

Spread and Adaptation of *Triticeae* Crops: From Ancient Origins to Global Distribution

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Abstract *Triticeae* crops, such as wheat, barley, and rye, are globally important food crops critical for human and animal nutrition and ecosystem sustainability. Understanding the origins, domestication, and global dissemination mechanisms of these crops is essential for improving their production efficiency and adaptability. This study reviews the early evolution of *Triticeae* crops and their wild relatives, the genetic changes during domestication, and the impact of early agricultural practices, trade, and migration routes on their spread. It explores the adaptation mechanisms of *Triticeae* crops to climate, soil, and pests, and summarizes the application of modern breeding technologies in enhancing yield and disease resistance. The research indicates that *Triticeae* crops underwent significant genetic changes during domestication, which have been elucidated through modern genetic techniques. Early agricultural practices and ancient civilizations played a crucial role in the dissemination of these crops. Modern genetic improvement technologies, such as genome editing and marker-assisted selection, have significantly enhanced crop yield and disease resistance. By comprehensively reviewing the domestication and dissemination history of *Triticeae* crops, this study provides valuable genetic resources and strategies for modern breeding programs. Understanding the adaptation mechanisms of these crops in different environments will aid in developing more resilient and high-yielding varieties to meet the growing global food demand.

Keywords *Triticeae*; Domestication; Dissemination mechanisms; Genetic adaptation; Genetic improvement

1 Introduction

The *Triticeae* tribe, encompassing vital cereal crops such as wheat, barley, and rye, has played a significant role in the development of human civilization. These crops have not only been fundamental to the sustenance of ancient societies but have also adapted and spread across diverse global environments. This systematic review aims to explore the historical spread and adaptation mechanisms of *Triticeae* crops, tracing their journey from ancient origins to their current global distribution.

The domestication of *Triticeae* crops began approximately 10 000 years ago in the Fertile Crescent, a region often referred to as the cradle of agriculture. Early domestication efforts focused on selecting traits that enhanced yield, resilience, and adaptability to local environments (Zhou et al., 2020; Gutaker and Purugganan, 2023). The genetic diversity within the *Triticeae* tribe, bolstered by introgression from wild populations, has been a key factor in the successful adaptation and spread of these crops (Zhou et al., 2020). Recent advancements in genomic technologies have provided deeper insights into the genetic makeup of *Triticeae* crops. Whole-genome sequencing of species such as wheat, barley, and their wild relatives has revealed complex genetic histories and significant genomic variations that have facilitated their adaptation to various environments (Mochida and Shinozaki, 2013; Gao et al., 2023). These genomic resources are crucial for ongoing breeding programs aimed at improving crop resilience and productivity (Mochida and Shinozaki, 2013).

Triticeae crops are indispensable in global agriculture due to their versatility and nutritional value. Wheat, barley, and rye are staple foods for millions of people and are also used extensively in animal feed and industrial applications (Hensel, 2019; Gao et al., 2023). The adaptability of these crops to different climatic conditions and soil types has enabled their cultivation in diverse regions, contributing to food security worldwide (Ceoloni et al., 2015; Ma et al., 2022). Moreover, the genetic improvement of *Triticeae* crops through modern breeding

techniques, including molecular biology and genomic selection, holds promise for addressing future agricultural challenges. These advancements can enhance traits such as disease resistance, drought tolerance, and nutrient use efficiency, ensuring sustainable crop production in the face of climate change (Ayalew et al., 2018; Maeda and Nakamichi, 2022).

This study synthesizes current knowledge on the spread and adaptation of *Triticeae* crops from their ancient origins to their present-day global distribution. By examining historical records, genetic studies, and modern breeding efforts, it provides a comprehensive understanding of the factors that have shaped the success of *Triticeae* crops. Understanding the genetic and environmental mechanisms underlying the adaptation of *Triticeae* crops is crucial for future crop improvement strategies. This knowledge can inform breeding programs aimed at developing resilient crop varieties capable of thriving in diverse and changing environments. This study highlights the significance of *Triticeae* crops in global agriculture and their potential contribution to food security and sustainable agricultural practices in the future.

