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In common Wheat, Yield-related Traits are Enhanced by the Introduction of QTL from Aegilops Tauschii

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Abstract

By crossing Ae, a collection of Aegilops tauschii-wheat introgression (A-WI) lines were created to break the wheat D genome's narrow diversity bottleneck tauschii promotion T015 with normal wheat first class cultivar Zhoumai 18 (Zhou18). Based on Single Nucleotide Polymorphism (SNP) markers, a high-density genetic map was created, and 15 yield-related traits were tested in 11 environments to find quantitative trait loci (QTL). In at least five environments, a total of 27 environmentally stable QTLs were discovered, 20 of which were derived from Ae. up to 24.27 percent of the phenotypic variations can be accounted for by tauschii T015. Based on nonsynonymous nucleotide mutations in the candidate gene AetT093-2Dv1G100900, three successful Kompetitive Allele Specific PCR (KASP) markers demonstrated that A-WI lines with the T015 haplotype had significantly longer. For breeding improvement, four primary valuable A-WIs with good trait performance and yield-related QTL were chosen. The outcomes will make it easier to transfer beneficial genes from Ae in an effective manner. tauschii into wheat cultivars to further develop wheat yield and different characteristics.

Keywords: A-WI; Aegilops tauschii; Wheat; QTL mapping; Yield-related traits

Introduction

The hybridization of diploid Aegilops tauschii and tetraploid T. turgidum approximately 8000 years ago in the Fertile Crescent gave rise to hexaploid wheat [1]. The wheat D genome has significantly lower genetic diversity than the A and B genomes. The low-level hereditary variety of the wheat D-genome has been an extreme hereditary bottleneck for choosing beneficial agronomic characteristics in wheat rearing. Thusly, it is important to increment hereditary variety in wheat reproducing pools to conquer this hereditary imperative and integrate novel alleles or qualities into present day cultivars [2].

Aegilops tauschii has many desirable genes for wheat improvement and has a significantly higher genetic diversity than the D-genome of common wheat. Numerous Ae genes and quantitative trait loci (QTL). tauschii have been found, including the SrTA1662 and Pm58 genes, which are resistant to disease [3]. Environmental stress resistance improvements, such as tolerance to drought stress, cadmium (Cd), and phosphorus (P) deficiency, were also reported in some studies. Relatively, there are just restricted reports connected with grain efficiency attributes. Consequently, investigating more Ae. To increase wheat's genetic diversity, tauschii accessions are required. Ae populations in the wild tauschii are normally circulated in focal Eurasia, spreading from northern Syria and Turkey to western China. Aegilops tauschii from China was accounted for to show a particular populace structure in view of agreement phylogenetic connections of Ae. exchange accessories. Consequently, Ae. tauschii, particularly those from China, is an important wild asset for enhancing the hereditary variety of normal wheat. Introgression and usage of valuable qualities from Ae. In breeding programs, tauschii has a lot of potential to improve wheat cultivars.

Various endeavors have been made to bridle a huge portion of the Ae. tauschii gene pool for the enhancement of wheat. Those endeavors have utilized two distinct strategies: backhanded, crossing Ae. tauschii with tetraploid wheat; and direct, passing through Ae [4]. with hexaploid wheat, tauschii A different approach to transfer desirable D genomic regions (carrying target alleles) without affecting adaptive allelic combinations in the A and B genomes is the direct approach. From Ae, some genes have been transferred. tauschii to common wheat, such as the SrTA1662 pre-harvest sprouting (PHS) resistance gene and the Cmc4 wheat curl mite resistance gene, evaluated the impact of the Ae introgression. tauschii into wheat cultivars on yield part qualities utilizing the immediate methodology and viewed that as up to 23% of the introgression lines delivered a bigger number of grains than their folks.

If the chromosome sets of the F1 hybrids were successfully doubled, direct hybridization can yield synthetic octoploid wheat. Then, at that point, SOW will be backcrossed with a receptor parent to foster Ae [5]. QTL from Ae can be identified using tauschii-wheat introgression (A-WI) populations. tauschii. For instance, utilized a stem of rust-resistant Ae to perform a direct cross. tauschii accession and a wheat breeding line that is resistant to stem rust. Utilizing the BC2F1 planning populace, a stem imperviousness to rust quality from an Ae. tauschii increase was situated on the chromosome arm 1DS. The SOW method identified two significant QTLs for seed dormancy on chromosomes 2D and 3D, which respectively explained 10.3% and 20.4 percent of the phenotypic variations [6]. These outcomes showed that SOW is an effective method for moving great qualities into world class wheat germplasm and recognize promising QTL got from Ae. tauschii by fostering A-WI populace containing Ae. tauschii chromosomal portions. However, there aren't many reports of studies using A-WI populations to find QTL in yield-related traits.

