SHORT COMMUNICATION

WheatQTLdb V2.0: a supplement to the database for wheat QTL

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Abstract We recently developed a database for hexaploid wheat QTL (WheatQTLdb; www.wheatqtl.db.net), which included 11,552 QTL affecting various traits of economic importance. However, that database did not include valuable QTL from other wheat species and/or progenitors of hexaploid wheat. Therefore, an updated and improved version of wheat QTL database (WheatQTLdb V2.0) was developed, which now includes information on hexaploid wheat (Triticum aestivum) and the following seven other related species: T. durum, T. turgidum, T. dicoccoides, T. dicoccum, T. monococcum, T. boeoticum, and Aegilops tauschii. WheatQTLdb V2.0 includes a much-improved list of QTL, including 27,518 main effect QTL, 202 epistatic QTL, and 1321 metaQTL. This newly released WheatQTLdb V2.0 also has additional valuable options to search and choose the QTL, category-wise, and trait-wise data for their use in research or breeding programs.

Keywords QTL · Epistatic QTL · metaQTL · Wheat · QTL database

Introduction

A database for wheat QTL (WheatQTLdb V1.0; www.wheatqtl.db.net) was recently developed by us (Singh et al. 2021a), which carried 11,552 QTL. A correction to this database was also published later (Singh et al. 2021b). The database included QTL reported in the literature till May 2020 and included QTL for only hexaploid wheat that were identified using interval mapping and genome-wide association studies (GWAS). For the purpose of this
database, marker-trait associations (MTAs) detected using GWAS were also treated as QTL. The database included not only main effect QTL (QTL which directly affect the trait in question), but also epistatic QTL (QTL which affect the trait due to first order QTL×QTL interactions) and metaQTL. The article received 23 citations, 1342 accesses, and 5485 visits to www.wheatqtldb.net in just one year, demonstrating the utility of this database (V1.0). The database is also being utilized on a regular basis for improvement of the widely used alignment system Pretzel Wheat (https://plantinformatics.io/), which is an interactive, web-based environment for navigating multi-dimensional wheat datasets, including genetic maps and chromosome-scale physical assemblies (Personal Communication, Rudi Appels, University of Melbourne, Australia).

After the acceptance of our WheatQTLdb V1.0 manuscript for publication in Molecular Genetics and Genomics, we have been continuously working on mining and manual curation of additional QTL reported either before or after May 2020. The purpose of this manuscript is to provide updated WheatQTLdb V2.0 including information not only on *T. aestivum* but also on the following seven other related species: *T. durum*, *T. turgidum*, *T. dicoccoides*, *T. dicoccum*, *T. monococcum*, *T. boeoticum*, and *Aegilops tauschii*. WheatQTLdb V2.0 now has 27,518 main effect QTL (25,422 of *T. aestivum* and 2096 of other related species), 202 epistatic QTL (162 of *T. aestivum* and 40 of *T. durum*), and 1321 metaQTL (1236 of *T. aestivum* and 85 of *T. durum*). This newly released V2.0 will provide users more options to search and retrieve the species-wise, trait-wise, and chromosome-wise data. This improved version of wheat QTL will prove useful to the community of wheat researchers.

WheatQTLdb V1.0 was based on three-tier architect of application programming interface (API), where user’s request (in PHP) was sent to the web server, which generated a query (in MySQL) to database (Singh 2021a, b). Then, database sent a response (in MySQL) to web server to be sent to user’s system (in PHP). Same architect of API is followed in V2.0. In WheatQTLdb V1.0, the traits were classified first into 09 broad categories (including biotic stresses, abiotic stresses, biofortification, quality, development, morphology, nutrient use efficiency, physiology, and yield) and then individual traits in each broad category. However, metaQTL and epistatic QTL were not classified into these categories. This pattern of classification of traits has been retained and the references for each QTL were hyperlinked to each pop-up arrow image in “Link to reference” column. While adding more QTL in each category, the data on main effect QTL, epistatic QTL, and metaQTL, has also been updated. No separate category of multi-trait QTL has been created and, wherever available, multi-trait QTL have been included in individual traits. Thus, during the present study, information for about 15,966 new main effect QTL, 95 epistatic QTL, and 991 metaQTL was extracted and curated to improve the list of QTL available in WheatQTLdb V1.0. The database largely includes main effect QTL, which make ~95% of the total QTL; the remaining ~5% QTL include metaQTL (~4.0%) and epistatic QTL (~1.0%). The species-wise distribution of different types of QTL including main effect QTL, epistatic QTL, and metaQTL is provided in Table 1, Fig. 1, and Table 2.

