

SorGSD: updating and expanding the sorghum genome science database with new contents and tools

Yuanming Liu

Institute of Botany Chinese Academy of Sciences

Zhonghuang Wang

Beijing Institute of Genomics Chinese Academy of Sciences

Xiaoyuan Wu

Institute of Botany Chinese Academy of Sciences

Junwei Zhu

Beijing Institute of Genomics Chinese Academy of Sciences

Hong Luo

Institute of Botany Chinese Academy of Sciences

Dongmei Tian

Beijing Institute of Genomics Chinese Academy of Sciences

Cuiping Li

Beijing Institute of Genomics Chinese Academy of Sciences

Jingchu Luo

Peking University School of Life Sciences

Wenming Zhao

Beijing Institute of Genomics Chinese Academy of Sciences

Huaiqing Hao (✉ hqhao@ibcas.ac.cn)

Institute of Botany Chinese Academy of Sciences <https://orcid.org/0000-0003-0653-0021>

Hai-Chun Jing

Institute of Botany Chinese Academy of Sciences

Research

Keywords: Sorghum, Bio-energy plant, Variation, SNPs, Small INDELs, Phenotype, Database

Posted Date: May 6th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-495905/v1>

License:  This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Version of Record: A version of this preprint was published at Biotechnology for Biofuels on August 3rd, 2021. See the published version at <https://doi.org/10.1186/s13068-021-02016-7>.

Abstract

Background

As the fifth major cereal crop originated from Africa, sorghum (*Sorghum bicolor*) has become a key C₄ model organism for energy plant research. With the development of high-throughput detection technologies for various omics data, much multi-dimensional and multi-omics information has been accumulated for sorghum. Integrating this information may accelerate genetic research and improve molecular breeding for sorghum agronomic traits.

Results

We updated the Sorghum Genome SNP Database (SorGSD) by adding new data, new features and renamed it to Sorghum Genome Science Database (SorGSD). In comparison with the original version SorGSD, which contains SNPs from 48 sorghum accessions mapped to the reference genome BTx623 (v2.1), the new version was expanded to 289 sorghum lines with both single nucleotide polymorphisms (SNPs) and small insertions/deletions (INDELs), which were aligned to the newly assembled and annotated sorghum genome BTx623 (v3.1). Moreover, phenotypic data and panicle pictures of critical accessions were provided in the new version. We implemented new tools including ID Conversion, Homologue Search and Genome Browser for analysis and updated the general information related to sorghum research, such as online sorghum resources and literature references. In addition, we deployed a new database infrastructure and redesigned a new user interface as one of the Genome Variation Map databases. The new version SorGSD is freely accessible online at <https://bigd.big.ac.cn/sorgsd/>.

Conclusions

SorGSD is a comprehensive integration with large-scale genomic variation, phenotypic information and incorporates online data analysis tools for data mining, genome navigation and analysis. We hope that SorGSD could provide a valuable resource for sorghum researchers to find variations they are interested in and generate customized high-throughput datasets for further analysis.

Background

Sorghum ranks fifth in cereal production and acreage behind maize, rice, wheat and barley (<http://www.fao.org>). It is cultivated in vast geographic areas in the Americas, Africa, Asia, and Oceania. Sorghum's excellent agronomic and biological properties, such as heat and drought tolerance, make it a vital grain crop in marginal land for production without competing against other major food crops [1]. With the increase of world population and the decrease of water resources, sorghum will become the preferred food crop all over the world in the future. Furthermore, sorghum is not only harvested for grain, but also often used to produce syrup, grazing and biomass production [2].

As a model organism that carries out C₄ photosynthesis, sorghum was the second sequenced cereal crop after the C₃ organism rice [3, 4]. The comparatively small genome of sorghum makes it a potential genetic model for the design of bioenergy crops compared with the larger and more repetitive genomes of other major C₄ crops, such as maize and sugarcane. With the improvement of the reference genome (BTx623) [4, 5] and the development of sequencing technologies, studies on domestication and genetic mechanism of distinct phenotype in sorghum have been greatly accelerated [2, 6–15].

During the past decade, diverse web resources have been constructed to exhibit numerous omics data, which is beneficial for the sorghum research community (Table 1). Plant specific genome databases such as Phytozome [16] and Gramene [17], as well as the most comprehensive Genome OnLine Database (GOLD) [18] are widely used as data sources and analysis platforms for sorghum research. On the other hand, sorghum included plant secondary databases such as PIGD [19], PlanTFDB [20], DNApod [21], PceRBase [22], PtRFdb [23] and GreenPhylDB [24] have vital modules about sorghum resources. Finally, the sorghum specific secondary databases, including MOROKOSHI [25], PGSB [26], SorghumFDB [27], Sorghum QTL Atlas [28], and Sorghum Genomics, are a cluster of websites dedicated to sorghum researches. Among them, SorghumFDB is the most comprehensive sorghum specific database, which contains extensive public genomic and functional annotations data, as well as useful analysis tools. With published sorghum genome re-sequencing data of 48 accessions, we developed a sorghum SNP database (SorGSD) in 2016, providing the sorghum user community with abundant SNPs and some other resources related to sorghum genetics and genomics [29].