An Ae-derived A-WI population was genotyped for this study. tauschii T015 and Zhou18 and distinguished QTL for 15 yield-related

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qualities assessed in 11 conditions [7]. Our goals were as follows: 1) Create a genetic linkage map of the A-WI population with a high density; ii) distinguish ecologically stable QTL that was critical for yield-related qualities in at least five conditions; (iii) identify potential candidate genes for the crucial QTL; and (iv) high-performing screen elite introgression lines. The findings make it easier to transfer advantageous yield-related genes from Ae and contribute to yield-related QTL that are environmentally stable. the elite wheat germplasm into tauschii [8].

Materials and Procedures

Plant materials and field preliminaries: Aegilops tauschii increase T015 was initially gathered from the Henan area of China. Zhoumai 18 (Zhou18) is a first class assortment enlisted in a similar region. By crossing Ae directly, 322 BC1F9 lines were used to create an A-WI population. the wheat cultivar Zhou18 and the tauschii accession T015 In each trial, a split-plot design with two replicates was used [9]. There were twenty plants in each of the three rows in each plot. The distance between rows was 30 cm, and the row length was 150 cm.

Non-denaturing fish detections: The A-WI lines and the parental lines were subjected to a karyotype based on non-denaturing fluorescent in situ hybridization (FISH) according to previously described procedures. oligo-pTa535, oligo-(GAA)10, oligo-pSc119.2, and oligo-pTa71 were the oligonucleotide probes.

Attribute appraisals: For each A-WI line of T015/Zhou18, ten plants in the inside columns were tested to explore the accompanying qualities: plant height (PH), spike length (SL), tiller number (TN), width (FLW). The mean of the ten plants was used to determine all traits. Seeds were collected from five arbitrarily chosen plants from each line. Using SC-G software (WSeen, Hangzhou, Zhejiang, China), 100 kernels were used to calculate their length (KL), width (KW), length-width ratio (KLWR), and perimeter (KP). Thousand-bit weight (TKW) was assessed by weighing three examples of 500 parts for every example from every one of the eight preliminaries.

Using IBM SPSS Statistics 20.0 software (SPSS, Chicago, USA), the mean values of yield-related traits (Mean), standard deviations (SD), coefficients of variation (CV), and an analysis of variance (ANOVA) were determined. The ANOVA model was used to evaluate the variance components based on the accession mean to calculate broad-sense heritability: where g2 is the genotypic variance, g2ge is the variance of the genotype's interaction with its environment, which is equal to (MSge MSe)/r, and g2e is the error variance; The mean squared error, genotype, and genotype by environment mean square are referred to as MSe, MSg, and MSge, respectively. The number of replications is denoted by r, and the number of environments is denoted by e. Using the GGally and R packages, Pearson's correlation coefficients between traits were determined.

Genotyping and the construction of genetic map: The T015/Zhou18 A-WI population and its two parents were genotyped with the Wheat 55K SNP array, and 12,892 SNP markers from the D genome were retained [10]. Minor allele frequencies of less than 5% or missing values of more than 10% were grounds for the removal of SNP markers. Flanking successions of SNPs were utilized to Impact against the reference genome groupings of Ae. Chinese Spring and tauschii (accession T093) to determine their physical positions. The BIN function in IciMapping 4.1 was used to remove redundant markers—also known as co-segregating markers—from the A-WI population in order to simplify the calculation. A Chi-squared test was used to look for significant segregation distortion in the retained markers. The MAP function in IciMapping was used to group SNPs into linkage groups. With a Logarithm of odds (LOD) score of 3.5 and a recombination fraction of 0.3, genetic distances in centimorgans (cMs) were determined using the Kosambi mapping function. Markers without linkage or linkage bunches with under 5 markers were disposed of in the ensuing examination and were utilized to draw the hereditary guide [11]. For the excess loci that were co-isolated in the A-WI populace, just a single exceptional enlightening marker was displayed in the hereditary guide.

