<u>Review Article</u>

ENHANCING THE PRODUCTIVITY OF WHEAT (TRITICUM SPP.) VIA GENETIC AND ENVIRONMENTAL VARIABILITY: A REVIEW

ABSTRACT

Significant advances in our understanding of the biological underpinnings of plant production have created fresh opportunities for innovative breeding approaches as compared to the 1950s. Although the enormous and intricate genomes of hexaploid wheat and diploid barley constitute a significant challenge, they also provide a substantial gene pool that may be used for breeding. We provide an overview of current biology's identification or characterization of productivity-related genes and/or mutations in wheat and barley. Because extreme weather events seriously impair agricultural productivity, climate change-induced variations in weather patterns will have an influence on agriculture's future environmental effects and the impending danger to yield sustainability. In order to fulfil the demands of an expanding population, future practical techniques will investigate and understand genotype, environment, phenological characteristics, GWAS, and QTL mapping in order to boost agricultural yield. Since the world's population is growing and requires food in the face of changing climate conditions and shrinking farmed lands, breeding and genetic modification are crucial methods for enhancing wheat yield under environmental stresses. It was claimed that the amount of yield might be measured by weighing a thousand grains or in kilogrammes per hectare.

Keywords: GWAS and QTL,phenological characteristics,Significant advances.weighing

1. INTRODUCTION

Triticum aestivum and Triticum durum wheat are a key source of calories and proteins for around a million people(ABBAS et al., 2023). Being one of the most extensively cultivated staple crops, it provides 18–20% of human calories and proteins, making it the mainstay of global food security. Since the mid-1990s, there has been a worldwide drop in wheat growth yields, which has resulted in an increasingly low wheat production that might jeopardise global food security.The threat of climate change continues to have a detrimental influence on crop yield(Arriagada et al., 2020). These days, plant scientists are focusing on developing strategies to mitigate the negative effects of climate change on agricultural production. Abiotic stressors such as temperature, salinization of the soil, and drought have the potential to significantly reduce agricultural yield by around fifty percent. Plants' cellular molecular reaction, which is meant to shield the plant from harm and sustain life, may be impacted by this(Bapela et al., 2022). In order to address the increasing demand for wheat worldwide and identify wheat genotypes with higher yields and yield components, this article will review studies that looked at wheat genetic diversity under current and future environmental conditions. Therefore, adding further improvements to specific sources and sink features like photosynthesis and leaf gas exchange, grain amount, and size, is the main objective of many researchers in this framework of wheat genotypes.To achieve significant gains in agricultural yields, effective coordination both within and across improved source and sink characteristics would be required(Beres et al., 2020).Examined were the number of tillers per plant, the 1000-Kernel weight (TKW), the Time of Falling (ToF), the days to heading, the Spike Length (SL), and other variables. In hexaploid wheat, the number of spikes per plant is strongly associated with the number of tillers per plant, which regulates grain yield(Chaudhary et al., 2022).

2. GREEN REVOLUTION GENETICS

The Green Revolution (GR) and its creator, Norman Borlaug, are widely acknowledged as iconic figures from the 20th century's agricultural history(Chauhan et al., 2023). In acknowledgment of his creative approach to crop variety development and the significant productivity rise he brought about—which was crucial in supplying food for nations facing poverty—Norman Borlaug was given the Nobel Peace Prize in 1970(Christian et al., 2022). The goal was aided by the development of high-yielding cultivars and the use of modern agrotechnologies including irrigation, artificial fertilisers, and herbicides. The semi-dwarf phenotype, which in wheat is reliant on the Reduced height-1 (Rht1) gene, is the most notable trait of GR cultivars. The gene was found in Japan and was created by crossing a Japanese semidwarf wheat cultivar with high-yielding American cultivars to generate Norin 10(De Vita & Taranto, 2019). The gene's two alleles, designated Rht-B1 and Rht-D1, are located at one of two loci on the hexaploid wheat's genome B and genome D, respectively(Drezner et al., 2007). They comprise the majority of cultivars planted worldwide. The mutant alleles feature single nucleotide alterations in the N-terminal coding region, which control premature stop codons(Filip et al., 2023). The Arabidopsis Gibberellin Insensitive (GAI) gene, maize dwarf-8 (d8), barley Slender1 (HvSln1), and the orthologs Rht-B1 and Rht-D1 are related. In addition to its direct effect of making plants shorter, the mutation has a notable pleiotropic effect that increases the number of grains per spike and assimilate partitioning to increasing ears(Gadisa, 2019). Moreover, resistance to disease is influenced by some Rht gene alleles. At the sdw1/denso locus in barley, the Green Revolution genes uzu1.a and semidwarf1 (sdw1) are implicated in the metabolism of GA and brassinosteroid hormones, respectively(Gupta et al., 2020). Genes dictate stronger, shorter culms that limit lodging and promote spikes. Both phytohormones cause a range of undesired agronomic traits, including smaller grains, as a consequence of their pleiotropic effects, which control many activities in different plant tissues(Guzman et al., 2016). Moreover, efforts have been made to replace the alleles of sdw1, which imparts late flowering and may be connected to inferior malt quality, and uzu1, which regulates temperature sensitivity, with those of alternative genes(Hossain et al., 2021).

