PanaxGDB: A Comprehensive Platform for Panax

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INTRODUCTION

The genus Panax (Araliaceae) consists of 16 species primarily distributed in southwestern and northeastern Asia and North America. The herb has been used as a traditional medicine for treating cardiovascular and cerebrovascular diseases and improving immune systems for thousands of years (Zuo et al., 2017). Three high-value species, Panax quinquefolius, Panax ginseng, and Panax notoginseng, have been successfully domesticated and are widely cultivated in Asia and North America to meet increasing market demands (Beedata, 2020; Zhang et al., 2020; Ibaogao, 2021). In 2019, the total global market for P. notoginseng, P. ginseng, and P. quinquefolius exceeded...
 geological distribution, morphology, and cultivar information on 16 Panax species. A section on the compounds of those species focuses on the distributions and characteristics of nearly 600 compounds as well as their metabolic pathways. For the published P. notoginseng genomes, the database also integrates the draft genomic sequence with structural and functional annotations and calculates the gene expression levels based on well-organized transcriptomes sampled from different tissues, growth stages, and treatments. The resequencing results of P. notoginseng were also uploaded on the Population page to perform genome-wide association analysis (GWAS) on agronomic traits associated with the yield of P. notoginseng. In addition, the powerful tools Blast and JBrowse are used to perform functional analysis.

MATERIALS AND METHODS

Oomics, Metabolome, and Germplasm Data Sets

The oomics data set includes transcriptome sequencing, genomes, metagenomes, and chloroplast genomes. The bioinformation of the data sets was summarized, and a list was formed for easy searching. Germplasm data include species and cultivar information. Information was also collected on more than 500 compounds from 13 Panax species by searching the literature on phytochemistry between 1963 and 2021. The above information and that on chemical compositions were manually collected from publications, online resources, and other literature.

Assembly and Gene Models of Genome Data

Genomic data sets primarily contain genome sequences, gene sequences, protein sequences, gff, gene functional annotations, and transcription factor (TF) annotations. Gene sequence and gff files of P. ginseng in the database were obtained from the ginseng genomic database (http://ginsengdb.snu.ac.kr/data.php). The 5th P. notoginseng genome assembly composed of 2.41 Gb from a previous study was included (Yang et al., 2021). Genome assemblies of P. ginseng and P. notoginseng included 59,352 and 47,870 genes, respectively. Genes were functionally annotated in InterPro (protein family; http://www.ebi.ac.uk/interpro/), pfam (protein family; http://pfam.xfam.org/), GO (Gene Ontology; http://geneontology.org/), NCBI non-redundant protein (Nr) database (http://www.ncbi.nlm.nih.gov), and Kyoto Encyclopedia of Genes and Genomes (KEGG) database (http://www.genome.jp/kegg) by using BLASTX (e-value < 10^{-5}; http://www.ncbi.nlm.nih.gov/BLAST/). The transcription factors were identified with PlantTFDB serve (http://planttfdb.gao-lab.org/).

Digital Gene Expression Profiles

RNA-Seq data sets of P. ginseng and P. notoginseng with biological duplication were selected. Data sets included different tissues, development times, and treatments. Filtered RNA-seq was mapped to the latest reference genome by HISAT2 (Zhang et al., 2021). Matched reads were subsequently presented to
StringTie for de novo assembly, during which the expression level of each gene and the isoform was estimated (Pertea et al., 2015). Gene expression maps were prepared by manual selection on the Gene page.

**Resequencing of *Panax notoginseng***

FastQC software (v0.11.5) was used for quality control of raw reads from Illumina HiSeqTM2000 (WuHang, HuNan, China) sequencing, and clean reads were mapped to the latest reference genome using the BWA software (v0.7.15-R1140; Li and Durbin, 2009; De Sena Brandine and Smith, 2019). The GATK software (v4.0.9.0) was used for single nucleotide polymorphisms (SNPs) identification (Tajima, 1989). The ANNOVAR software was used to calculate the number of mutation types of SNP sites in each sample (Wang et al., 2010). The software LUMPY (v0.2.13) was used to detect structural variation (SV) in this project (Layer et al., 2014). PCA of the sample group structure was performed by using PLINK (v1.9b6) and EIGENSOFT (EIG-6.1.4) software (Patterson et al., 2006; Price et al., 2006; Purcell et al., 2007). The software ADMIXTURE (v1.3.0; Alexander et al., 2009) was used to analyze population structure. The software SNPhylo 2 (Lee et al., 2014) was used to construct evolutionary relations between different samples, and Phylogeny.IO (https://github.com/oist/phylogeny-io) was used to construct the phylogenetic tree. A graph of linkage disequilibrium was obtained by PopLDdecay (v3.40) analysis (Zhang et al., 2019). GCTA (v1.93.2) software was performed for GWAS analysis, and a mixed linear model (MLM) was adopted as a modeling method (Yang et al., 2011).