2 Historical Origins and Domestication

2.1 Early evolution and wild relatives

The early evolution of *Triticeae* crops is deeply rooted in the Fertile Crescent, a region that spans modern-day Israel, Jordan, Lebanon, western Syria, southeastern Turkey, and parts of Iraq and Iran. This area is recognized as the cradle of Western agriculture, where wild progenitors of modern cereal species, such as wild wheats (*Triticum urartu*, *T. boeoticum*, *T. dicoccoides*), wild barley (*Hordeum spontaneum*), and wild rye (*S. vavilovii*), naturally intersect. The presence of these wild species in early archaeological sites, followed by domesticated forms, provides substantial evidence for the region's role in the advent of agriculture (Ozkan et al., 2002).

Molecular evolutionary studies have further elucidated the origins of these crops. Techniques such as amplified fragment length polymorphism (AFLP) have been instrumental in identifying the specific natural stands from which wild crops were domesticated. For instance, AFLP analysis has pinpointed the Karacadag Mountains in southeastern Turkey as the site of einkorn wheat domestication, supported by genetic similarities between wild and domesticated populations. This genetic evidence is complemented by archaeobotanical remains from early settlements in the region, reinforcing the significance of the Fertile Crescent in the early evolution of *Triticeae* crops (Ozkan et al., 2002).

2.2 Domestication process and regions

The domestication of *Triticeae* crops, including wheat and barley, marked a pivotal transition from hunting and gathering to agriculture, significantly impacting human societies. Wild emmer wheat (*Triticum dicoccoides*) was among the first cereals to be domesticated in the Fertile Crescent around 12 000 to 10 000 years ago, laying the foundation for subsequent bread wheat evolution. The geographic distribution of wild emmer today spans the western Fertile Crescent, including Jordan, Syria, Israel, southeastern Turkey, and parts of Iraq and Iran, indicating the broad region involved in its domestication (Özkan et al., 2010).

The domestication process of tetraploid wheats appears to have been multiregional. Genotyping-by-sequencing (GBS) studies have shown that domesticated tetraploid wheats have genetic affinities with wild emmers from both the northern Fertile Crescent and the southern Levant. This suggests a complex domestication scenario involving admixture and allele sharing between domesticated and wild populations from different regions. Archaeological evidence supports the initial cultivation of tetraploid wheats in the southern Levant, followed by their spread and mixing with wild populations in southeastern Turkey, leading to the fixation of domestication traits (Oliveira et al., 2020).

2.3 Genetic changes during domestication

The domestication of *Triticeae* crops involved significant genetic changes that enhanced their suitability for agriculture. One of the key outcomes of domestication was the increase in yield, driven by traits such as larger seed size, greater plant size, and reduced chaff or pod material. These changes resulted in domesticated cereals and pulses having, on average, 50% higher yields than their wild progenitors. The increase in seed mass and

number, along with a reduction in non-reproductive biomass, were crucial adaptations that improved the productivity of these crops (Preece et al., 2016).

Genetic studies have revealed that domesticated wheat populations have undergone substantial introgression from wild populations, contributing to their genetic diversity and adaptive success. Whole-genome sequencing of bread wheat has shown that introgression from wild populations accounts for a significant portion of the bread wheat genome, enhancing its ability to adapt to diverse environments. This genetic diversity, combined with convergent adaptation to human selection, has played a critical role in the global spread and success of wheat as a major crop (Zhou et al., 2020).

3 Mechanisms of Spread and Expansion

3.1 Early agricultural practices

The domestication of *Triticeae* crops, including wheat and barley, began in Southwest Asia around 10 000 to 11 000 years ago. This marked the transition from hunter-gatherer societies to agrarian communities, fundamentally altering human lifestyles. Early agricultural practices involved the cultivation of wild ancestors of these crops, which led to the development of Neolithic cultures characterized by food production, permanent settlements, and specialized tools. The spread of these agricultural practices from the Near East into Europe and other regions was facilitated by the adaptability of these crops to different environmental conditions. For instance, barley's genetic diversity allowed it to thrive in various climates, contributing to its widespread cultivation (Zhou et al., 2020).

The processing of wild cereal grains also played a crucial role in early agricultural practices. Evidence from the Upper Palaeolithic site of Ohalo II in Israel indicates that humans were processing barley and possibly wheat as early as 12 000 years ago. This involved grinding the hard, fibrous seeds into flour and baking it into dough, which made the grains more digestible and nutritious (Piperno et al., 2004). Such practices not only improved the utility of these crops but also likely encouraged their cultivation and spread as staple foods in early agrarian societies.

