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RESEARH STATUS OF QTL MAPPING OF GRAIN NUMBER PER SPIKE IN WINTER WHEAT

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Abbreviations

| | | | |
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| QTL | Quantitative trait locus | GWAS | Genome-wide association study |
| SN | Spike number per unit area | GNS | Grain number per spike |
| TGW | Thousand-grain weight | FSN | Fertile spikelet number per spike |
| SSN | Sterile spikelet number per spike | TSS | Total spikelet number per spike |
| SNP | Single-nucleotide polymorphism | RIL | Recombinant inbred line |
| SSR | Simple sequence repeats | DART | Diversity array technology |
| GY | Grain yield | | |

Wheat originated in the Fertile Crescent 10,000 years ago, and since then it has become one of the largest and important food crops around the world [1-3]. It is reported that yields in the main wheat-producing regions of the world have stagnated, including the United States, Asia and Australia, and it is predicted that by 2050 the world population will increase from the current 7 billion to 9.7 billion, and grain yield must increase by more than 30% to meet The increasing consumer demand of mankind [4-6] ,it has caused people to worry about global food security in the future. Therefore, it is necessary to continuously increase grain yield to achieve global food and nutrition security [7-8]. Due to the complexity of genetics, polygenes, low heritability, and obvious environmental impact, increasing yield is still a huge challenge. Yield is a complex trait involving multiple genes and is affected by environmental conditions. Yield is divided into three main components, namely spike number per unit area, grain number per spike and thousand-grain weight [9-10]. Among these factors, the heritability of thousand-grain weight is more stable, and it is composed of multiple sub-components [11-12]. The structural characteristics of grains (grain number per spike and grain size) directly affect all key components of grain yield, and it has been proposed to adjust the structure of wheat grains as a key strategy to increase the yield potential of future wheat varieties [13-16].

Yield is a complex trait, which is restricted by environmental factors. Yield is composed of spike number per unit area, grain number per spike, and thousand grain weight. Increasing spike number per unit area and the thousand-grain weight has reached a bottleneck, breaking through increasing grain number per spike to increase yield. This article mainly describes the research on grain number per spike by molecular marker-assisted selection technology QTL in recent years, and discusses the gene regulation pathway of the traits of multiple grain number per spike, which provides a theoretical basis for the subsequent creation of new wheat germplasm the cultivation of new high-yielding wheat varieties.

With the current these genes must seek new mutations. It is now believed that the yield potential can be further improved through a detailed understanding of its genetic structure combined with Marker Assisted Selection (MAS). MAS is considered to be a key technology to break through the bottleneck of conventional breeding and further increase the potential of wheat yield. The application potential of MAS depends on the number of available genes and tightly connected molecular markers. There are many reports on quantitative QTL mapping and genome-wide association studies (GWAS) of yield and related traits [17-22]. Single nucleotide polymorphism (SNP) arrays are developed from the transcriptomes of plants and animals, and provide the most advanced method for finding candidate genes for economic traits using QTL mapping (GWAS) [23]. Wheat 90k and 660 K SNP arrays are gradually replacing simple sequence repeat (SSR) markers for genetic research on yield, quality, disease resistance and stress resistance [24-27].

Li et al. selected a total of 326,570 single nucleotide polymorphism (SNP) markers from the wheat 90 K and 660 K SNP arrays for GY and related traits of GWAS, resulting in a physical distance of 14,064.8 Mb. The 3A chromosome of 714.4–725.8 Mb is positively correlated with yield, grain number per spike, grain width and plant height [28]. Liu et al. used recombinant inbred line (RIL) populations (173 F8:9 lines) in 5 environments using 90K SNP array, diversity array technology (DArT) and simple sequence repeat (SSR) markers to construct high-density genetics Map, conduct linkage analysis. Additive quantitative trait loci (QTL) were found on chromosomes 1A, 2D, 4B, 5B, 6B, and 6D, including 11 stable QTLs. The EX_C101685 and RAC875_C27536 marker intervals of 4B chromosome showed pleiotropic effects on GW, SL, GNS, FSN, SSN and TSS, and its phenotypic variation (PVE) interpretation range was 5.40 ~ 37.70%. 2-164 and RAC875_c17479_359 on 3A for SL and GNS in multiple environments were detected through linkage analysis and a genome-wide association study (GWAS)[29].

