inform the design of breeding programs, this review will give an overview of population improvement, selection, and line development techniques related to wheat breeding. It will also discuss the benefits and drawbacks of these techniques and provide a summary of empirical studies that have assessed them.

The initial stage in creating new genetic combinations is usually making crosses between several parental plants, regardless of the employed line development technique. The F1 progeny will be identical if the two parents utilized for crossing are also inbred(Reif et al., 2005). The F1 progeny will exhibit "segregation," or genetic and phenotypic variety, if neither of the crossing parents is inbred (Baenziger, 2016). Using a mutagenization process, a breeder can induce genetic mutations in a selected number of plants before crossing to produce a new genetic variety. (Allen et al., 2017).

Depending on the line development strategy used(Baenziger, 2016), different actions are taken after the generation of F1 seed or mutagenized plants(Kuchel et al., 2007). After several generations of line development, a breeder can release several lines as varieties or a multiline variety comprising several carefully selected inbred lines. Using several molecular marker sets and platforms, wheat has been the focus of genome-wide association studies (GWAS), also known as linkage mapping and association analysis(Larkin et al., 2019).

Thus, it is laborious but necessary to cross-reference locus and QTL. The mapping's findings between genetic materials and experiments reveal improved mapping accuracy and map the distribution of alleles and haplotypes in breeding pools and germplasm collections throughout the QTLome (Paux et al., 2012). Meta-analyses that aggregate and compare the findings of several QTL studies offer a useful way to order the QTLs required to be focused on with MAS (Heffner et al., 2011). In the long run, this analysis attempts to clone them, creating a more accurate mapping of QTLs and their overall significance in different environments (Kuchel et al., 2005).

Research Problem

The issue is that although Afghanistan grows this cereal on over 2.7 million hectares yearly, the nation must import it to meet domestic demand (Tiwari et al., 2020). The Ministry of Agriculture, Irrigation, and Livestock (MAIL) has designated the accurate evaluation of the wheat cultivated domestically output as a priority to handle any potential difficulties related to food security(Tiwari et al., 2020). In Afghanistan, the agriculture industry provides a living for around 75% of the people and makes up roughly 28% of the country's GDP(Muradi & Boz, 2018). Growth in agriculture is, therefore, essential to sustaining the nation's economy and guaranteeing food security at home(Reynolds et al., 2011).

Afghanistan's most important crops are wheat, barley, cotton, and rice (MAIL). Mostly, grain harvests are used by the harvesters directly. Wheat is grown in each province of the country and is an essential aspect of all major farming systems. It dominates the estimated 2.7 to 3 million hectares of total farmed cereal area(Tiwari et al., 2020). Even though wheat is

Afghanistan's most common cereal crop, domestic demand is not met by wheat output. To meet domestic needs, almost a million tons (or 25% of the total demand) of wheat are imported each year (Martínez & Gilabert, 2009). As a result, Afghanistan now ranks among the world's top wheat importers. Afghanistan mostly buys wheat from five bordering countries: Turkmenistan, Uzbekistan, Tajikistan, Kazakhstan, and Pakistan.

Research Objectives:

The study aims to discuss the issue of improving wheat cultivars, particularly in Afghanistan, supplying background data on population improvement, creating variable combination lines, and selecting an enhanced wheat variety in Afghanistan. Furthermore, it encourages critical thinking regarding the functions of population enhancement, selection techniques, and variety development in the design of breeding activities for wheat. The main bullet points are: 1) To provide precise background based on line development approaches in wheat breeding. 2) To facilitate critical thinking around the roles of population improvement and selection methods in the design of wheat breeding programs. 3) Wheat Improvement – Food Security is about fast environmental and climate changes. 4) Highlight the need for integration of all disciplines of wheat improvement

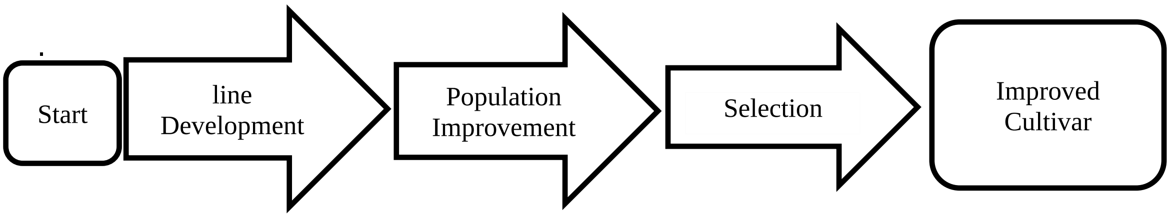


Fig.1: Complete cycle of breeding for an improved wheat variety

Genetic Variability and Line Development

Traditional Breeding Approaches

Pedigree Breeding. Every inbreeding generation might have a selection among individual plants and entire families through the pedigree approach of variety development(Heffner et al., 2011). As the plants get closer to homozygosity, the method prioritizes visual evaluation in selecting individual field plants over several years(Qiao et al., 2000). F1s from a single cross are space-planted to enhance seed yield and enable distinct plant identification to start pedigree breeding (Poland et al., 2012). The resulting F2s are sowed in rows following the pedigree so that individual plants within families can be identified and harvested individually(Allen et al., 2017). F1 plants are harvested separately or in large numbers. Among the F2 plants, selection is imposed, and only the chosen plants are propagated. A distinct identity (ID) is assigned to every chosen F2 and is documented alongside its lineage(Kuchel et al., 2007). For its F3 seed, F2 plants are taken one at a time. F2-derived F3 families (F2:F3) are F3s that originate from a single F2 plant. The F2:F3 families are typically space-planted in rows to enable the selection of one or more single plants or single spikes from different plants within each family (Baenziger, 2016).