**Table 1** Distribution of three different types of QTL in *T. aestivum* and other wheat species in WheatQTLdb V1.0 (Singh et al. 2021a, b) and V2.0

| Types of QTL | V1.0 | V2.0 |
|--------------|------|------|
| *T. aestivum* |      |      |
| Main effect QTL | 11,552 (25 removed due to redundancy) | 25,422 |
| Epistatic QTL | 107  | 162  |
| metaQTL      | 330  | 1236 |
| Other species|      | 85   |
| Total        | 27,518 (~95%) | 2096 |
|              | 202 (~1%)    |      |
|              | 1321 (~4%)   |      |

**Data summary and availability**

The salient features of QTL data available in V1.0 and V2.0 are compared in Table 1. It can be seen that the number of main effect QTL and metaQTL in V2.0 is more than double relative to the corresponding numbers in V1.0. The current version 2.0 of wheat QTL database is available at http://wheatqtldb.net and has no access restriction to its use.

**Main effect QTL for different traits**

In WheatQTLdb V2.0, now there are 27,518 QTL from 997 publications, of which 25,422 QTL belong
to *T. aestivum* and the remaining 2096 QTL belong to other seven wheat species; in contrast, V1.0 had 11,552 QTL all belonging to *T. aestivum* only. The distribution of QTL in other species (Fig. 1) is as follows: *T. durum* (2055), *T. monococcum* (02), *T. boeoticum* (05), *T. turgidum* (11), *T. dicoccoides* (09), *T. dicoccum* (05), and *Aegilops tauschii* (09). These QTL belong to 21 different traits placed in nine major categories (Table 2). The maximum number of QTL is available for yield followed by abiotic and biotic stresses. Figure 2 shows chromosome-wise distribution of QTL in hexaploid wheat and related species; it is apparent that B sub-genome has maximum percentage of QTL (40.57%), followed by A sub-genome (37.28%) and D

![Species-wise distribution of main effect QTL, metaQTL, and epistatic QTL in WheatQTLdb V2.0](image)

**Table 2** Frequencies of QTL for each trait belonging to nine categories of traits available in WheatQTLdb V1.0 (Singh et al. 2021a, b) and V2.0

| Trait category          | Trait                  | V1.0  | V2.0  | V2.0 Other species | V2.0 Total |
|-------------------------|------------------------|-------|-------|--------------------|-----------|
| Nutrient use efficiency | Phosphorus use efficiency | 185   | 236   | 0                  | 236       |
|                         | Nitrogen use efficiency | 1338  | 1702  | 0                  | 1702      |
|                         | Potassium use efficiency | 745   | 1049  | 0                  | 1049      |
| Abiotic stress          | Waterlogging tolerance | 282   | 277   | 0                  | 277       |
|                         | Salt stress tolerance  | 687   | 1603  | 58                 | 1661      |
|                         | Heat stress tolerance  | 453   | 1812  | 396                | 2208      |
|                         | Pre-harvest sprouting tolerance | 593 | 574 | 25 | 599 |
|                         | Drought tolerance      | 1414  | 1685  | 383                | 2068      |
| Biotic stress           | Nematode resistance    | 85    | 162   | 02                 | 164       |
|                         | Insect resistance      | 111   | 150   | 0                  | 150       |
|                         | Bacterial resistance   | 24    | 29    | 0                  | 29        |
|                         | Fungal resistance      | 3007  | 3421  | 285                | 3706      |
| Biofortification         | Zinc content           | 449   | 526   | 15                 | 541       |
|                         | Selenium content       | 71    | 62    | 15                 | 77        |
|                         | Iron content           | 312   | 367   | 25                 | 392       |
| Yield                   | Yield                  | 712   | 6863  | 651                | 7514      |
| Development             | Developmental          | 56    | 779   | 89                 | 868       |
| Physiology              | Physiological          | 391   | 427   | 0                  | 427       |
| Morphology              | Morphological          | 153   | 951   | 61                 | 1012      |
| Quality                 | Quality                | 484   | 2747  | 91                 | 2838      |
| **Total**               |                        | 11,552| 25,422| 2096               | 27,518    |
sub-genome (20.58%). A total of 429 QTL were not assigned to any particular chromosome. Chromosome 2B carries the maximum number of QTL followed by chromosomes 1B, 5A, and 3B. Figure 3 shows frequency of QTL in hexaploid wheat and related species according to the year of publication. It can be seen that major progress in QTL discovery was made during the last 5 years, mainly due to major focus in the area of GWAS and increased activity in the area of QTL interval mapping.