3.2 Trade and migration routes

The expansion of *Triticeae* crops was significantly influenced by ancient trade and migration routes. For example, the spread of wheat into China is believed to have occurred through three primary routes: across the Eurasian Steppe, by sea from India to the east coast of Eurasia, and along the Hexi Corridor, part of the Silk Road in western China (Jones et al., 2016). These routes facilitated the exchange of agricultural knowledge and practices, as well as the movement of seeds and crops, thereby promoting the spread of *Triticeae* crops across vast regions.

In Europe, the spread of Neolithic agriculture, including the cultivation of barley, was influenced by adaptive genetic traits that allowed these crops to thrive in diverse climates. The photoperiod response gene PPD-H1 in barley, for instance, enabled the crop to flower in response to increasing day lengths in spring, which was crucial for its successful cultivation in northern and higher altitude regions (Jones et al., 2012). This genetic adaptation, along with the movement of early farming communities, contributed to the widespread distribution of *Triticeae* crops across Europe.

3.3 Role of ancient civilizations

Ancient civilizations played a pivotal role in the spread and adaptation of *Triticeae* crops. The Fertile Crescent, often referred to as the cradle of agriculture, was the initial center of domestication for wheat and barley. From this region, these crops spread to other parts of the world, facilitated by the agricultural practices and trade networks established by ancient civilizations (Levy and Feldman, 2022). The genetic diversity of these crops, enhanced by introgression from wild populations, allowed them to adapt to various environmental conditions, further aiding their global distribution (Zhou et al., 2020).

The role of ancient civilizations is also evident in the genetic adaptations observed in *Triticeae* crops. For instance, the selection of specific genetic variants, such as the barley homolog of Antirrhinum CENTRORADIALIS (HvCEN), contributed to the successful adaptation of barley to new environments encountered as early farming

spread from the Near East (Comadran et al., 2012). These genetic adaptations were crucial for the establishment of *Triticeae* crops in diverse regions, highlighting the interplay between human selection and environmental factors in the spread of these important agricultural species.

4 Genetic Adaptation to Diverse Environments

4.1 Adaptation to climate and soil

The genetic adaptation of *Triticeae* crops to diverse climates and soils has been a key factor in their global distribution. Bread wheat, for instance, has expanded from the Fertile Crescent to various global environments over approximately 10 000 years. This expansion was facilitated by composite introgression from wild populations, which contributed significantly to the genetic diversity of bread wheat, allowing it to adapt to different climates and soils (Zhou et al., 2020). Similarly, barley has shown remarkable adaptability to different environments, with ancient landraces demonstrating exceptional tolerance to micronutrient deficiencies in marginal soils. These landraces have developed unique genetic traits over centuries, enabling them to thrive in adverse soil conditions by efficiently acquiring and translocating essential nutrients like manganese, zinc, and copper (Schmidt et al., 2018).

Moreover, the genetic diversity within barley landraces from Ethiopia highlights the role of altitude in shaping genetic adaptation. Barley populations from different altitudinal gradients exhibit significant genetic variation, suggesting that selection for adaptation to varying altitudes has been a major driving force in their evolution. This local adaptation is crucial for maintaining crop productivity in diverse environmental conditions and provides a valuable genetic resource for breeding programs aimed at improving crop resilience to climate change (Hadado et al., 2010).

4.2 Resistance to pests and diseases

Resistance to pests and diseases is another critical aspect of the genetic adaptation of *Triticeae* crops. The draft genome sequence of *Aegilops tauschii*, a wild relative of wheat, has revealed a rich repertoire of genes associated with disease resistance. This genetic information is invaluable for understanding the mechanisms of disease resistance in wheat and can aid in the development of more resilient wheat varieties (Jia et al., 2013). Similarly, rye, known for its wide adaptation to harsh environments, has been studied for its resistance to the fungal pathogen *Pyrenophora tritici-repentis*. Genome-wide association studies have identified specific genomic regions in rye that confer resistance to this pathogen, providing insights into the genetic basis of disease resistance and potential targets for breeding programs (Sidhu et al., 2019).

In addition, the genetic diversity within wheat germplasm has been explored to identify genotypes with better yield stability and resistance to pests and diseases under semi-arid conditions. Field screening of diverse wheat genotypes has revealed significant variability in traits related to yield and disease resistance, highlighting the potential of certain genotypes for cultivation in challenging environments (Mahpara et al., 2022). These findings underscore the importance of genetic diversity in developing pest and disease-resistant crops, which is essential for ensuring food security in the face of changing environmental conditions.