To choose among families more precisely, the F2:F3 families can also be assessed for quality or yield. Similar to the previous generation, a record of the ID of the F2 plant of origin is kept with the IDs of the chosen F3 plants(MAURYA, 2019). The chosen F3 plants yield F4 seed, then planted in rows as the F3:F4 family. Many entire families may be eliminated based on quantitative data on qualities like grain production or visual evaluations of features like disease resistance or flowering time, as the majority of variability at this point occurs across families rather than within them(Akhtar et al., 2015; Shamaya et al., 2017). The top individual F4 plants are chosen and assigned an ID from among the greatest families. The most suitable F4 plants are harvested for use as F5 seed. These days, the F4:F5s are often referred to as "fixed lines" or "inbred lines." Since F4:F5s are predicted to be 87.5% homozygous, their phenotypes should be consistent and stable across generations(Zhou et al., 2016).

After the F4:F5s are planted in rows, each row's bulk harvest yields F4:F6 seed, which can be used to create disease nurseries and multi-environment performance experiments. F4 plants that have been selected are harvested to provide F5 seeds. These days, the F4:F5s are known as "fixed lines" or "inbred lines"(Kiszonas & Morris, 2018). Since F4:F5s are predicted to be 87.5% homozygous, their phenotypes should be consistent and persistent from generation to generation(Bonnett et al., 2005). They plant the F4:F5s in rows, which results in bulk harvests of each row, providing F4:F6 seed that can be used to set up disease nurseries and yield trials across many environments (Koebner & Summers, 2003). Assuming that selection during line development was successful, the F4-developed lines are anticipated to be superior to the average of their F1 parents for the attributes chosen during pedigree breeding because multiple generations of selection have already been applied(Paux et al., 2012). One benefit of the pedigree breeding method is the ability to improve selection accuracy through among-family selection by taking into account phenotypic information from linked families.

Bulk Breeding

In bulk techniques of generating lines, initial generation families will be planted and collected together. The F1 plants are gathered in bulk according to their genetics for the start of this process. The F2 seed from each F1 bulk shall be sown as a row or piece of land during the following season(Randhawa et al., 2013). The seed of F3 will be harvested in large quantities from each selection of the F2 family. Each F3 family shall be planted again as a plot in the following season, and the selection of plots may be made(Poland et al., 2012).

In bulk variety development procedures, initial generation families are cultivated and collected as bulk populations(Dong et al., 2009). F1 plants are first harvested in large quantities following their pedigree. Each F1 bulk's F2 seed is sown as only one row or a small plot in the next growing season. To create an F3 seed, each chosen F2 family is harvested in large quantities(Poland et al., 2012). Next year, each F3 family will be sown as a plot, and plot selection will be required. The process is done once again after achieving the required degree of homozygosity and uniformity. At this time, specific spikes within the bulk plots are taken out to create fixed lines(Reynolds et al., 2011). Planted fixed lines are given IDs and planted as rows for the next time when row selection is regularly imposed. Next, yield and other characteristics are assessed using the seed taken from the chosen rows. Abiotic and biotic challenges will be used in bulk breeding to help cull individuals in bulk populations who are ill-adapted through generations of inbreeding. This will allow lines to be evaluated(Allen et al., 2017; Baenziger, 2016; Bonnett et al., 2005).

Several modifications to the bulk breeding approach have been proposed to streamline or enhance the procedure further. To create what is known as a "composite cross population," suggested mass progeny from many cross combinations(Larkin et al., 2019). With this method, progeny from a wide range of cross-combinations can be sampled, and among them, natural selection can subsequently be applied(Poland et al., 2012).

The primary benefit of bulk breeding techniques is their simplicity and cost-effectiveness, as individual plants do not need to be picked and recorded separately. The evaluation of fixed lines in various conditions can be funded with cost savings, a more efficient way to enhance low heritability qualities like grain production(Bartoš et al., 2002). Although it was often believed that bulk breeding benefited from the process of natural selection among bulk populations, numerous investigations showed that selective pressure within bulk populations usually favors genotypes that perform poorly in real-world production situations(Baenziger, 2016; Kuchel et al., 2007).

The main disadvantage of bulk breeding procedures is that natural selection favors traits that are beneficial to natural populations but not to agricultural production systems (Koebner & Summers, 2003).

Single Seed Descent

To mitigate the negative impacts of natural selection in bulk breeding populations, the single seed descent methodology (SSD) was proposed as a fast way to generate lines without allowing natural selection (Allen et al., 2017). This revolutionary idea made it possible to avoid selection for adaptability to these undesirable conditions, which allowed for the use of controlled environments and off-season nurseries for generation improvement(Bonnett et al., 2005). The SSD method is used to identify F1 plants and harvest these individuals for their F2 seed(Baenziger, 2016). Every generation, just one seed is sown to produce lines from each F2. To be more precise, each F2 plant has one spike that is harvested, and one seed is planted to create an F2:F3 seed, which is subsequently sown by the family(Allen et al., 2017). To create the F3:F4 seed, one F3 spike is taken from each family, and one seed is sown. Every F4 plant has one spike taken, just like the previous generation, and one seed is sown(Kiszonas & Morris, 2018). The procedure is repeated until the lines achieve the required degree of homozygosity. The phenotypic traits in the F2 population will be similar to the F2-derived inbred lines for features expressed by additive effects (Bonnett et al., 2005). Transgressive segregation will continue to exist, notwithstanding the possibility of certain oddities, attrition, or selection (Koebner & Summers, 2003). Concerns over neglected possibilities for selection throughout generational advancement are frequently highlighted. However, it has been discovered that the yield improvement of the SSD and pedigree methods are similar (Kuchel et al., 2005). This is expected as early generations of selection for yield result in minimal or no genetic gain (Kuchel et al., 2007).