Table 1
Online databases for sorghum genome

Name	URL / Description	PubMed ID
<i>Comprehensive genome databases and analysis platforms</i>		
Phytozome	https://phytozome.jgi.doe.gov/ Plant genome database portal and analysis platform	[16] 22110026
Gramene	http://www.gramene.org/ Plant genome database portal and analysis platform	[17] 33170273
GOLD	https://gold.jgi.doe.gov/ Genomes online database	[18] 33152092
<i>Sorghum included plant secondary databases</i>		
PIGD	http://pigd.ahau.edu.cn/ A database for intronless genes in <i>Poaceae</i>	[19] 25270086
PlantTFDB	http://planttfdb.gao-lab.org/ A database of plant transcription factors	[20] 27924042
DNApod	http://tga.nig.ac.jp/dnapod DNA polymorphism annotation database	[21] 28234924
PceRBase	http://bis.zju.edu.cn/pcernadb/ A database of plant competing endogenous RNA	[22] 28053167
PtRFdb	http://www.nipgr.res.in/PtRFdb A database for plant tRNA-derived fragments	[23] 29939244
GreenPhylDB	https://www.greenphyl.org/ A comparative pangenomic database for plant genomes	[24] 33237299
<i>Sorghum specific secondary databases</i>		
MOROKOSHI	http://sorghum.riken.jp/ Sorghum transcriptome database	[25] 25505007
SorGSD	http://sorgsd.big.ac.cn/ Sorghum SNP database	[29] 26884811
PGSB	http://pgsb.helmholtz-muenchen.de/plant/sorghum/ Plant genome and systems biology	[26] 26527721

Name	URL / Description	PubMed ID
SorghumFDB	http://structuralbiology.cau.edu.cn/sorghum/ A database for sorghum functional genomics	[27] 27352859
Sorghum QTL Atlas	https://aussorgm.org.au/sorghum-qtl-atlas/ Tool for searching QTL landscape in sorghum	[28] 30343386
Sorghum Genomics	https://www.purdue.edu/sorghumgenomics/ Functional Gene Discovery Platform for Sorghum	N/A

Here we announce and describe the second major release of the sorghum genome science database (SorGSD). The goal of the redesign is to construct a comprehensive database with sorghum genomic variations and phenotypes. Compared with the first version SorGSD which contains SNPs of 48 sorghum accessions, the second version provides a more extensive set of genomic variation data for both SNPs and small INDELs of 289 sorghum accessions, as well as characteristic phenotypic information and panicle pictures of critical sorghum lines. We also provide three useful tools, including ID Conversion, Homologue Search and Genome Browser, in the new release. The back-end database framework and the web interface were redesigned as a part of the Genome Variation Map at the National Genomics Data Center (NGDC) and China National Center for Bioinformation (CNCB). We hope that these data and tools are beneficial for exploring genetic variations and evolution studies of sorghum and other species. The new version SorGSD is freely accessible at <https://bigd.big.ac.cn/sorgsd/>.

Results And Discussion

New data contents

The new version SorGSD was mainly built on sorghum reference genome BTx623 (v3.1) with improved assembly and gene annotations [5]. Currently, SorGSD contains 33,825,236 SNPs and 5,722,385 small INDELs identified from the re-sequencing data of 289 sorghum lines [6, 30, 31], including three accessions of *sorghum propinquum*, 50 wild/weedy sorghums and 236 cultivated sorghums (Table S1). After annotation and calculation, we obtained detailed information about the distribution of variations in different genomic regions, including genic, intergenic, and intronic regions (Table 2). On the other hand, we also collected about 70 kinds of phenotypic data over 183 accessions with plant ID (PI) from the U.S. National Plant Germplasm System (GRIN-Global) and panicle pictures of 174 critical accessions taken in our laboratory. Besides, we renewed the introduction about sorghum genome, sorghum resources websites including general information, genome and transcriptome databases, research institutions and sorghum producers around the world, as well as critical references about sorghum genetics and genomics.

Table 2
Distribution of variations in different genomic regions

Consequence type	SNPs	small INDELS
Intergenic	20683922	2248312
Upstream	12974750	4145728
Downstream	11.903259	3904589
Intron	4263151	1386417
5' UTR	489036	272597
3' UTR	805777	313469
Missense	784695	-
Synonymous	667205	-
Splice region	100793	33979
Start lost	2152	849
Stop lost	1813	722
Stop gained	16102	4730
Stop retained	1002	409
Splice acceptor	4160	3292
Splice donor	3686	3858
Coding sequence	89	4480
Inframe deletion	-	52218
Inframe insertion	-	41617
Frameshift	-	104763
Protein altering	-	3656

New features of the database

SorGSD is free and open to the public with comprehensive functions (Fig. 1). In this update, we put the main page under the National Genomics Data Center of the China National Center for Bioinformation (CNCB-NGDC) (Fig. 1a, h) [32]. Links to each page are shown at the menu bar (Fig. 1b), and a simple welcome message is displayed under the menu bar (Fig. 1c). Four shortcuts of core functions and prompt of citation can be found on the home page (Fig. 1d, e). Our laboratory's major publications and website browsing history could be acquired easily on the right side (Fig. 1f, g)

It is worth mentioning that we still keep the original version up and running, and users could browse it by clicking the "V1.0" button on the menu bar and switch back to the new version by clicking the "V2.0" button of the old version. We optimized the presentation interface to make it easier for users to search for variations. Phenotypic details of each accession could be searched directly. The browsing interface of critical references was redesigned for a better user experience. We also provide three new tools: ID conversion, Homologue Search and Genome Browser. Online documentation is provided to help users get familiar with the database. More detailed information is described as follows.