4.3 Advances in genetic mapping

Advances in genetic mapping have significantly enhanced our understanding of the genetic basis of adaptation in *Triticeae* crops. Whole-genome sequencing and exome sequencing have been pivotal in identifying key genetic regions associated with adaptive traits. For instance, the sequencing of bread wheat populations has revealed the role of specific genes in adaptation to different growing zones and human selection pressures, providing new perspectives on crop improvement (Zhou et al., 2020). Similarly, exome sequencing of barley has elucidated the genetic basis of adaptation by identifying genes related to key life history traits and their interactions with the environment (Figure 1). This has enabled the prioritization of genomic regions for breeding efforts aimed at developing climate-resilient barley varieties (Bustos-Korts et al., 2019).

Bustos-Korts et al. (2019) conducted a gene association analysis on barley's days to heading, plant height, thousand kernel weight, and awn length using a multi-environment GWAS approach. The results revealed

significant associations between several chromosomal regions and these traits, particularly on chromosomes 2H and 5H. The presence of known key genes, such as *HvFT1*, *HvCEN*, and *Vrs1*, within these associated regions further confirmed the reliability of the study's findings. By identifying these critical genes, the research significantly enhances the understanding of the genetic basis of barley adaptation. These findings provide valuable insights into the genetic foundation of agronomic traits in barley and will aid in improving barley varieties through marker-assisted selection.

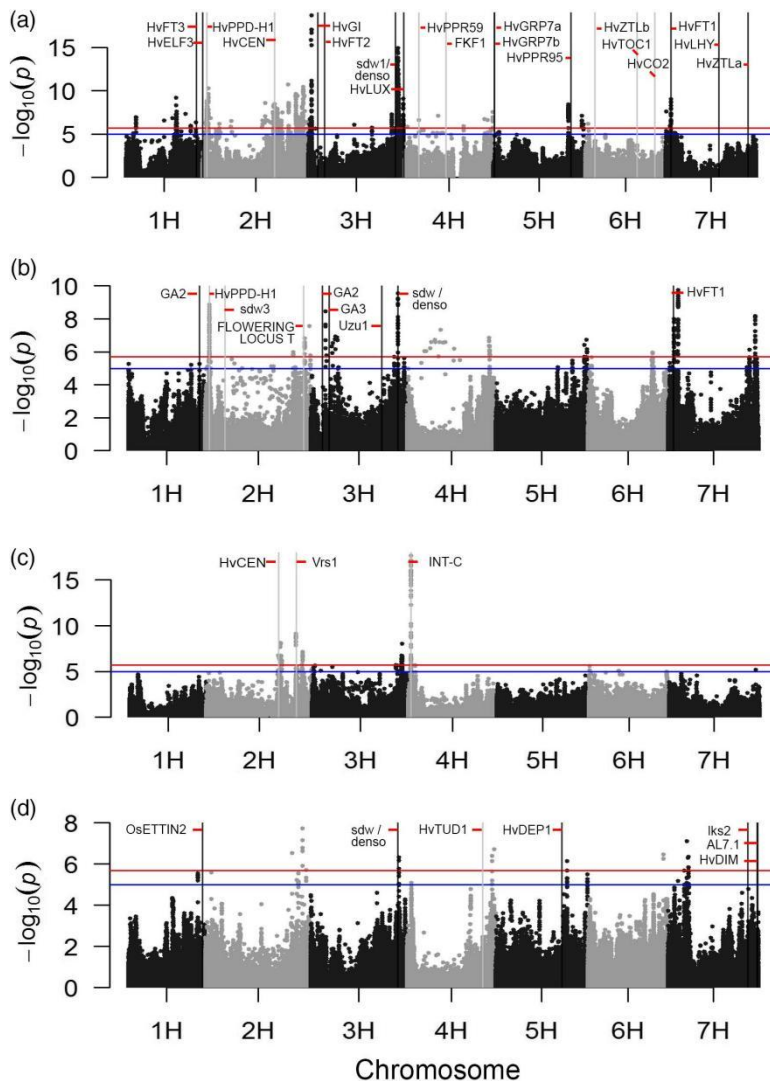


Figure 1 Multi-environment Genome-wide Association Study (GWAS) Reveals Key Genes for Agronomic Traits in Barley (Adapted from Bustos-Korts et al., 2019)