The main advantage of the SSD method is that it can rapidly establish lines in a nursery or greenhouse during the off-season. The swift generation progress in greenhouses, often known as "speed breeding" (Koebner & Summers, 2003), is gaining popularity as a means of expediting line development by bulk or SSD techniques. Plant growth and development are accelerated by the stressors imposed by these accelerated breeding techniques. Interestingly, breeders are returning to the randomized bulk approach to speed up the process because of the quick advancement of generations (Water Agric. Sustain. Strateg.," 2010).

Backcross

Backcross breeding techniques can introduce a particular feature of interest from various donors to a different cultivar known as a recurrent parent (Bolton et al., 2006). Using this procedure, the parent donor line is continuously crossed with a recurrent parent to produce a line nearly genetically identical to the recurrent parent. Still, it incorporates one or a few traits from the original parent, conferring the desired trait (Kiszonas & Morris, 2018). In actuality, linkage can cause unwanted connected genes to be conveyed, particularly in crosses where the donor parent is an exotic germplasm(Mohandas & Ravishankar, 2016).

The backcrossing process depends on whether the trait being transferred is inherited recessively or dominantly(Kiszonas & Morris, 2018). This causes heterozygosity as the heterozygous plants display a dominant trait in each generation and are selected for transfer to the recurrent parent (Kim et al., 2007).

Doubled-Haploids

By employing doubled-haploids (DHs), breeders can produce completely homozygous lines from heterozygous lines in a single generation of the F1 or over two generations in the F2 (Paux et al., 2012). Fast-line development with DH techniques is common for winter wheat, which might take eight weeks or longer to vernalize. In wheat, DHs can be generated by chromosomal elimination or another culture, with the latter method being more dependable for wheat improvement(Mwathi et al., 2020). Chromosome deletion by Double Haploid production in wheat starts with hybridizing F1 wheat with Zea mays (corn) plants, then employing colchicine to rescue embryos and double chromosomes(Mwathi et al., 2020; Zhang et al., 2021). To read a thorough analysis of DH production techniques in cereals (M. Gupta et al., 2016).

When DH production is successful, fully homozygous plants are produced and subsequently subjected to phenotypic analysis and seed increase(Paux et al., 2012). In theory, even in the absence of selection, the variation of DH populations created from F1s might differ from those of identical SSD individuals due to favorable loci linkage and interactive effects (Reynolds et al., 2011). Unless population sizes are raised, it may be more difficult to identify individuals with superior phenotypic distributions than the population mean in DH populations due to their higher kurtosis than SSD populations(Luo et al., 2021).

On the other hand, empirical research comparing the phenotypic distributions of SSD and DH populations has revealed little to no differences (P. K. Gupta et al., 1999). It has been suggested that instead of creating DHs from F1s, F2s or F3s should be used to increase recombination opportunities and reduce the variations between the SSD and DH populations (Larkin et al., 2019).

DHs are used for certain applied wheat breeding initiatives. Still, their use has been limited because they are expensive to produce and difficult to set up internally with a specialist DH production facility or find a suitable DH supplier (Kuchel et al., 2005). In the spring breeding of wheat setting at CIMMYT, two generations of line improvement are carried out annually; using DH to produce permanent lines proved ineffective (P. K. Gupta et al., 1999). In winter wheat, options for DH methods may yield lines in the same amount of time and at a cheaper cost for fast generation development in the greenhouse or off-season nurseries.(Bonnett et al., 2005)

It is important to remember that fresh populations and lineages are produced yearly by an established breeding program, and the only way to accelerate line progress is to recycle new lines as parents(Mwadzingeni et al., 2016). Breeders should always review their alternatives for quick line development and use the most effective approach accessible as generation improvement methods, and DH continues to develop (Kuchel et al., 2007).