Improved Variation Search function

Users may search variation by typing in the variation type, genome position or gene ID. Furthermore, it is also possible to filter variation through consequence type and minor allele frequency (MAF) value. In our previous work, we found that the *Dry* gene encoded a plant-specific NAC transcription factor which had a few loss-of-function mutations in sweet sorghum [31]. An inframe deletion variation (Chr06:50898132) within the conserved functional NAC domain could turn the pithy stem into a juicy stem, which is one reason for the origin of sweet sorghum. Here we take the *Dry* gene as an example to search this inframe deletion (Chr06:50898132). Firstly, we enter the "Variation Search" page and choose the variation type as "INDEL"; secondly, type the gene ID of version 3.1 (*Sobic.006g147400*) in the edit box "Gene ID"; thirdly, tick "inframe deletion" in "MODERATE" under "Consequence Type"; finally, click "Submit" and we can get the list of target small INDELS at the region of *Dry* on the right hand of the page (Fig. 2a).

In the list, we could see that the first one is the target small INDEL we searched (Fig. 2a). The details of the variation could be obtained by clicking the variation ID. Users may browse the no-redundant and individual SNPs with text format in three tables and the chromosome-based graphical Genome Browser interface (Fig. 2b). In the text format tables, variation details (e.g., chromosome location, reference allele and three-fifths flank sequences), individual alleles and details of the annotated gene of the variation are given. Users can enter the gene page by clicking the gene ID with a blue background in the "Gene Annotation" table. The gene detail, gene annotation and all the variations locating gene, including SNPs and small INDELS without filtered, will be listed in three tables, respectively (Fig. 2c).

On the other hand, the demand of searching all the SNPs in the position of *Dry* could be obtained on the "Variation Search" page (Fig. 2a) by the following steps: (1) choose the variation type as "SNP"; (2) choose the chromosome as "Chr06"; (3) input the physical location (Chr06:50896169..50898604) and submit, we can get all the SNPs in the site of *Dry*.

New Phenotype Search function

A user-friendly web interface is provided for users to browse and retrieve phenotypic information (Fig. 3). On this page, users can search for important information of samples using several keywords, including Sample ID, Plant ID, Plant Name, Origin, Taxonomy and Usage. When we input "sweet sorghum" in the search box, we can obtain all accessions with the keyword of individual information (Fig. 3a). A high-resolution image could be exhibited by clicking each sample's picture to see the detail of panicle and seed

appearance. For example, sample "101" is improved sweet sorghum from Zimbabwe. By clicking the "Sample ID: 101" tab, the result page will list all agronomic traits' values (Fig. 3b). It is noteworthy that users could also enter the phenotypic page to view the value of this trait from the variation detail page by clicking the tab of "Sample ID" in the "Individual Alleles" table (Fig. 2b).

New online tool

SorGSD provides three online tools (e.g., ID Conversion, Homologue Search and Genome Browser) for users to analyze their data. ID Conversion is a useful tool to convert sorghum gene IDs from one to other ID systems of v1.4, v2.1 and v3.1, as well as the IDs of UniProt and PANTHER databases. Users could access directly to the corresponding pages of the IDs of UniProt and PANTHER through the hyperlink.

To better understand the evolution of sorghum genes, Homologue Search is built to identify homologous genes among sorghum, maize, rice and *Arabidopsis*. Besides, we provided a Genome Browser to visualize the locus of variation in the genome. Users only need to type in the genome position (e.g. *dry* gene, Chr06:50896169..50898604), corresponding transcript information of the gene and the positions of SNPs and INDELS in the relevant range will appear on the results page.

Revised Resource page

The Resource page is divided into three sections, including "Genome", "Website" and "Reference". The "Genome" part introduces the general information of sorghum genome. Users could enter the homepages of website resources promptly on the "Website" page. It is worth mentioning that we updated 162 vital publications of sorghum and classed them into six broad categories in "Reference". By clicking the class title heading in the directory on the left of the page, all papers in the target category will be listed on the right hand. Consumers could read the abstract or download the article from the links by clicking the button "Abstract".