QTL investigation: Examination of QTL was directed involving the BIP capability in IciMapping 4.1. The ICIM-ADD QTL method (inclusive composite interval mapping of additive) was chosen. The phenotypic upsides of the A-WI populace in every climate were utilized for individual climate QTL planning examination. The stepwise regression probability was 0.001 and the walking speed was 1.0 cm for QTL detection. 1000 permutations were used to calculate the LOD scores, with a 0.05 type I error. Using inclusive composite interval mapping of epistatic QTL (ICIM-EPI), QTL IciMapping V4.1 was used to examine digenic epistasis and the interaction of QTL with their environment [12]. The digenic epistasis QTL was found with a 5.0 LOD score. ICIM-ADD was used to scan the QTL and environment interactions with QTL IciMapping V4.1. QTL with overlapping confidence intervals were assumed to be equivalent for a given trait. Each QTL was identified.

The candidate genes: Reference genomic sequences were used to create a set of conserved primers for cloning. Positive clones were selected and sequenced after PCR products from the two parents were gel-purified and inserted into the pGEM-T Easy Vector (Promega, Beijing, China). DNAMAN was used to align the parents' nucleotide sequences.

Transformation of SNPs to KASP markers: In view of the nonsynonymous nucleotide transformations of the competitor quality somewhere in the range of T015 and Zhou18, we fostered a bunch of Kompetitive Allele Explicit PCR (KASP) markers. In reaction mixtures containing 50 ng dried DNA, 0.14 liters assay mix, 5.0 liters of water, 5.0 liters of 2 KASPar reaction mix, and 5.0 liters of water, the polymorphisms of newly designed KASP markers were examined. In a Roche LightCycler 480 Real-Time PCR system, the PCR profile was set at 94 °C for 15 minutes (activation), followed by 10 cycles of 94 °C for 20 s, 61–55 °C for 60 s (drop 0.6 °C per cycle), and then 26 cycles of 94°C for 20 s and 55 °C for 60 s [13]. The LightCycler software was used to analyze the fluorescence signal.

Results and Discussion

Chromosome constitutions of T015/Zhou18 A-WI lines: To assess the chromosome solidness of the T015/Zhou18 A-WI populace, 22 A-WI lines were haphazardly chosen and screened by ND-FISH. The karyotype investigation uncovered that each of the A-WI lines were euploid with 42 chromosomes. In contrast, the A-WI lines and Zhou18 shared very little in common on the chromosomes of the A and B subgenomes, while the D subgenome contained a high number of homozygous variations, indicating that multiple alleles from Ae were successfully introduced. tauschii T015 into A-WI lines. As a result, it was established that A-WIs inherited distinct Ae alleles. tauschii T015 and chromosomes were practically steady in the BC1F9 age.

Phenotypic variation and correlation analysis: The A-WI population's and their parents' phenotypic performance for the 15 traits. The phenotypic values of each trait varied widely and continuously

across the A-WI lines. The seven traits had coefficients of variation greater than 10%, indicating that the values of these traits varied between population lines. These outcomes indicated Ae's introgression. Introducing tauschii T015 into bread wheat may result in significant phenotypic variation in the resulting A-WIs.

Assessed connection coefficients among the 15 attributes [14]. For the three yield characteristics, TKW had a positive relationship with portion size-related qualities like KL, KW, and KP. There was a positive correlation between trait KNS and traits related to flag leaves and spikes. Attribute TN had positive connections with KLWR and FLL and negative relationships with KW, FLW, and HD. Critical relationships were seen among spike-related attributes. With a r value of 0.89, trait TSS had the strongest positive correlation with FSS. KL had a strong positive correlation with KP for the five traits that were related to the kernel (r = 0.94). Quality KLWR had a negative relationship with KW and didn't essentially correspond with TKW.

Linkage map development: The T015/Zhou18 A-WI populace was genotyped with the Wheat 55K SNP exhibit and a last arrangement of 3131 polymorphic markers on the D genome were held [15]. The genetic map that was produced after unlinked markers were removed contained 1426 markers that were mapped within 506 bins. In order to build the genetic map, a single marker was chosen to represent each bin.