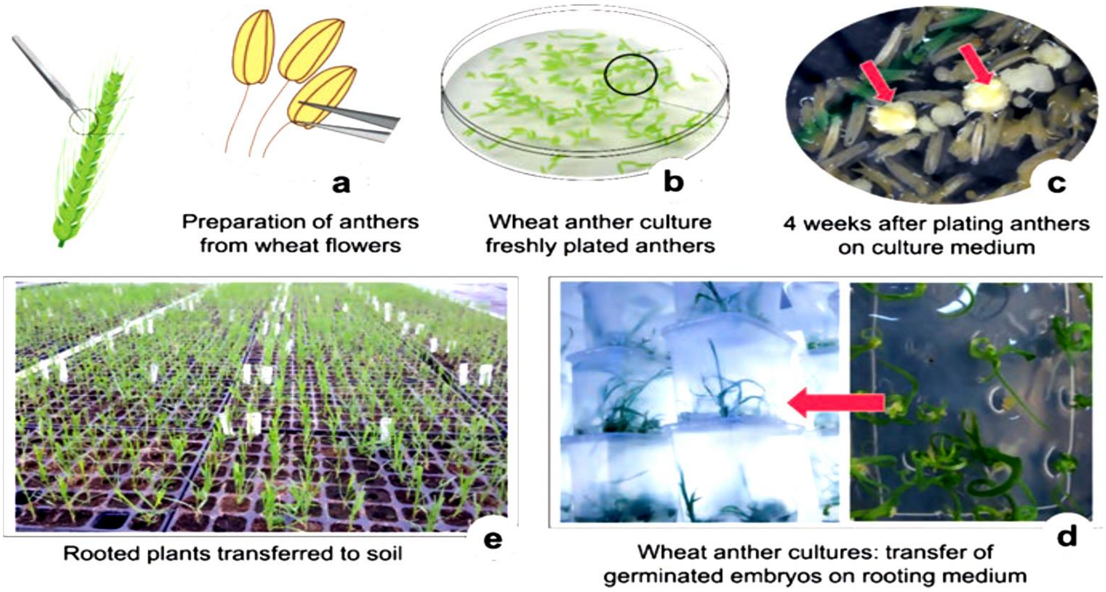


Figure 2: *a summary of the procedures that are included in creating wheat DH lines improvement using the anther culture approach, such as a) collecting the chosen wheat plants' anthers, b) producing organs, c) initiating the callus, d) transferring embryos to the rooting media, and e) inserting rooted vegetation into the soil (Kuchel et al., 2005)*

Cultivar Improvement Molecular Marker-Based Breeding Approaches

Evolutionary Breeding

The goal of increasing the bulk breeding method's efficiency gave rise to the concept of evolutionary plant breeding (Kiszonas & Morris, 2018). The bulking of F1 progeny is the initial action in the evolutionary breeding methods. This is followed by several generations of extended natural selection (as well as accidental synthetic selection) in increasing more natural environments (Baenziger, 2016). The concept is straightforward: minimize the work involved in traditional genotype selection and testing by allowing nature to gradually choose the best-adapted genotypes(Paux et al., 2012).

Evolutionary breeding is a population improvement approach because the production of new combinations of genes depends upon natural crossing and selection and gradually enhances the population (Larkin et al., 2019). These diverse mixes are subject to several generations of natural selection, which results in populations with superior environmental adaption. Like large-scale breeding to develop lines, natural selection might favor unfavorable features in agricultural environments(Poland et al., 2012). When populations of evolving breeding are replanted, a small amount of the seed, often 1/30 to 1/50th or fewer, is sampled so that it can be utilized by the next generation (Allen et al., 2017).

Recurrent Selection Approach

Continual Selection is a population improvement technique that uses recombination and crossing to improve the overall breeding population. Recurrent selection(Mwadzingeni et al., 2016) is an ongoing cycle that involves four steps in order: (1) breeding materials by crossing;(2) producing novel breeding individuals, which may be inbred lineages, families, or non-inbred plants;(3) genotyping as well as phenotyping the breeding individuals; and(4) choosing the finest breeding individuals to employ in the subsequent crossing cycle. Recurrent selection, in its most basic form, occurs in wheat when the program's finest new breeding lines are chosen and interbred, or recycled, each year to produce F1s that move on to the line development stage(Koebner & Summers, 2003). A new group of the "best" breeding lines will be selected every year for intercrossing due to the improved breeding germplasm(Reynolds et al., 2011).

Selection Methods

Mass Selection. During line creation, mass selection is a common process that uses facilitated male sterile recurrent selection and bulk or pedigree methods(Baenziger, 2016). It includes making decisions about individual plants according to their traits(Kweon et al., 2011). Although mass selection is a reasonably common selection technique due to its ease of use and low cost, its value in wheat breeding has generated debate. The trait of interest's heritability is a significant barrier to mass selection's efficacy(Mwadzingeni et al., 2016).