Conclusions And Future Directions

SorGSD is committed to providing a wide range of sorghum genome data, including genomic information, detailed phenotypic data, sorghum resources and analysis tools for sorghum scientists and breeders. The interface of new version SorGSD is under the CNCB-NGDC and also an essential part of the Genome Variation Map (GVM), a data repository of genome variations of human, as well as cultivated plants and domesticated animals [33]. In this upgrade, we added 241 varieties of whole-genome variation data (including SNPs and small INDELS) based on the latest sorghum reference annotation (version 3.1). The total number of accessions is seven times to the first version. We also added about 70 kinds of traits information of 183 variations, which provides detailed reference data of each line for breeders. Tools of ID Conversion, Homologue Search and Genome Browser provide visual, convenient and quick queries for scientific workers engaged in sorghum study. Besides, we carried out a brand new page design to optimize the user experience and make the interaction friendlier. The simple and straight forward user guide allows users to be familiar with the web page's overall design and realize various functions of the webpage quickly.

In the future, we will update SorGSD regularly and add variations with newly available re-sequenced sorghum accessions. In the next step, we anticipate integrating phenotypic data, genomic variation data, transcriptome data, proteome data, and epigenomic data, as well as metabolomics and metabolic interaction networks to build a comprehensive sorghum research and analysis database. At the same time, we hope to receive comments and suggestions, aiming to make SorGSD a one-stop sorghum research platform with multi-faceted omics data and analysis tool.

Methods And Materials

Data resources

Currently, we collected re-sequencing raw data with a deep of 5.7 ~ 54× coverage from three sets of sorghum germplasms comprising a total of 289 accessions of wild and cultivated sorghum. The most extensive set of germplasm is a diverse panel of 241 sorghum lines which we published to explore the origin of sweet sorghum through the selection of *Dry* gene [31]. The second dataset is 44 sorghum lines which revealed untapped genetic potential in Africa's indigenous cereal crop sorghum by Jordan's Lab in 2013 [6]. The last dataset is also our group's work which contains three accessions of cultivated sorghums [30]. The entire set of original sequence data could be obtained from Genome Sequence Archive [34]. Phenotypic data cover the breed and agronomic-trait information collected from GRIN-Global (npgsweb.ars-grin.gov/). Finally, panicle pictures were taken when the sorghum plant reached maturity in the experimental fields of the Institute of Botany, Chinese Academy of Sciences (Beijing, China) in 2019.

Data processing

After trimming the adapter and filtering low-quality reads of the second [6] and third [30] datasets in the first dataset [31], the remaining clean reads were mapped to the reference genome BTx623 (v3.1) with BWA (v0.7.8) [35]. The mapping results were converted to BAM format, and the duplicated reads and multi-aligned reads were eliminated by the SAMtools package (v1.3) [36]. GVCF files of these lines were generated by *HaplotypeCaller* in GATK (v3.1) [37]. All the GVCF files of the three datasets were used to call SNPs and Indels by *GenotypeGVCFs* in GATK (v3.1) [37]. In total, 33,825,236 SNPs and 5,722,385 small INDELs were identified across 289 sorghum lines. Finally, we predicted and annotated the effects of variations by using the VEP program (v84) [38]. Besides, we also calculated the MAF of each variant using *vcftools* (v0.1.13) [39].

Database design and implementation

SorGSD was designed based on the framework of the iDog database [40], which was implemented using Spring Boot (<http://spring.io>), a free and prevailing Model-View-Controller (MVC) framework, and Mybatis (<https://mybatis.org/mybatis-3/>), a first-class persistence framework with support for custom SQL, stored procedures and advanced mappings. In the back-end part, metadata and reference data are stored in MySQL (<https://www.mysql.com>). Web user interfaces were developed using JSP, JQuery as well as

BootStrap. The Biodalliance genome browser (<http://www.biodalliance.org/>) was used for genome synteny visualization.

List Of Abbreviations

SNP: single nucleotide polymorphism

INDEL: insertion/deletion

NGDC: national genomics data center

CNCB: China national center for bioinformation

PI: plant ID

MAF: minor allele frequency

GVM: genome variation map

BWA: burrows-wheeler alignment

GATK: genome analysis toolkit

VEP: variant effect predictor

MVC: Model-View-Controller

SQL: structured query language

JSP: java server pages.

Declarations

Authors' contributions

HCJ initiated the project with assistance from HL, YML and XYW. HQH organized and coordinated the project. WMZ, YML, HL and XYW designed the database structure. YML and ZHW designed the web interface. ZHW constructed and maintained the webserver. YML, ZHW, JWZ, XYW, DMT and CPL participated in data analysis. YML drafted the manuscript. JCL, HQH, ZHW, XYW, HCJ, WMZ, and HL revised the manuscript. All authors read and approved the final manuscript.

Availability of data and materials

All datasets are available at <https://bigd.big.ac.cn/sorgsd/download>.

Acknowledgements

The authors would like to thank Zhiquan Liu and Zhigang Li for their field management of the panel, and all the staffs of Haichun Jing's Lab for their vital suggestions on improving the website.

Competing interests

The authors declare that they do not have any possible conflicts of interest.

Funding

This work was financially supported by grants from National Key R&D Program of China (2018YFD1000701), the CAS-Commonwealth Scientific and Industrial Research Organization Bilateral Collaboration Project (151111KYSB20180049), the Strategic Priority Research Program of Chinese Academy of Sciences (XDA26050101) and the National Natural Science Foundation of China (32072026).