3. METHODS FOR IDENTIFYING THE MAIN GENES THAT DETERMINE YIELD

A suggestion is made to use modern genetics to study the vast mutant resources. The NordGengenebank contains these resources. Barley mutants have been used to study nitrate reductas, the row-type gene SIX-ROWED SPIKE 1, the semi-dwarf, slender-type plant architecture SLENDER1, and the short culm UZU DWARF(Khan et al., 2022). A unique barley phytomer model was created to explain the characteristics of a number of grain morphological mutants. In the complicated, polyploid wheat genome, selecting for these mutations is very difficult. Hundreds of yield-related quantitative trait loci (QTL) have been identified by molecular marker-based genetic mapping; several of these QTL have been cloned in species with smaller genomes, such as rice(Mahdy et al., 2022). Direct cloning of yield-related genes in wheat and barley using techniques of gene high-resolution mapping and map-based cloning remains very difficult due to the complexity of the genomes. Technology will enable the production of new functional alleles or the inactivation of genes. Moreover, a team of scientists from the Chinese Academy of Sciences proved the efficiency and specificity of TALEN and CRISPR-Cas9 technologies in allopolyploid species like common wheat (T. aestivum) using triplicate homoeologous genes of the three genomes(Mahpara et al., 2022). To apply the approaches to yield-related variables, further progress in technology, genotype adaptability, and heritability documentation are required. RNAi-based methods for gene silencing may still be the better approach in polyploid species, even if one of the potential primary benefits of genome editing tools is the capacity to develop plants that would not be subject to GMO restrictions(Mălinaş et al., 2022).

4. INFLUENCE OF GENOTYPE ON WHEAT YIELD

Hexaploid wheat, 2n=6x=42, is cultivated as a major food crop all over the globe. The family to which it belongs is Poaceae. The three different genomes found in each nucleus of cultivated wheat make it a polyploid plant(Miransari & Smith, 2019). Every set has 2n=2x=14, which is the basic set of chromosomes. Triticum urartu provided the A, B, and D subgenomes of Triticum aestivum, whereas Aegilops speltoides provided the B-genome and the D-genome(Mourad et al., 2019). A multitude of yield-related factors, such as plant height, the number of productive tillers, the number of grain spikes per spike, the weight of each spike, and thousand-grain mass, all have an impact on wheat production, a complex and polygenic trait.According to investigations, differences in the genotype of wheat cause changes in the number of spikelets on each spike.Furthermore, it was found that a plant's tiller count controlled the number of spikelets on each spike; plants with fewer tillers and spikelets per spike had larger seed weights because they were better at loading grains and absorbing nutrients(PALABIYIK & Poyraz, 2022). The fertility of spikelets, or the number of kernels or spikelets, is one factor influencing the final grain yield. Recent research using the genetic and phenotypic analysis of wheat spike and kernel traits revealed long-term and geographic trends resulting from the breeding process(Roy et al., 2021). Furthermore, small-effect QTL contributes to the quantitative inheritance of traits and is supported by genomic prediction(Saeidnia et al., 2023).