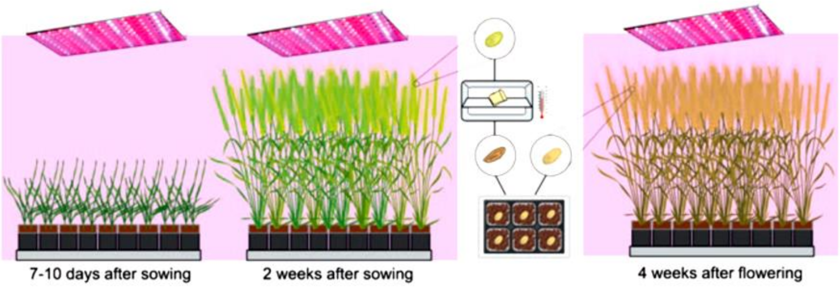
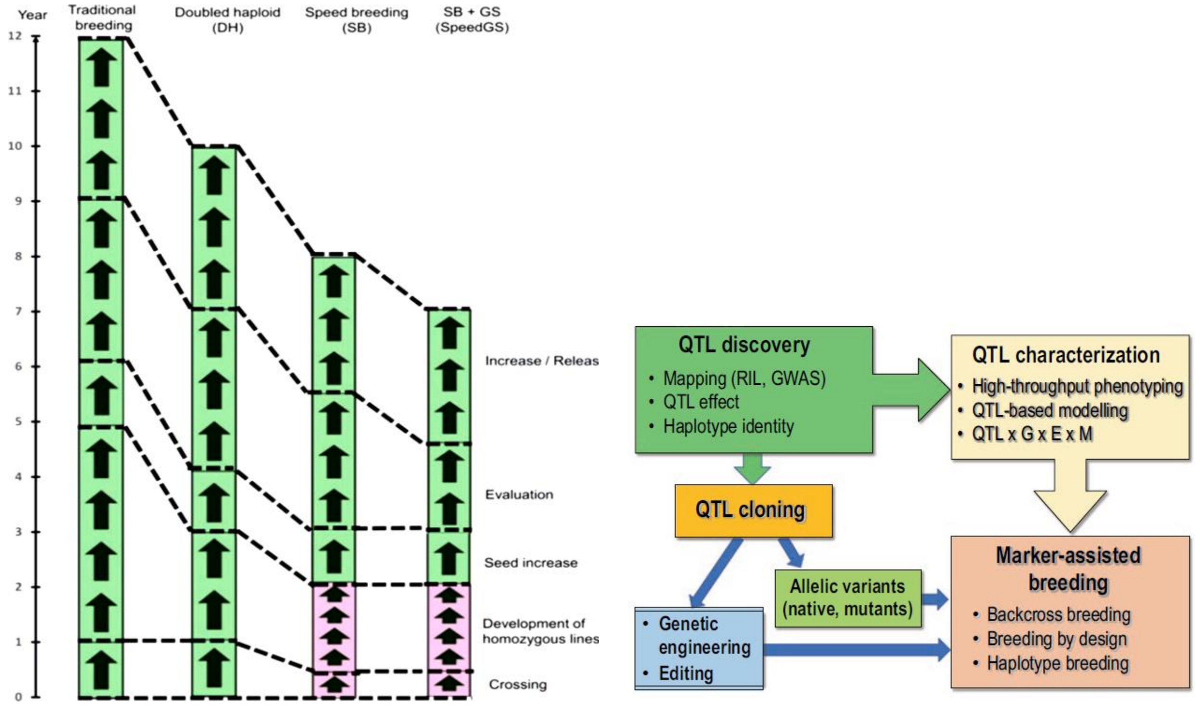


***Figure 3 illustrates a high-density wheat breeding population growing under speed breeding conditions**. Wheat seedlings enter the 2-3 leaf growth stage seven to ten days after seeding. For most spring wheat genotypes, the time to bloom usually varies from 4 to 6 weeks. Wheat spikes can be harvested and preserved two weeks in advance, allowing plant growth to be completed in eight weeks and then dried for three days at 35 °C in an air-forced dehydrator(Larkin et al., 2019).*

Marker-Assisted Selection. The method of marker-assisted selection is based on the theory that selection using DNA markers could be more effective or successful than selection utilizing phenotypes (Rajaram et al., 2009). This article presents conventional MAS, which covers MAS techniques except for genomic selection. In plant breeding, conventional MAS entails the following steps(Reynolds et al., 2011): (1) finding diagnostic markers that are strongly associated with genes influencing the desired traits; (2) confirming the presence of certain markers in the genotypes in which MAS is to be implemented; and making normal selections during the breeding process based on the validated markers. Because it suggested that breeders might make direct allele-based selections without using phenotyping, MAS was a groundbreaking concept (Dong et al., 2009). While phenotyping and traditional selection techniques were never completely supplanted by MAS, it is currently a significant factor in wheat development, backcross introgression, pyramiding of genes, and line development (Lehnert et al., 2018). The Backcross method was the first to use DNA markers to improve plant breeding. When they made it easy to select over the elite background haplotype and recognize recombinants close to one or more genes, or QTLs (Quantitative trait loci), from a donor parent, molecular markers evolved into a contemporary breeding tool for crop improvement(Vats, 2018). This technique, known as marker-assisted backcrossing(Kulkarni et al., 2017), significantly increased the effectiveness of backcrossing genes that influence qualities that are difficult to quantify on a single plant basis, are recessive, or are epistatic(Larkin et al., 2019). To attain an optimal genotype involving several genes or QTL Originating from different parents, marker-assisted backcrossing was also suggested, as well as gene or QTL pyramiding using markers (Randhawa et al., 2013) detailed the use of MAS forward breeding on a few breeding populations to improve the ability to withstand Fusarium head blight. Multiple loci in F2 and F3 generations of MAS are used, and lines resulting from these populations undergo phenotypic assessment(Kulkarni et al., 2017).



a b

***Figure 3**: **a)** A comparison of three wheat breeding systems (SpeedGS, SB, and DH) and how long the breeding cycle takes for each. Lowering the requirement for thorough phenotyping and combining genomic selection with speed breeding, or SpeedGS shortens the breeding cycle even more. Black arrows show one plant generation. Steps taken under normal growing conditions are indicated by green, whereas steps taken under rapid breeding conditions are indicated by pink(Paux et al., 2012). b) How genomics-assisted breeding enables the detection of advantageous QTL alleles and increases the frequency of beneficial allelic variations in breeding populations by genetic engineering (GE), selection assisted by markers (MAS), and genome editing (Fu & Somers, 2009).*

Genomic Selection: The method used in the selection of genomic (GS) is a type of multiple approach sampling (MAS) that differs greatly from traditional MAS(Heffner et al., 2011). In contrast to many other MAS procedures, the objective of GS aims to improve the overall breeding material for all desired characteristics throughout several iterations of population development. Calculations known as genetic estimated breeding values (GEBVs) on the parents based on genetic markers are the foundation of GS(Poland et al., 2012). A "training population"'s phenotypic and genotypic data are necessary to estimate GEBVs accurately (Larkin et al., 2019). A genomics prediction system uses this information to predict GEBVs for selecting individuals who may or may not have undergone phenotyping but have been genotyped (Poland et al., 2012). As far as these lines' phenotypic & genome-wide marker data are accessible, breeding lines established in the last several years are used for an ongoing wheat breeding effort.