Image caption: This figure displays the results of a multi-environment genome-wide association study (GWAS) conducted on 371 domesticated barley accessions; The Manhattan plots show the distribution of single nucleotide polymorphisms (SNPs) associated with the traits: (a) days to heading, (b) plant height, (c) thousand kernel weight, and (d) awn length; The blue and red lines represent the significance thresholds for multiple testing corrections at $\alpha = 0.05$ and $\alpha = 0.01$, respectively (Adapted from Bustos-Korts et al., 2019)

Furthermore, the genetic mapping of adaptation genes in wheat, such as those controlling vernalization and photoperiod responses, has provided valuable tools for breeders. These genes play a crucial role in determining the flowering time and overall adaptability of wheat to different climates. Understanding the genetic control of these traits allows for ideotypic selection, ensuring that wheat varieties are well-suited to their target environments (Sanchez-Garcia and Bentley, 2019). Advances in genetic mapping continue to drive the development of more resilient and adaptable *Triticeae* crops, contributing to global food security.

5 Modern Distribution and Cultivation

5.1 Global production and economic importance

Triticeae crops, particularly wheat (*Triticum* spp.) and barley (*Hordeum* spp.), have expanded from their origins in the Fertile Crescent to become globally significant crops. Bread wheat, for instance, has adapted to diverse environments worldwide, thanks to genetic introgression from wild populations, which has increased its genetic diversity and facilitated its adaptation to various climates (Zhou et al., 2020). Durum wheat, another important *Triticeae* crop, is cultivated across a wide range of international agroenvironments, with significant genotype and environment interactions influencing its yield and stability (Bassi and Sanchez-Garcia, 2017). The economic importance of these crops is underscored by their role in food security and their extensive use in food, beverages, and animal feed (Hensel, 2019).

5.2 Regional cultivation practices

Regional cultivation practices for *Triticeae* crops vary significantly based on local environmental conditions and agricultural traditions. In the Southern Great Plains of the United States, triticale, a hybrid of wheat and rye, is cultivated for both grain and forage production, benefiting from its adaptability to less favorable environments and its potential to improve soil health as a cover crop (Ayalew et al., 2018). In the Gansu–Qinghai region of Northwest China, the spread of barley and wheat during the Late Neolithic and Bronze Age transformed local millet agriculture, with these crops being primarily cultivated along rivers and at specific altitudes with suitable climatic conditions (Ma et al., 2020). Additionally, the adaptation of wheat to different environmental conditions has been facilitated by the expansion and functional diversification of *MIKC-type MADS-box* genes, which play crucial roles in plant development and stress responses (Schilling et al., 2019).

5.3 Challenges in modern agriculture

Modern agriculture faces numerous challenges in the cultivation of *Triticeae* crops, particularly wheat. Climate change is a significant threat. A study by Pequeno et al. (2021) simulated wheat yield changes under the 2050 RCP 8.5 scenario using three crop simulation models (CROPSIM-CERES-wheat, CROPSIM, and Nwheat) and five global climate models. The results indicated that climate change would significantly reduce wheat yields in Africa and South Asia, with declines of 15% and 16%, respectively (Figure 2). However, the introduction of crop genetic traits (CGTs) significantly mitigated these yield losses, with some regions even experiencing yield increases. Additionally, the application of extra nitrogen fertilizers led to widespread increases in wheat yields globally. This study demonstrates that genetic improvement and optimized fertilization strategies can effectively counteract the adverse impacts of climate change on wheat yields, thereby significantly enhancing wheat production and ensuring food security.

Additionally, the use of biotechnological methods, including CRISPR/Cas technology, for genetic modification of *Triticeae* cereals offers potential solutions for enhancing disease resistance, improving water and nitrogen use efficiency, and developing varieties suited for drought or saline soils (Hensel, 2019). However, the successful implementation of these strategies requires coordinated international efforts and region-specific approaches to address the specific challenges faced by different regions (Bassi and Sanchez-Garcia, 2017; Pequeno et al., 2021).