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

References

1. Hao HQ, Li ZG, Leng CY, Lu C, Luo H, Liu YM, Wu XY, Liu ZQ, Shang L, Jing HC. Sorghum breeding in the genomic era: opportunities and challenges. *Theor Appl Genet.* 2021. doi:10.1007/s00122-021-03789-z.
2. Boyles RE, Brenton ZW, Kresovich S. Genetic and genomic resources of sorghum to connect genotype with phenotype in contrasting environments. *Plant J.* 2019;97:19–39.
3. Sorghum Genomics Planning Workshop p. Toward sequencing the sorghum genome. A U.S. National Science Foundation-sponsored workshop report. *Plant Physiol.* 2005;138:1898–902.
4. Paterson AH, Bowers JE, Bruggmann R, Dubchak I, Grimwood J, Gundlach H, Haberer G, Hellsten U, Mitros T, Poliakov A, et al. The *Sorghum bicolor* genome and the diversification of grasses. *Nature.* 2009;457:551–6.
5. McCormick RF, Truong SK, Sreedasyam A, Jenkins J, Shu S, Sims D, Kennedy M, Amirebrahimi M, Weers BD, McKinley B, et al. The *Sorghum bicolor* reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. *Plant J.* 2018;93:338–54.
6. Mace ES, Tai SS, Gilding EK, Li YH, Prentis PJ, Bian L, Campbell BC, Hu WS, Innes DJ, Han XL, et al. Whole-genome sequencing reveals untapped genetic potential in Africa's indigenous cereal crop sorghum. *Nat Commun.* 2013;4:2320.

7. Morris GP, Rhodes DH, Brenton Z, Ramu P, Thayil VM, Deshpande S, Hash CT, Acharya C, Mitchell SE, Buckler ES, et al. Dissecting genome-wide association signals for loss-of-function phenotypes in sorghum flavonoid pigmentation traits. *G3*. (Bethesda). 2013;3:2085–94.
8. Morris GP, Ramu P, Deshpande SP, Hash CT, Shah T, Upadhyaya HD, Riera-Lizarazu O, Brown PJ, Acharya CB, Mitchell SE, et al. Population genomic and genome-wide association studies of agroclimatic traits in sorghum. *Proc Natl Acad Sci USA*. 2013;110:453–8.
9. Boyles RE, Cooper EA, Myers MT, Brenton Z, Rauh BL, Morris GP, Kresovich S. Genome-wide association studies of grain yield components in diverse sorghum germplasm. *Plant Genome*. 2016;9.
10. Brenton ZW, Cooper EA, Myers MT, Boyles RE, Shakoor N, Zielinski KJ, Rauh BL, Bridges WC, Morris GP, Kresovich S. A genomic resource for the development, improvement, and exploitation of sorghum for bioenergy. *Genetics*. 2016;204:21–33.
11. Thurber CS, Ma JM, Higgins RH, Brown PJ. Retrospective genomic analysis of sorghum adaptation to temperate-zone grain production. *Genome Biol*. 2013;14:R68.
12. Hayes CM, Burow GB, Brown PJ, Thurber C, Xin ZG, Burke JJ. Natural variation in synthesis and catabolism genes influences dhurrin content in sorghum. *Plant Genome*. 2015;8.
13. Maina F, Bouchet S, Marla SR, Hu Z, Morris GP. Population genomics of sorghum (*Sorghum bicolor*) across diverse agroclimatic zones of Niger. *Genome*. 2018;61:223.
14. Anami SE, Zhang LM, Xia Y, Zhang YM, Liu ZQ, Jing HC. Sweet sorghum ideotypes: genetic improvement of the biofuel syndrome. *Food Energy Secur*. 2015;4:159–77.
15. Anami SE, Zhang LM, Xia Y, Zhang YM, Liu ZQ, Jing HC. Sweet sorghum ideotypes: genetic improvement of stress tolerance. *Food Energy Secur*. 2015;4:3–24.
16. Goodstein DM, Shu S, Howson R, Neupane R, Hayes RD, Fazo J, Mitros T, Dirks W, Hellsten U, Putnam N, Rokhsar DS. Phytozome: a comparative platform for green plant genomics. *Nucleic Acids Res*. 2012;40:D1178–86.
17. Tello-Ruiz MK, Naithani S, Gupta P, Olson A, Wei S, Preece J, Jiao Y, Wang B, Chougule K, Garg P, et al. Gramene 2021: harnessing the power of comparative genomics and pathways for plant research. *Nucleic Acids Res*. 2021;49:D1452–63.
18. Mukherjee S, Stamatis D, Bertsch J, Ovchinnikova G, Sundaramurthi JC, Lee J, Kandimalla M, Chen IA, Kyrpides NC, Reddy TBK. Genomes OnLine Database (GOLD) v.8: overview and updates. *Nucleic Acids Res*. 2021;49:D723–33.
19. Yan HW, Jiang CP, Li XY, Sheng L, Dong Q, Peng XJ, Li Q, Zhao Y, Jiang HY, Cheng BJ. PIGD: a database for intronless genes in the Poaceae. *BMC Genom*. 2014;15:832.
20. Jin J, Tian F, Yang DC, Meng YQ, Kong L, Luo J, Gao G. PlantTFDB 4.0: toward a central hub for transcription factors and regulatory interactions in plants. *Nucleic Acids Res*. 2017;45:D1040–5.
21. Mochizuki T, Tanizawa Y, Fujisawa T, Ohta T, Nikoh N, Shimizu T, Toyoda A, Fujiyama A, Kurata N, Nagasaki H, et al. DNApod: DNA polymorphism annotation database from next-generation sequence read archives. *PLoS One*. 2017;12:e0172269.