A GEBV may be more effective than selection based on a phenotypic or BLUP calculated without genetic linkages (Paux et al., 2012). However, the primary benefit of GEBV-based selection is that it allows for the estimation of GEBVs for individuals who have not yet undergone phenotyping. This makes it possible for breeders to identify parents earlier during the breeding cycle, which can be used in crossing (Larkin et al., 2019). For instance, in a traditional wheat breeding program, breeding lines that have passed two to three years of testing and line development are usually subject to selection. A conservative genetic selection (GS) approach is commonly used in wheat breeding programs, where selection is applied to breeding populations that have passed two to three years of line development and one to one year of screening (Heffner et al., 2011).

Before using GS in wheat breeding, a few prerequisites must be satisfied. Initially, after tissue sampling and DNA extraction for one to six months, the breeding effort is expected to be able to acquire low-cost genome-wide marker information consistently (Poland et al., 2012). By accelerating the collection of genome-wide marker information and reducing the cost of genotyping compared to phenotyping, the potential for using GS to reduce the length of breeding cycles and expedite rates of genetic information can be improved (Paux et al., 2012). The recycling of superior lines by the program is necessary to accomplish genetic gain throughout cycles and to help train a precise prediction system for GS in subsequent generations based on marker and phenotypic information gathered from the breeding populations (Larkin et al., 2019; Reynolds et al., 2011). Last but not least, the breeding program should gather and meticulously handle superior phenotypic data on all characteristics of relevance and highly correlated traits—referred to as "secondary traits"—with the traits of interest(Allen et al., 2017).

Conclusions

Particularly since the Green Revolution, wheat breeding has been incredibly successful. Much of this success may be attributed to the free exchange among wheat science and germplasm experts, which continues today. As long as hybrid wheat is not widely accepted—especially in the Global South, where most wheat is produced—wheat research is anticipated to remain a significant government effort.

Multiple line development strategies are frequently used in different phases of the pipeline for breeding in wheat breeding efforts. Breeders need to carefully integrate population improvement, selection, and line development techniques to create better varieties. In most wheat-growing nations, tolerance to heat and drought stress will become more and more essential breeding goals.

Marker-assisted selection emerged in connection with the early advances in genetic mapping and the discovery of the most significant markers for wheat biology, genetics, and improvement(Barkley et al., 2014). Nowadays, a wide range of methods and genomic resources are available for wheat breeding, such as the newly finished wheat genome, which allowed M. Maccaferri et al. to create assays for molecular sequences that allow for high-throughput MAS. Notably, during the last five years, a consistent rise has been recorded in the number of cloned wheat loci/QTLs, distinct MAS techniques, and genetic stocks generated. Gene editing, selection of genomics through MAS in pre-breeding and breeding programs, gene/QTL discovery, and integrated and combined use are now required to improve our knowledge of wheat functional genomics and better leverage and bridge the biodiversity of the tetraploid with hexaploid A and B genomes.

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References

Akhtar, S. S., Andersen, M. N., & Liu, F. (2015). Residual effects of biochar on improving growth, physiology, and yield of wheat under salt stress. *Agricultural Water Management*, *158*, 61–68. https://doi.org/10.1016/j.agwat.2015.04.010

Allen, A. M., Winfield, M. O., Burridge, A. J., Downie, R. C., Benbow, H. R., Barker, G. L. A., Wilkinson, P. A., Coghill, J., Waterfall, C., Davassi, A., Scopes, G., Pirani, A., Webster, T., Brew, F., Bloor, C., Griffiths, S., Bentley, A. R., Alda, M., Jack, P., … Edwards, K. J. (2017). Characterization of a Wheat Breeders' Array suitable for high-throughput SNP genotyping of global accessions of hexaploid bread wheat (Triticum aestivum). *Plant Biotechnology Journal*, *15*(3), 390–401. https://doi.org/10.1111/pbi.12635

Baenziger, P. S. (2016). Wheat Breeding and Genetics. *Reference Module in Food Science*, *December 2016*. https://doi.org/10.1016/b978-0-08-100596-5.03001-8

Barkley, A., Tack, J., Nalley, L. L., Bergtold, J., Bowden, R., & Fritz, A. (2014). Weather, disease, and wheat breeding effects on Kansas wheat varietal yields, 1985 to 2011. *Agronomy Journal*, *106*(1), 227–235. https://doi.org/10.2134/agronj2013.0388

Bartoš, P., Šíp, V., Chrpová, J., Vacke, J., Stuchlíková, E., Blažková, V., Šárová, J., & Hanzalová, A. (2002). Achievements and prospects of wheat breeding for disease resistance. *Czech Journal of Genetics and Plant Breeding*, *38*(1), 16–28. https://doi.org/10.17221/6107-cjgpb