6 Technological Advances in Crop Improvement

6.1 Genetic transformation and biotechnology

Genetic transformation has been a cornerstone in the advancement of *Triticeae* crops, including wheat, barley, rye, and triticale. Over the past three decades, significant progress has been made in developing stable transgenic lines, which are crucial for both functional genomics and precise crop engineering (Kumlehn and Hensel, 2009; Hensel, 2019). These advancements have enabled the introduction of traits that are difficult or impossible to achieve through conventional breeding, such as resistance to viral and fungal diseases, improved water and nitrogen use efficiency, and the ability to grow in dry or salty conditions (Hensel, 2019). Despite these successes, challenges remain, particularly in the transformation and regeneration of certain crop genotypes that are recalcitrant to established tissue culture methods (Anjanappa and Gruissem, 2021). Innovations such as the use of

morphogenetic transcriptional regulators and the development of non-tissue culture-based transformation methods offer promising alternatives to overcome these bottlenecks (Altpeter et al., 2016; Anjanappa and Gruissem, 2021).

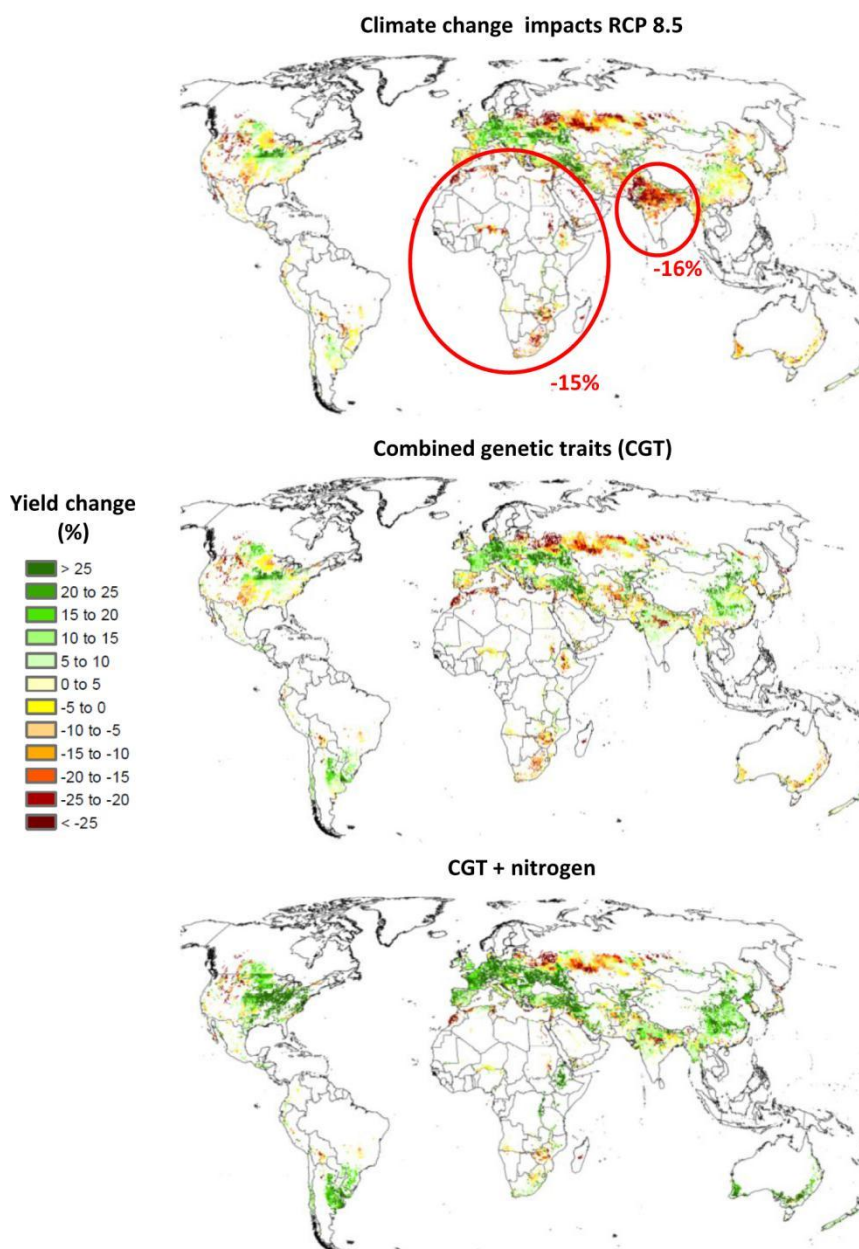


Figure 2 Impact of climate change, genetic traits, and nitrogen fertilization on global wheat yields (Adapted from Pequeno et al., 2021)
 Image caption: This figure presents the simulated effects of climate change, crop genetic traits (CGT), and the combination of CGT with nitrogen fertilization on global wheat yields under the RCP 8.5 scenario; The top panel shows the impact of climate change on wheat yields, with red circles and numbers representing the combined data for countries in Africa and South Asia (India, Pakistan, Bangladesh, and Nepal); The middle panel illustrates yield changes when genetic traits (CGT) are incorporated, while the bottom panel displays the combined effect of CGT and additional nitrogen fertilization (Adapted from Pequeno et al., 2021)