Conclusion

Using an A-WI population and the Wheat 55K SNP array, we created a high-density genetic map and carried out QTL mapping for 15 traits related to yield in 11 environments. 27 earth stable QTLs were recognized in something like five conditions, 20 of which were gotten from Ae. up to 24.27 percent of the phenotypic variations can be accounted for by tauschii T015. The major QTL QKl-2D.5 for KL was recognized in seven conditions and showed a constructive outcome with the T015 allele. There was speculation that the QKl-2D.5 candidate gene was AetT0932Dv1G100900.1. There are four primary valuable introgression lines that carry Ae-derived yield-related loci and exhibit excellent trait performance. In breeding programs, tauschii T015 was selected for wheat improvement. The effective transfer of beneficial genes from Ae may be made easier by these findings. for the purpose of improving wheat, tauschii into elite wheat germplasm.

Acknowledgement

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Conflict of Interest

None

References

1. Mcfadden ES, Sears ER (1946) The origin of Triticum spelta and its free-threshing hexaploid relatives. J Hered 37: 81-89.
2. Kou H, Zhang Z, Yang Y, Wei C, Xu L, et al. (2023) Advances in the Mining of Disease Resistance Genes from Aegilops tauschii and the Utilization in Wheat. Plants (Basel) 12: 880.
3. Huang S, Sirikhachornkit A, Su X, Faris J, Gill B, et al. (2002) Genes encoding plastid acetyl-CoA carboxylase and 3-phosphoglycerate kinase of the Triticum/Aegilops complex and the evolutionary history of polyploid wheat. Proc Natl Acad Sci U S A 99: 8133-8138.
4. Braglia L, Gavazzi F, Morello L, et al. (2020) On the applicability of the Tubulin-Based Polymorphism (TBP) genotyping method: a comprehensive guide illustrated through the application on different genetic resources in the legume family. Plant Methods 16: 86.
5. Zhou Y, Zhao X, Li Y, Xu J, Bi A, et al. (2020) Triticum population sequencing provides insights into wheat adaptation. Nat Genet 52: 1412-1422.
6. Zhou Y, Bai S, Li H, Sun G, Zhang D, et al. (2021) Introgressing the Aegilops tauschii genome into wheat as a basis for cereal improvement. Nat Plants 7: 774-786.
7. Wiersma AT, Pulman JA, Brown LK, Cowger C, Olson EL, et al. (2017) Identification of Pm58 from Aegilops tauschii Theor Appl Genet 130: 1123-1133.
8. Xue S, Hu S, Chen X, Ma Y, Lu M, et al. (2022) Fine mapping of Pm58 from Aegilops tauschii conferring powdery mildew resistance. Theor Appl Genet 135: 1657-1669.
9. Liu Y, Wang L, Deng M, Li Z, Lu Y, et al. (2015) Genome-wide association study of phosphorus-deficiency-tolerance traits in Aegilops tauschii. Theor Appl Genet 128: 2203-2212.
10. Qin P, Lin Y, Hu Y, Liu K, Mao S, et al. (2016) Genome-wide association study of drought-related resistance traits in Aegilops tauschii. Genet Mol Biol 39: 398-407.
11. Olson EL, Rouse MN, Pumphrey MO, Bowden RL, Gill BS, wt al. (2013) Simultaneous transfer, introgression, and genomic localization of genes for resistance to stem rust race TTKSK (Ug99) from Aegilops tauschii to wheat. Theor Appl Genet (5):1179-88.
12. Zhang D, He J, Huang L, Zhang C, Zhou Y, et al. (2017) An advanced backcross population through synthetic octaploid wheat as a “bridge”: development and QTL detection for seed dormancy. Front Plant Sci 8: 2123.
13. Zhang D, Zhou Y, Zhao X, Lv L, Zhang C, et al. (2018) Development and utilization of introgression lines using synthetic octaploid wheat (Aegilops tauschii × hexaploid wheat) as donor. Front Plant Sci 9: 1113.
14. Turner MK, Kolmer JA, Pumphrey MO, Bulli P, Chao S, et al. (2017) Association mapping of leaf rust resistance loci in a spring wheat core collection. Theor Appl Genet 130: 345-361.
15. Zhang L, Wang X, Wang K, Wang J (2022) GAHP: An integrated software for genetic linkage map construction and quantitative trait locus mapping in biparental populations. Front Genet 13: 1021178.