22. Yuan CH, Meng XW, Li X, Illing N, Ingle RA, Wang JJ, Chen M. PceRBase: a database of plant competing endogenous RNA. *Nucleic Acids Res.* 2017;45:D1009–14.
23. Gupta N, Singh A, Zahra S, Kumar S. PtRFdb: a database for plant transfer RNA-derived fragments. *Database (Oxford).* 2018;2018:bay063.
24. Valentin G, Abdel T, Gaetan D, Jean-Francois D, Matthieu C, Mathieu R. GreenPhylDB v5: a comparative pangenomic database for plant genomes. *Nucleic Acids Res.* 2021;49:D1464–71.
25. Makita Y, Shimada S, Kawashima M, Kondou-Kuriyama T, Toyoda T, Matsui M. MOROKOSHI: transcriptome database in *Sorghum bicolor*. *Plant Cell Physiol.* 2015;56:e6.
26. Spannagl M, Nussbaumer T, Bader KC, Martis MM, Seidel M, Kugler KG, Gundlach H, Mayer KF. PGSB PlantsDB: updates to the database framework for comparative plant genome research. *Nucleic Acids Res.* 2016;44:D1141–7.
27. Tian T, You Q, Zhang LW, Yi X, Yan HY, Xu WY, Su Z. SorghumFDB: sorghum functional genomics database with multidimensional network analysis. *Database.* 2016;2016:baw099.
28. Mace E, Innes D, Hunt C, Wang XM, Tao YF, Baxter J, Hassall M, Hathorn A, Jordan D. The Sorghum QTL Atlas: a powerful tool for trait dissection, comparative genomics and crop improvement. *Theor Appl Genet.* 2019;132:751–66.
29. Luo H, Zhao WM, Wang YQ, Xia Y, Wu XY, Zhang LM, Tang BX, Zhu JW, Fang L, Du ZL, et al. Erratum to: SorGSD: a sorghum genome SNP database. *Biotechnol Biofuels.* 2016;9:37.
30. Zheng LY, Guo XS, He B, Sun LJ, Peng Y, Dong SS, Liu TF, Jiang S, Ramachandran S, Liu CM, Jing HC. Genome-wide patterns of genetic variation in sweet and grain sorghum (*Sorghum bicolor*). *Genome Biol.* 2011;12:R114.
31. Zhang LM, Leng CY, Luo H, Wu XY, Liu ZQ, Zhang YM, Zhang H, Xia Y, Shang L, Liu CM, et al. Sweet sorghum originated through selection of *Dry*, a plant-specific NAC transcription factor gene. *Plant Cell.* 2018;30:2286–307.
32. Members C-N, Partners. Database Resources of the National Genomics Data Center, China National Center for Bioinformation in 2021. *Nucleic Acids Res.* 2021;49:D18–28.
33. Li CP, Tian DM, Tang BX, Liu XN, Teng XF, Zhao WM, Zhang Z, Song SH. Genome Variation Map: a worldwide collection of genome variations across multiple species. *Nucleic Acids Res.* 2021;49:D1186–91.
34. Wang YQ, Song FH, Zhu JW, Zhang SS, Yang YD, Chen TT, Tang BX, Dong LL, Ding N, Zhang Q, et al. GSA: Genome Sequence Archive. *Genom Proteom Bioinf.* 2017;15:14–8.
35. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. *Bioinformatics.* 2009;25:1754–60.
36. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, Marth G, Abecasis G, Durbin R. Genome Project Data Processing S. The Sequence Alignment/Map format and SAMtools. *Bioinformatics.* 2009;25:2078–9.

37. McKenna A, Hanna M, Banks E, Sivachenko A, Cibulskis K, Kernytsky A, Garimella K, Altshuler D, Gabriel S, Daly M, DePristo MA. The Genome Analysis Toolkit: a mapreduce framework for analyzing next-generation DNA sequencing data. *Genome Res.* 2010;20:1297–303.
38. McLaren W, Gil L, Hunt SE, Riat HS, Ritchie GR, Thormann A, Flicek P, Cunningham F. The Ensembl Variant Effect Predictor. *Genome Biol.* 2016;17:122.
39. Danecek P, Auton A, Abecasis G, Albers CA, Banks E, DePristo MA, Handsaker RE, Lunter G, Marth GT, Sherry ST, et al. The variant call format and VCFtools. *Bioinformatics.* 2011;27:2156–8.
40. Tang BX, Zhou Q, Dong LL, Li WL, Zhang XQ, Lan L, Zhai S, Xiao JF, Zhang Z, Bao YM, et al. iDog: an integrated resource for domestic dogs and wild canids. *Nucleic Acids Res.* 2019;47:D793–800.