Bolton, M. D., Thomma, B. P. H. J., & Nelson, B. D. (2006). Sclerotinia sclerotiorum (Lib.) de Bary: Biology and molecular traits of a cosmopolitan pathogen. *Molecular Plant Pathology*, *7*(1), 1–16. https://doi.org/10.1111/j.1364-3703.2005.00316.x

Bonnett, D. G., Rebetzke, G. J., & Spielmeyer, W. (2005). Strategies for efficient implementation of molecular markers in wheat breeding. *Molecular Breeding*, *15*(1), 75–85. https://doi.org/10.1007/s11032-004-2734-5

Dong, C., Dalton-Morgan, J., Vincent, K., & Sharp, P. (2009). A Modified TILLING Method for Wheat Breeding. *The Plant Genome*, *2*(1), 39–47. https://doi.org/10.3835/plantgenome2008.10.0012

Fu, Y. B., & Somers, D. J. (2009). Genome-wide reduction of genetic diversity in wheat breeding. *Crop Science*, *49*(1), 161–168. https://doi.org/10.2135/cropsci2008.03.0125

Gupta, M., Atri, C., Agarwal, N., & Banga, S. S. (2016). Development and molecular-genetic characterization of a stable Brassica allohexaploid. *Theoretical and Applied Genetics*, *129*(11), 2085–2100. https://doi.org/10.1007/s00122-016-2759-2

Gupta, P. K., Varshney, R. K., Sharma, P. C., & Ramesh, B. (1999). Molecular markers and their applications in wheat breeding. *Plant Breeding*, *118*(5), 369–390. https://doi.org/10.1046/j.1439-0523.1999.00401.x

Heffner, E. L., Jannink, J., & Sorrells, M. E. (2011). Genomic Selection Accuracy using Multifamily Prediction Models in a Wheat Breeding Program. *The Plant Genome*, *4*(1), 65–75. https://doi.org/10.3835/plantgenome2010.12.0029

Kim, Y. T., Prusky, D., & Rollins, J. A. (2007). An activating mutation of the Sclerotinia sclerotiorum pac1 gene increases oxalic acid production at low pH but decreases virulence. *Molecular Plant Pathology*, *8*(5), 611–622. https://doi.org/10.1111/j.1364-3703.2007.00423.x

Kiszonas, A. M., & Morris, C. F. (2018). Wheat breeding for quality: A historical review. *Cereal Chemistry*, *95*(1), 17–34. https://doi.org/10.1094/CCHEM-05-17-0103-FI

Koebner, R. M. D., & Summers, R. W. (2003). 21st century wheat breeding: Plot selection or plate detection? *Trends in Biotechnology*, *21*(2), 59–63. https://doi.org/10.1016/S0167-7799(02)00036-7

Kuchel, H., Fox, R., Reinheimer, J., Mosionek, L., Willey, N., Bariana, H., & Jefferies, S. (2007). The successful application of a marker-assisted wheat breeding strategy. *Molecular Breeding*, *20*(4), 295–308. https://doi.org/10.1007/s11032-007-9092-z

Kuchel, H., Ye, G., Fox, R., & Jefferies, S. (2005). Genetic and economic analysis of a targeted marker-assisted wheat breeding strategy. *Molecular Breeding*, *16*(1), 67–78. https://doi.org/10.1007/s11032-005-4785-7

Kulkarni, M., Soolanayakanahally, R., Ogawa, S., Uga, Y., Selvaraj, M. G., & Kagale, S. (2017). Drought response in wheat: Key genes and regulatory mechanisms controlling root system architecture and transpiration efficiency. *Frontiers in Chemistry*, *5*(DEC), 1–13. https://doi.org/10.3389/fchem.2017.00106

Kweon, M., Slade, L., & Levine, H. (2011). Solvent retention capacity (SRC) testing of wheat flour: Principles and value in predicting flour functionality in different wheat-based food processes and in wheat breeding-A review. *Cereal Chemistry*, *88*(6), 537–552. https://doi.org/10.1094/CCHEM-07-11-0092

Larkin, D. L., Lozada, D. N., & Mason, R. E. (2019). Genomic selection—considerations for successful implementation in wheat breeding programs. *Agronomy*, *9*(9), 1–18. https://doi.org/10.3390/agronomy9090479

Lehnert, H., Serfling, A., Friedt, W., & Ordon, F. (2018). Genome-wide association studies reveal genomic regions associated with the response of wheat (triticum aestivum l.) to mycorrhizae under drought stress conditions. *Frontiers in Plant Science*, *871*(December). https://doi.org/10.3389/fpls.2018.01728

Luo, X., Yang, J., Zhu, Z., Huang, L., Ali, A., Javed, H. H., Zhang, W., Zhou, Y., Yin, L., Xu, P., Liang, X., Li, Y., Wang, J., Zou, Q., Gong, W., Shi, H., Tao, L., Kang, Z., Tang, R., … Fu, S. (2021). Genetic characteristics and ploidy trigger the high inducibility of double haploid (DH) inducer in Brassica napus. *BMC Plant Biology*, *21*(1), 1–17. https://doi.org/10.1186/s12870-021-03311-z

Martínez, B., & Gilabert, M. A. (2009). Vegetation dynamics from NDVI time series analysis using the wavelet transform. *Remote Sensing of Environment*, *113*(9), 1823–1842. https://doi.org/10.1016/j.rse.2009.04.016