MetaQTL for different traits

In WheatQTLdb V1.0, there were 330 metaQTL belonging to drought tolerance, heat stress tolerance, root depth, and leaf rust resistance. V2.0 has 1321 metaQTL from 22 publications, of which 1236 metaQTL belong to *T. aestivum* for the following traits: earliness, grain yield, protein content, heading time, iron content, zinc content, multiple disease resistance, nitrogen use efficiency, phosphorus use efficiency, and plant height. The remaining 85 metaQTL belong to *T. durum* for the following categories of traits: biotic stresses, abiotic stresses, and quality traits. This rise in frequency of metaQTL is mainly due to results of several recent studies on metaQTL published during 2019–2021. Figure 4 shows year-wise frequencies of metaQTL for *T. aestivum* and *T. durum* according to the year of publication. Similarly, Fig. 5 shows chromosome-wise distribution of metaQTL in *T. aestivum* and *T. durum* available in V2.0; it can be seen that the B sub-genome has the maximum number of metaQTL followed by A and D sub-genomes.

Epistatic QTL information

In WheatQTLdb V1.0, there were 107 epistatic QTL for *T. aestivum* belonging to the following traits: heat stress tolerance, insect resistance, physiological traits, quality-related traits, stem rust resistance, stripe rust resistance, and yield-related traits. V2.0 has 202 epistatic QTL from 21 publications, of which 162 QTL belong to *T. aestivum* pertaining to salt stress tolerance and nitrogen use efficiency along with traits mentioned in V1.0. The remaining 40 epistatic QTL belong to *T. durum* pertaining to quality and yield-related traits. Figure 4 also shows year-wise distribution of epistatic QTL.
**Fig. 3** Frequencies of year-wise reported main effect QTL in WheatQTLdb V2.0

**Fig. 4** Frequencies of year-wise reported epistatic QTL and metaQTL in *T. aestivum* and *T. durum* in WheatQTLdb V2.0
Enhanced features of WheatQTLdb V2.0

Following updates have been made in WheatQTLdb V2.0 web-resource to improve its utility for wheat researchers: (i) availability of additional 15,966 main effect QTL, 991 metaQTL, and 95 epistatic QTL; (ii) inclusion of a tutorial section to guide users through the exploration of WheatQTLdb data; (iii) updated genetic maps for QTL, hyperlinked to each element of the position/interval (cM/bp) column of QTL, and metaQTL data; (iv) better search options in drop-down menus, such as species-wise, chromosome-wise, and
parameter-wise search within QTL of a particular trait; (v) a search option through QTL name written from user’s end, making the web server more user-friendly; (vi) new graphs for better representation of data in the statistics section (all written in Java scripts to provide interactive images except the bar graph image for species-wise distribution of QTL, metaQTL, and epistatic QTL); (vii) updated website for improved user experience while handling web-resource (Fig. 6 shows layout of updated web-page of WheatQTLdb V2.0).

Conclusions

A large number of main effect QTL, epistatic QTL, and metaQTL have been added to WheatQTLdb V1.0, which was already the largest collection of QTL, metaQTL, and epistatic QTL in a single database for *T. aestivum*. WheatQTLdb V2.0 replaces V1.0 and provides much more inclusive data for QTL of *T. aestivum* and seven other related species, published till December 2021. Hopefully, the V2.0 will serve better to the wheat research community including research scholars, wheat geneticists, and wheat breeders. The WheatQTLdb V2.0 is available at http://wheatqtldb.net.

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Author contribution PKG, HSB, DKS, GS, and KS conceived and planned the study and also finalized the manuscript. KS prepared the database and jointly with DKS and GS also prepared the first draft of the manuscript. RB, TG, RS, SP, MK, IJ, SaS, AK, HS, JC, KK, SoK, VKS, VPS, DKS, ShiS, SK, RK, SS, SSG, and PKS collected and tabulated the data for different traits. The chromosome maps showing the markers linked to QTLs for different traits were prepared by DKS. All authors have read and approved the final manuscript.

Data availability Updated database (WheatQTLdb V2.0) can be accessed online from the following URL: www.wheatqtldb.net through any internet browser (Mozilla Firefox/Chrome/Safari/Internet Explorer) compatible as per the operating system (Windows/Linux/Mac OSX).

Code availability Not applicable.

Declarations

Ethics approval Not applicable.

Consent to participate Not applicable.

Conflict for publication Not applicable.

Conflict of interest The authors declare no competing interests.

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