The grain number per spike is a quantitative trait, and quantitative trait locus (QTL) analysis is an important tool to determine the chromosome region or locate the basic genes of its genetic variation [30]. QTL research will help to better understand the relationship between grain number and yield. The seed setting rate of the top and basal spikelets of wheat spikes directly affects grain number per spike. Foliar spraying with exogenous 6-BA during the development of the floret primordium can increase the number of fertile florets in the basal and central spikelets by inhibiting floret abortion, Increase wheat production [31]. Boden et al. found that the Ppd-1 (Photoperiod-1) gene

can cause wheat spikelets to change from alternate to opposite by regulating the expression of FT (FLOWERING LOCUS T) gene, and the spikelet density increases, thereby increasing the number of grains per spike [32]. Zhai et al. identified a new TaGW2-A1 allele from the stable and robust QTL regions of wheat thousand-grain weight, grain number per spike, and grain morphology parameters [33].

Through the evaluation of 191 recombinant inbred lines in 11 field trials, we identified TGW and GNS gene regions on chromosomes 1B, 3A, 3B, 5B, and 7A, respectively, and also identified TGW and GNS on chromosome 6A. Gene region. The QTL of interest on chromosome 6A, composed of wsnp_BE490604A_Ta_2_1 and wsnp_RFL_Contig1340_448996, is designated as QTgw/Gns. Using near-isogenic lines (NILs) to fine-map the genetic range less than 0.538 cM. Elite NILs of QTgw/Gns. In 6 field trials, cau-6A increased TGW by 8.33% and decreased GNS by 3.05%. In conclusion, these results expand our knowledge of the genetic and molecular basis of TGW-GNS trade-offs in wheat. The QTLs and the novel TaGW2-A1 allele are likely useful for the development of cultivars with higher TGW and/or higher GNS. (2012) have reported SSR stable loci for spike length on chromosomes 1B, 2A, 2D, 3A, 3D, 4A, 5A, 5B, 5D, 6B, and/or 7D; for spikelet number per spike on 1A, 1B, 2A, 2D, 3B, 4A, 5A, and/or 5D; for grain number per spike on 1B, 2A, 2B, 2D, 3A, 4A, 4D, and/or 5A; and for thousand-grain weight on 2A, 2B, 2D, 3B, and/or 5A using a GWAS [34-35]. Tobias Würschum used 407 wheat materials to perform QTL mapping for the structure of 6 ears. The results showed that the number of grains per ear was significantly positively correlated with the number of spikelets, and there was a significant negative correlation with the thousand-grain weight. The genome-wide association map only identified small-effect QTL and medium-effect QTL, as well as the effects of phenological loci Rht-D1 and pd-d1 on some traits [36].

An International Triticeae Mapping Initiative (ITMI) mapping population comprising 105 recombinant inbred lines (RIL) developed from a cross between a Synthetic hexaploid wheat (*Triticum aestivum*) 'W7984' and a spring wheat variety «Opata M85» was used to identify quantitative trait loci (QTL) associated with grain number per spike under two treatment conditions, normal watering and water stress during meiosis. Two major QTL for grain number per spike on the main stem Q. Gnu.uwa-5A-1 and Q. Gnu.uwa-5A-2 with phenotypic variations of 25.71% and 24.93% respectively. The two major QTL—Q. Gnu.uwa-5A-1 and Q. Gnu.uwa-5A-2—contributing to variations in grain number per spike under water stress during meiosis, were found to be located close to the vernalisation gene *Vrn-A1* based on the physical positions (obtained by blasting against the wheat reference genome) of the gene and the identified QTL (<https://urgi.versailles.inra.fr>) [37]. The collection of tetraploid wheat was evaluated in seven environments, and the genotype was typed by 90K SNP analysis to identify major and stable quantitative trait loci (QTL) to show the grain number per spike (GNS), spike number (SN) and thousand-grain weight (TGW), and the genetic relationship between yield components was analyzed at the QTL level. Genome-wide association analysis detected the QTLs of KNS, TKW and GYS as 8, 11 and 10, which were significant in at least three or two environments and the entire environment. It was found that most QTLs of TKW and KNS were located in different

marker intervals, which indicated that they were genetically independent of each other. Of the eight KNS QTLs, three were associated with a significant increase in GYS [38].

In the past few decades, the increase in wheat production has been the main focus of breeding programs in many countries around the world. Although there are many genes for QTL mapping and cloning of the three factors of wheat yield and yield, there are few in actual production and breeding. Therefore, in the following research, more theoretical research should be used for breeding selection, because traditional breeding The method takes a long time. The use of molecular marker-assisted selection technology provides a favorable way for germplasm innovation and genetic improvement. In addition, the three factors of yield must be coordinated.

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