5. BIOTIC AND ABIOTIC STRESSES

- **SALTING OF SOILS**

After drought, salt stress is the most dangerous abiotic stressor that reduces field crop productivity. When crops are stressed by salt, they respond in different ways(Santhoshini et al., 2023). Salinity stress reduces most crops' yield, growth, and productivity. Salt stress also has a significant impact on the area's biological balance and soil physicochemical characteristics. The region where salinity exists exhibits a variety of drawbacks, including poor crop yield, low agricultural economic return, and losses from soil erosion(Sharma et al., 2015). the harm that salt does to a plant's morphology, physiology, and biochemistry, including nutrition and water intake, seed germination, and plant development. Salinity inhibits plant development in all respects, including seed germination, vegetative growth, and reproductive development(Sharma & Sood, 2022). Ion toxicity, a scarcity of important elements (N, Ca, K, P, Fe, and Zn), osmotic stress, and a decrease in plant water intake are only a few effects of salt in the soil. Certain elements, such as boron, sodium, and chlorine, may be harmful to plants if applied in excess.A cell that receives too much sodium suffers from osmotic stress and eventually dies as a result of too much sodium building up in the cell wall(Sissons et al., 2020). Salinity stress causes the leaves to become shorter and consequently less chlorophyll-containing. It also affects the stomatal opening, which directly impacts the plants' ability to photosynthesize. Numerous processes related to reproductive development are impacted by salinity, including ovule absorption, microsporogenesis, elongation of stamen filament, enhanced cell death in tissues, and senescence of fertilisedembryos(Šramková et al., 2009). One important environmental factor that impacts plant development and productivity is salinity. The detrimental impacts of saltwater surroundings lead plants to perish, which lowers production 298 Walli, Al-Jubouri, Madumarov, Margaryta, and Aldibe. To counteract this damage, plants either transport salts outside of their cells or carry them within using a variety of techniques. Saline soils affect energy generation, protein synthesis, photosynthesis, and fat catabolism. While rice (*Oryza sativa L.*) perishes before development under salty conditions (100 mM NaCl), wheat yields little in these conditions. Temperate regions are ideal for growing wheat (*T. aestivum*), a crop that can withstand salt. Barley, a salt-tolerant crop (*Hordeum vulgare*), perishes after constant salt treatment (250 mM NaCl)(Studnicki et al., 2016). Compared to bread wheat, durum wheat has a reduced tolerance to salt. These elements are all to blame for the detrimental impacts on plant growth and development at the physiological, biochemical, and molecular levels.

- **DROUGHT**

The ultimate determinant of drought tolerance, including both drought avoidance and dehydration tolerance, is yield in fields of barley and wheat that are subjected to drought stress.Tolerance to salt and drought are two different things(Tadesse et al., 2019). There is no set aim for drought tolerance; instead, controlling salt absorption by the roots and transport throughout the plant are crucial components of salt tolerance. The complicated dynamics of crop performance during droughts are caused by a variety of erratic environmental elements and their interactions with other biotic and abiotic factors(Taghouti et al., 2017). Depending on the conditions, various traits and/or genes that increase yield during a severe drought may not operate during a mild drought or even have negative impacts when well water is available. Drought has varying effects on crop production. Enhancements in drought tolerance have to be carried out in conditions that are specifically targeted(Tillett et al., 2022) .Plants use a range of defence mechanisms to stave against drought stress. Plants control their stomatal opening and closing, osmotic homeostasis, antioxidant systems, hormone signalling, miRNA family, light protection, and metabolic pathways to prevent or lessen drought stress damage(Tomar et al., 2021). This regulatory network involves a number of genes and processes. Therefore, the synthesis of metabolites and the expression of many genes are impacted by drought stress.A high sink potential created by abundant photosynthesis around flowering enables the plant to yield a lot later on . The most crucial time frame for figuring out grain number is the ten to fifteen days before to anthesis. It could be especially crucial to understand the molecular processes, such as sugar supply and signalling, that are crucial for figuring out grain number at this time in order to increase production(Tshikunde et al., 2019). Grain counts are mostly dependent on the availability of carbon assimilates and nitrogen .