Figures

The image shows a schematic diagram of the SorGSD website home page. The page is divided into several sections, each annotated with a letter in a yellow box:

- (a)** The top navigation bar, including the CNCB-NGDC logo and links for Databases, Tools, Standards, Publications, and About.
- (b)** The main menu bar with links for Home, Variation, Phenotype, Tools, Download, Resource, Tutorial, Contact Us, and the version number V1.0.
- (c)** The welcome message: "Welcome to SorGSD!". Below it is a paragraph describing SorGSD as a comprehensive database of sorghum genomic variations (SNPs and INDELs) of 289 accessions, with links to phenotypes, practical tools, resources, and critical references.
- (d)** A central area with four shortcut boxes: "Variation" (39,547,621 variations), "Phenotype" (289 phenotypes), "ID Conversion" (Versions, UniProt, PANTHER), and "Homologue Search" (Sorghum, Maize, Rice, Arabidopsis). A central image shows a Yin-Yang symbol made of sorghum grains.
- (e)** The "Please cite" section, which includes a citation for Luo H, Zhao W, Wang Y, Xia Y, Wu X, Zhang L, Tang B, Zhu J, Fang L, Du Z, Bekele WA, Tai S, Jordan DR, Godwin ID, Snowdon RJ, Mace ES, Luo J, Jing HC. SorGSD: a sorghum genome SNP database. *Biotechnol Biofuels*. 2016 Feb 15;9:37. (PDF)
- (f)** The "Our work about sorghum" section, listing major publications such as "Sweet sorghum originated through selection of *Dry*, a plant-specific NAC transcription factor gene. *Plant Cell*. 2018. 30:2286-2307."
- (g)** The "Global visitors" section, featuring a world map with red markers indicating visitor locations.
- (h)** The footer, which includes the CNCB-NGDC logo, contact information, and a grid of links for Research & Resources, Featured, Conference & Outreach, and Alliance & Collaboration.

Figure 1

Schematic diagram of the SorGSD home page. The background of CNCB-NGDC is shown in (a) and (h). The menu bar (b), welcome message (c), shortcuts of core functions (d) and prompt of citation (e) are placed from up to bottom. Our laboratory's major publications (f) and website browsing history (g) could be acquired on the right side.

Variation Search

Variation Type: INDEL **1**

Total items: 4 Page size: 30 Page 1 / 1

Position: sbi37408707

Chromosome: Chr06:508985

From (bp): 100000 To (bp): 200000

Gene Information: Gene ID: Sobic.006G147400 **2**

Consequence Type: HIGH, MODERATE, Inframe deletion **3**, Chromosome variant, Eprotein altering variant, Chrframe insertion, LOW, MODIFIER

Minor Allele Frequency: 0.017

Submit **4** Reset

Variation ID : sbi37408707 **b**

Variation Detail

Variation ID	sbi37408707
Type	INDEL
Position	Chr06:50898132-50898144
Ref/Alleles	ACTGGGTGCTGTG/ A
MAF	A: 0.017
5' Flank	TTGCTGATGTGCATCGCTGCTGCAGGAGG
3' Flank	CAGGGTGTCCAGAAAGCGAAAGACAGCGCA

Individual Alleles

Sample Id	Type	Alleles
101	Improved	N/N
103	Improved	N/N
107	Improved	ACTGGGTGCTGTGA CTGGGTGCTGTG
11	Improved	N/N
110	Improved	ACTGGGTGCTGTGA CTGGGTGCTGTG
123	Landrace	ACTGGGTGCTGTGA CTGGGTGCTGTG

Gene Annotation

Variation ID	Gene	Consequence	Transcript	Type	cDNA	Source/target codon	Protein Name	protein pos	source/ Amino a
sbi37408707	Sobic.006G147400	Inframe deletion (MODERATE)	Sobic.006G147400.1	mRNA	402	gaCT:gaC	Sobic.006G147400.1.p	134	DWVLC
sbi37408707	Sobic.006G147450	upstream gene variant (MODIFIER)	Sobic.006G147450.1	mRNA			Sobic.006G147450.1.p		

Genome Browser

CNCB-NGDC SorGSD

Home Variation Phenotype Tools Download Resource Tutorial Contact Us V1.0

Gene ID : Sobic.006G147400 **c**

Gene Detail

Gene ID	Sobic.006G147400
Position	Chr6:50896169-50898604
Strand	+
Source	Phytozome V12