6.2 Advances in genome editing

Genome editing technologies, particularly the CRISPR/Cas system, have revolutionized the field of crop improvement by enabling precise and efficient modifications of plant genomes. These tools have been applied to various plant species, including *Triticeae* crops, to enhance yield, nutritional value, and resistance to environmental stresses (Zhang et al., 2018; Ahmar et al., 2021; Li et al., 2021). The integration of nanotechnology with genome editing has further improved transformation efficiency and reduced the time required for genetic modifications (Figure 3) (Ahmar et al., 2021). The application of nanomaterials in agriculture shows multifaceted

potential. Genome editing technologies utilize nanoparticles for gene delivery, aiding in crop quality improvement. Nano-bullets/carriers can precisely deliver compounds to specific organelles, enhancing crop transgene efficiency. By boosting crops' resistance to pests and tolerance to biotic and abiotic stresses, nano-fertilizers and nano-pesticides significantly improve crop yield and quality.

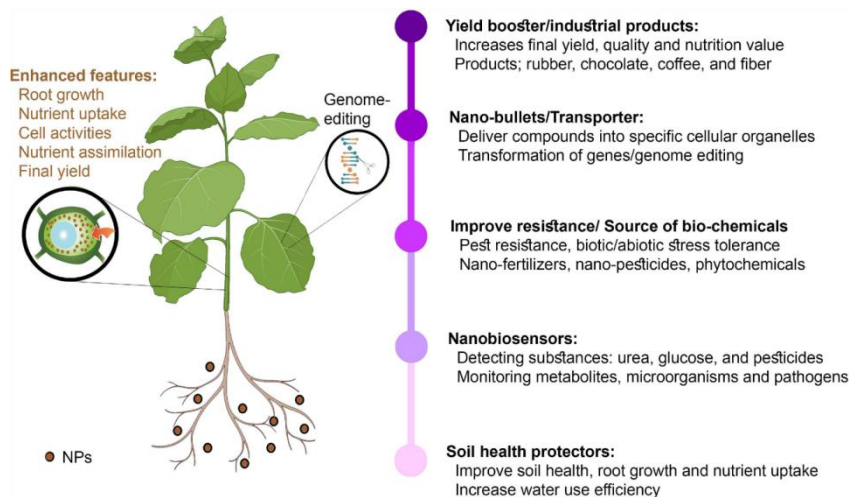


Figure 3 Applications of nanomaterials in agriculture (Adapted from Ahmar et al., 2021)

However, the complexity of the hexaploid wheat genome and gene redundancy pose significant challenges to precise gene editing (Li et al., 2021). Despite these obstacles, integrating genome editing with other molecular breeding strategies, such as speed breeding and high-throughput genotyping, holds great potential for accelerating the development of elite crop varieties (Watson et al., 2017; Li et al., 2021).

6.3 Integration of genomic resources

The integration of genomic resources, such as whole-genome sequencing and genome-wide association studies (GWAS), has provided new insights into the genetic mechanisms underlying the adaptation and evolution of *Triticeae* crops. For instance, population sequencing of bread wheat has revealed significant introgression from wild populations, which has increased genetic diversity and facilitated adaptation to diverse environments (Zhou et al., 2020). These genomic resources are invaluable for identifying key genes involved in crop resilience and adaptation, which can be targeted for improvement through genome editing and other biotechnological approaches (Zhou et al., 2020; Li et al., 2021). The use of synthetic biology and the development of universal transformation systems are also being explored to enhance the efficiency and precision of crop genetic modifications (Altpeter et al., 2016).

In summary, the integration of genetic transformation, advanced genome editing technologies, and comprehensive genomic resources is driving significant advancements in the improvement of *Triticeae* crops. These technological innovations are essential for meeting the growing global demand for food and ensuring the sustainability of agricultural practices in the face of environmental challenges.