MAURYA, A. K. (2019). Impact of different substrates for spawn production and production of milky mushroom (Calocybe indica). *International Journal of Pharma and Bio Sciences*, *10*(3). https://doi.org/10.22376/ijpbs.2019.10.3.b5-10

Mohandas, S., & Ravishankar, K. V. (2016). Banana: Genomics and transgenic approaches for genetic improvement. In *Banana: Genomics and Transgenic Approaches for Genetic Improvement*. https://doi.org/10.1007/978-981-10-1585-4

Muradi, A. J., & Boz, I. (2018). The contribution of Agriculture Sector in the Economy of Afghanistan. *International Journal of Scientific Research and Management (IJSRM)*, *6*(10), 750–755. https://doi.org/10.18535/ijsrm/v6i10.em04

Mwadzingeni, L., Shimelis, H., Dube, E., Laing, M. D., & Tsilo, T. J. (2016). Breeding wheat for drought tolerance: Progress and technologies. *Journal of Integrative Agriculture*, *15*(5), 935–943. https://doi.org/10.1016/S2095-3119(15)61102-9

Mwathi, M. W., Gupta, M., Quezada-Martinez, D., Pradhan, A., Batley, J., & Mason, A. S. (2020). Fertile allohexaploid Brassica hybrids obtained from crosses between B. oleracea and B. juncea via ovule rescue and colchicine treatment of cuttings. *Plant Cell, Tissue and Organ Culture*, *140*(2), 301–313. https://doi.org/10.1007/s11240-019-01728-x

Paux, E., Sourdille, P., Mackay, I., & Feuillet, C. (2012). Sequence-based marker development in wheat: Advances and applications to breeding. *Biotechnology Advances*, *30*(5), 1071–1088. https://doi.org/10.1016/j.biotechadv.2011.09.015

Poland, J., Endelman, J., Dawson, J., Rutkoski, J., Wu, S., Manes, Y., Dreisigacker, S., Crossa, J., Sánchez-Villeda, H., Sorrells, M., & Jannink, J. (2012). Genomic Selection in Wheat Breeding using Genotyping-by-Sequencing. *The Plant Genome*, *5*(3). https://doi.org/10.3835/plantgenome2012.06.0006

Qiao, C. G., Basford, K. E., DeLacy, I. H., & Cooper, M. (2000). Evaluation of experimental designs and spatial analyses in wheat breeding trials. *Theoretical and Applied Genetics*, *100*(1), 9–16. https://doi.org/10.1007/s001220050002

Rajaram, S., Borlaug, N. E., & Ginkel, M. Van. (2009). CIMMYT international wheat breeding. *Program*, *January 2002*, 1–24.

Randhawa, H. S., Asif, M., Pozniak, C., Clarke, J. M., Graf, R. J., Fox, S. L., Humphreys, D. G., Knox, R. E., Depauw, R. M., Singh, A. K., Cuthbert, R. D., Hucl, P., & Spaner, D. (2013). Application of molecular markers to wheat breeding in Canada. *Plant Breeding*, *132*(5), 458–471. https://doi.org/10.1111/pbr.12057

Reif, J. C., Zhang, P., Dreisigacker, S., Warburton, M. L., Van Ginkel, M., Hoisington, D., Bohn, M., & Melchinger, A. E. (2005). Wheat genetic diversity trends during domestication and breeding. *Theoretical and Applied Genetics*, *110*(5), 859–864. https://doi.org/10.1007/s00122-004-1881-8

Reynolds, M., Bonnett, D., Chapman, S. C., Furbank, R. T., Manés, Y., Mather, D. E., & Parry, M. A. J. (2011). Raising yield potential of wheat. I. Overview of a consortium approach and breeding strategies. *Journal of Experimental Botany*, *62*(2), 439–452. https://doi.org/10.1093/jxb/erq311

Shamaya, N. J., Shavrukov, Y., Langridge, P., Roy, S. J., & Tester, M. (2017). Genetics of Na+ exclusion and salinity tolerance in Afghani durum wheat landraces. *BMC Plant Biology*, *17*(1), 1–8. https://doi.org/10.1186/s12870-017-1164-6

Tiwari, V., Matin, M. A., Qamer, F. M., Ellenburg, W. L., & Hanan, N. P. (2020). *Wheat Area Mapping in Afghanistan Based on Optical and SAR Time-Series Images in Google Earth Engine Cloud Environment*. *8*(June). https://doi.org/10.3389/fenvs.2020.00077

Vats, S. (2018). Biotic and abiotic stress tolerance in plants. *Biotic and Abiotic Stress Tolerance in Plants*, 1–367. https://doi.org/10.1007/978-981-10-9029-5

Water and Agricultural Sustainability Strategies. (2010). In *Water and Agricultural Sustainability Strategies*. https://doi.org/10.1201/b10533

Zhang, K., Mason, A. S., Farooq, M. A., Islam, F., Quezada-Martinez, D., Hu, D., Yang, S., Zou, J., & Zhou, W. (2021). Challenges and prospects for a potential allohexaploid Brassica crop. *Theoretical and Applied Genetics*, *134*(9), 2711–2726. https://doi.org/10.1007/s00122-021-03845-8

Zhou, J., Tan, C., Cui, C., Ge, X., & Li, Z. (2016). Distinct subgenome stabilities in synthesized Brassica allohexaploids. *Theoretical and Applied Genetics*, *129*(7), 1257–1271. https://doi.org/10.1007/s00122-016-2701-7