Gene Annotation

Transcript Name	Sobic.006G147400.1
Peptide Name	Sobic.006G147400.1.p
Pfam	PF02365
Panther	PTHR31744.PTHR31744.SF9
Kog	
Ec	
KO	
GO	GO:0006355,GO:0003677
Best Hit Arabi Name	AT4G28530.1
Arabi Symbol	anac074.NAC074
Arabi Define	NAC domain containing protein 74
Best Hit Rice Name	LDC_Os04g43560.1
Rice Define	no apical meristem protein, putative, expressed
Arabi Define	NAC domain containing protein 74

Variations Locating Gene

Variation ID	Type	Position	Ref/Alleles	MAF	Gene	Consequence Type Effect
sbi20487752	SNP	Chr06:50891180	A/ G	0.014	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487753	SNP	Chr06:50891189	G/ T	0.026	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487754	SNP	Chr06:50891295	C/ T	0.005	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487755	SNP	Chr06:50891296	A/ G	0.019	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487756	SNP	Chr06:50891299	A/ G	0.010	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487757	SNP	Chr06:50891328	C/ A	0.481	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487758	SNP	Chr06:50891337	A/ T	0.010	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487759	SNP	Chr06:50891431	T/ C	0.010	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487760	SNP	Chr06:50891467	A/ G	0.020	Sobic.006G147400	upstream gene variant (MODIFIER)
sbi20487761	SNP	Chr06:50891513	T/ A	0.019	Sobic.006G147400	upstream gene variant (MODIFIER)

Figure 2

Steps and results of variation search. a. The search page of variations. Numbers in (a) shows the steps of the search. b. Detail page of the target variation. c. Detail page of the gene with target variations.

Phenotype

Total items: 87 Jump to: 1 100 sweet sorghum search

Sample ID: 101
Plant ID: PI 287603
Plant Name: FETERITA
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 103
Plant ID: PI 287817
Plant Name: ASU DIGAS
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 11
Plant ID: PI 144134
Plant Name: Inyangentombi
Origin: South Africa, KwaZulu-Natal
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 110
Plant ID: PI 302131
Plant Name: MN 3998
Origin: Portugal
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 131
Plant ID: PI 482605
Plant Name: TGR 38
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 132
Plant ID: PI 482606
Plant Name: TGR 39
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 135
Plant ID: PI 482609
Plant Name: TGR 151
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 137
Plant ID: PI 482658
Plant Name: Mhonda
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

Sample ID: 138
Plant ID: PI 482660
Plant Name: Mhonda
Origin: Zimbabwe
Taxonomy: Sorghum bicolor subsp. bicolor
Usage: Sweet sorghum

1 2 3 4 5 6 7 8 Next Last

Phenotype/101

Phenotype Information

Plant ID: PI 287603
Plant Name: FETERITA
Taxonomy: Sorghum bicolor subsp. bicolor
Origin: Zimbabwe
Type: Improved
Usage: Sweet sorghum
Race: Caudatum

Phenotype Detail

Category	Descriptor	Value	Study Environment
DISEASE	Anthraxnose	1.0 - Resistant	SORGHUM ISABELA 1994
DISEASE	Rust	2.0 - (1.0 = Resistant, 5.0 = Susceptible)	SORGHUM ISABELA 1994
GROWTH	Height Uniformity	2.0 - (1.0 = Very uniform, 5.0 = Not uniform)	SORGHUM ISABELA 1994
GROWTH	Plant Height	141	SORGHUM ISABELA 1994
INSECT	Greenbug Biotype-E	9 - Susceptible (death of the plant)	SORGHUM GREENBUG
MORPHOLOGY	Amount of Kernel Covered	3 - 50% kernel covered	SORGHUM ISABELA 1994
MORPHOLOGY	Awns	4 - None	SORGHUM ISABELA 1994
MORPHOLOGY	Basal Tiller	0	SORGHUM ISABELA 1994
MORPHOLOGY	Branch Angle	1 - Erect	SORGHUM ISABELA 1994
MORPHOLOGY	Endosperm Color	1 - White	SORGHUM ISABELA 1994
MORPHOLOGY	Endosperm Texture	3 - Partly corneous	SORGHUM ISABELA 1994
MORPHOLOGY	Endosperm Type	1 - Non-waxy	SORGHUM ISABELA 1994
MORPHOLOGY	Glume Color	1 - Purple	SORGHUM ISABELA 1994
MORPHOLOGY	Glume Pubescence	3 - No	SORGHUM ISABELA 1994
MORPHOLOGY	Inflorescence Exsertion	3	SORGHUM ISABELA 1994
MORPHOLOGY	Kernel Color	4 - Brown	SORGHUM ISABELA 1994
MORPHOLOGY	Kernel Plumpness	1 - Plump	SORGHUM ISABELA 1994
MORPHOLOGY	Kernel Shape	2 - Oval	SORGHUM ISABELA 1994
MORPHOLOGY	Mesocarp	1 - Thick	SORGHUM ISABELA 1994
MORPHOLOGY	Mid-Fib Color	2 - Green	SORGHUM ISABELA 1994
MORPHOLOGY	Nodal Tiller	2 - No	SORGHUM ISABELA 1994

Figure 3

Searching page (a) of accessions and result page (b) of the target accession.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Additionalfile1SorGSDupdateBFB.xlsx](#)