7 Future Challenges and Opportunities

7.1 Impact of climate change

Climate change poses a significant threat to *Triticeae* crops, particularly wheat, which is the most widely grown food crop globally. Projections indicate a potential decrease in global wheat production by 1.9% by mid-century, with the most severe impacts expected in developing countries in tropical regions. For instance, yields in African and Southern Asian countries are predicted to decline by 15% and 16%, respectively, by 2050 (Pequeno et al., 2021). The suitability for wheat cultivation is expected to increase in middle- and high-latitude areas but decrease in low-latitude regions due to higher temperatures, heat waves, and droughts (Yue et al., 2019). Adaptation strategies, such as the introduction of new crop genetic traits (CGT) like increased heat tolerance and improved nutrient management, are essential to mitigate these impacts (Pequeno et al., 2021).

7.2 Sustainable agriculture practices

Sustainable agriculture practices are crucial for the long-term viability of *Triticeae* crops. Intercropping systems, for example, have shown promise in reducing pest abundance without the need for harmful insecticides, although additional practices may be required to enhance the effectiveness of natural enemies (Lopes et al., 2016). Additionally, the diversification of crops, such as the inclusion of underutilized crops like teff, can enhance food and nutrition security while providing resilience against climate change (Cheng et al., 2017). Advanced technologies, including genome editing and synthetic biology, offer opportunities to improve crop traits such as disease resistance, water and nitrogen use efficiency, and adaptability to various environmental conditions (Hensel, 2019; Li et al., 2021).

7.3 Policy and research recommendations

To address the challenges posed by climate change and ensure sustainable agriculture, several policy and research recommendations are necessary. First, there is a need for region-specific adaptation strategies that consider local growing conditions and climate impacts (Pequeno et al., 2021). Policies should support the development and dissemination of advanced agricultural technologies, such as genome editing and high-throughput phenotyping, to accelerate crop improvement (Li et al., 2021). Additionally, participatory approaches like crowdsourced citizen science can enhance the scalability and effectiveness of variety evaluations, helping farmers select the best-suited crop varieties for their specific environments (Etten et al., 2019). Finally, policies should promote the diversification of crops to reduce dependency on a few major cereals and enhance overall food security (Cheng et al., 2017).

8 Concluding Remarks

The spread and adaptation of *Triticeae* crops, particularly wheat and barley, have been pivotal in shaping agricultural practices and food security globally. The genetic diversity and adaptability of these crops have been enhanced through various mechanisms, including introgression from wild populations and human selection, which have allowed them to thrive in diverse environments. The spatiotemporal distribution of these crops, especially in regions like the Gansu-Qinghai area of Northwest China, highlights the significant role of geographical and environmental factors in their spread. Local adaptation, driven by both abiotic and biotic factors, has been a crucial evolutionary process, enabling these crops to optimize their growth and reproduction in specific environments. The genetic transformation and biotechnological advancements in *Triticeae* cereals have further accelerated their adaptation and improvement, addressing challenges such as disease resistance and environmental stress tolerance.

Continued research in the field of *Triticeae* crop adaptation is essential for several reasons. Firstly, understanding the genetic mechanisms underlying their adaptability can provide insights into improving crop resilience against climate change and environmental stresses. Secondly, exploring the historical pathways and genetic diversity of these crops can inform breeding programs aimed at enhancing their productivity and nutritional value. Additionally, investigating local adaptation and the role of microbial symbionts can lead to more sustainable agricultural practices by optimizing plant-soil-microbe interactions. Finally, advancements in genetic engineering and molecular breeding techniques hold promise for developing new crop varieties with improved traits, ensuring food security for a growing global population.

The journey of *Triticeae* crops from their ancient origins to their current global distribution is a testament to their remarkable adaptability and the intricate interplay between genetics, environment, and human intervention. As we face the challenges of a changing climate and increasing food demand, the lessons learned from the spread and adaptation of these crops will be invaluable. Continued interdisciplinary research, combining historical, genetic, and biotechnological approaches, will be crucial in unlocking the full potential of *Triticeae* crops and securing a sustainable agricultural future. The ongoing efforts to understand and enhance the adaptability of these crops will not only benefit current agricultural practices but also pave the way for future innovations in crop science.

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Conflict of Interest Disclosure

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

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