- **TEMPERATURE**

Wheat yield is harmed by heat stress.Scholars have endeavoured to evaluate the significance of genetic pathways in agricultural plants' responses to heat stress . For every degree Celsius that the global mean temperature rises, there is expected to be a 4-6% decrease in wheat yields on average worldwide .The timing and different degrees of heat stress determine how it affects grain filling and development. Heat stress lowers the flag leaf's assimilatory efficiency, which may prevent the buildup and movement of 14C assimilate and drastically lower grain output and quality(Walli et al., 2022).

- **INSECT PATHOGENS**

Plant disease is a concern as agriculture tries to feed the world's rapidly expanding population.A study of genetic diversity and environmental factors for increased wheat production 299 reduces crop yields, fibre content, and biofuel generation.Crop losses may range from catastrophic to chronic, but they typically represent 45% of the output of the six most essential food crops. Postharvest disease losses may be catastrophic, particularly in cases where farms are far from markets and if supply chain procedures and infrastructure are subpar(Desheva et al., 2021). In addition, several postharvest infections generate toxins that pose a major risk to consumers' health. It is believed that changing climatic conditions, particularly global warming, contribute to the spread of pathogens and the aggressiveness of infestations. Crop losses due to phytopathogens are projected to reach 20–30% each year. They reduce food security at the household, governmental, and international levels and result in significant economic losses. Worldwide, losses from direct pathogen-caused grain production losses range from 25 to 45 percent of total agricultural output(Kumar et al., 2021).

OTHER GENES PROMOTING CELL DIVISION AND AFFECTING WHEAT GRAIN SIZE

It has been shown that GW2 encoding E3 RING ligase adversely regulates rice grain size .Lower weight and size grains were formed by plants exhibiting decreased TaGW2 expression. As a result, the gene's function differed from that of its wild rice ortholog OsGW2, which controlled grain size in an antagonistic manner . Results from a different set of transgenic lines that acquired and described were in accordance with the gene's predicted role as a negative regulator of grain size.Grain weight and breadth were inversely correlated with TaGW2 transcript abundance (Paw et al., 2020).Two sets of contradicting findings might either be due to the wheat type utilised in the research or come from an off-target impact generated by the RNAi cassette in the experiments described . Our experience with RNAi-based silencing in wheat suggests that the transformation technique, which may have an impact on the outcome, is a crucial component to achieving the quiet phenotype without an off-target effect . Recent work employing the TILLING population disproves these contradicting findings. It discovered the gw2-A1 mutant allele with a G to A transition at the splice acceptor position of exon 5. In tetraploid and hexaploid wheat, the mutation caused mis-splicing in the wild gene TaGW2-A1, which led to a significant 6.6% rise in TGW and an increase in grain width and length.Grain weight in rice is determined by a protein called thousand-grain weight6 (TGW6), which is encoded by indole-3-acetic acid (IAA)-glucose hydrolase activity . It is known that the gene controls rice stigma length and stigma extension. Grain weight was substantially correlated with TaGS-D1. Higher or lower TGW was regulated by InDels discovered in the gene's introns in various genotypes(Šućur et al., 2023).

CONCLUSION

Exciting advancements in our knowledge of the genes and mechanisms underlying characteristics crucial for increasing yield, such grain size and number, stomatal function and number, leaf architecture, and carbohydrate, have occurred over the second part of the 20th century. Variations in wheat quality and grain yield might be unanticipated outcomes of genotype-environment interactions.This is a barrier: inbreeding and genotype assessment programmes. Rainfall, temperature during ripening, soil quality, and nitrogen availability are some of the most important environmental factors that affect genotypic performance. It is improbable that a single gene or even a single process adjustment would result in yield gains greater than the few percent seen in the preceding cases. Due to wheat's hexaploid structure, single gene modifications are ineffective unless they can affect each of the three homologues, for example, by gene discovery or editing. GWAS and QTL mapping, which provide a more comprehensive approach to yield improvement, have not yet produced any appreciable advances to the general yield enhancement of crops, with the exception of situations when adaptations to more particular circumstances are required. Gene editing is promising for grains since it might target negative yield regulators first.The creation of improved agricultural cultivars that are more resistant to drought and other stresses may be accelerated by the identification of new molecular markers and their successful use in plant breeding. Once again, the distribution of biomass in roots and shoots is necessary to balance carbon benefits against water losses.

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