**Transcriptome of *Panax notoginseng***

A total of 20.3 G of PacBio Iso-Seq data and 92.6 G of raw RNA-seq data of three representative tissues (roots, stems, leaves) were acquired from *P. notoginseng* sequencing. The RNA from the three tissues was mixed to establish two SMRT cells for SMRT sequencing. Smrtlink 5.0 software was used to process the raw data, and the obtained redundant sequences were clustered by an iterative clustering for error correction algorithm to obtain full-length consensus sequences (FL; Pertea et al., 2015). Quiver was used to align FL sequences and non-FL reads. The high-quality sequence with accuracy >0.99 obtained in the previous step was further aligned with the assembled data from Illumina RNA-seq by using Lordec (v0.9) and mapped to the reference genome by using GMAP software (Wu and Watanabe, 2005).

**Database Implementation**

PanaxGDB is based on the Apache web server (http://www.apache.org), adopted ThinkPHP5.1 (http://www.thinkphp.cn)-based FastAdmin templates, included frameworks of Codegigniter (https://www.codeigniter.com/) and Bootstrap (https://getbootstrap.com), and applied programming languages including CSS, PHP-HTML5, and JavaScript. MySQL (https://
FIGURE 2 | Query interface to retrieve information on germplasm, genomic application, and compounds. (A) Species page. 16 species information on this page. (B) Cultivars page. 62 cultivars information on this page. (C) Gene page. Search for genetic information including functional annotation, CDS, and protein sequence, etc. JBrowse (D) based on JavaScript for visual analysis of the genome annotation. Blast server (E) to perform homology searches with different data sets. (F) Compounds page. Search for the distribution, known metabolic pathways, or other characteristics of a particular compound.

www.mysql.com) was used for data sorting, storage, and management, and the AJAX asynchronous loading scheme was used for quick data loading and function implementation. To provide an interactive user experience, Echarts (https://echarts.apache.org/zh/index.html), JBrowse (http://jbrowse.org), Phylogeny.IO (https://github.com/oist/phylogeny-io),
and JQuery (https://jquery.com) were applied. The File Transfer Protocol-based download function was also provided with a transfer speed of up to 50 Mbps. Additionally, all functions in PanaxGDB were tested for web browsing on Safari, Chrome, Firefox, IE, and Edge by mobile phone, pad, and computer.

RESULTS
Database Structure
PanaxGDB with a user-friendly web interface includes nine pages: Home, Species, Cultivars, Gene, Compounds, Population, Tools, and Download (Figure 1). The Home page presents an overview of PanaxGDB as well as links to popular ginseng sites and biological tools. Other pages represent the five main topics of PanaxGDB.

Germplasm of Panax
Two modules of the germplasm resources of Panax are included in PanaxGDB: Species (Figure 2A) and Cultivars (Figure 2B). These two pages can help users quickly understand the species structure of Panax and the breeding status of Panax cultivars, respectively. To determine species, authoritative plant taxonomic keys were used. Species not authenticated were identified according to morphological and molecular data in various public references, and species of uncertain status were indicated. Panax assamicus found in northeast India, which was not accepted by the Board of Trustees of the Royal Botanic Gardens, was cited as P. bipinnatifidus var. angustifolius. Similarly, Panax shangianus and Panax omiensis were not included in the authoritative source for plant nomenclature. Although Panax vietnamensis var. fuscidiscus and P. vietnamensis var. langbianensis were not included in authoritative plant taxonomies, morphological and molecular evidence indicate they are new varieties (Van Duy et al., 2016).

Sixteen Panax species are summarized in the database, and eight categories of information are provided for each species on the Species page, including pictures, common name, synonyms, chromosome number, utilization, distribution, description, and references (Figure 2A). In China, local provincial authorities register and identify cultivars of medicinal plants, and as a result, information on various cultivars is not concentrated. Therefore, enterprises and producers involved in Panax cultivation are limited in the collection of cultivar information, which is difficult to meet market demand. On the Cultivars page, those participating in the Panax industry can easily obtain the current breeding status of Panax cultivars to screen optimal cultivars for different products under local environmental conditions. The Cultivars page contains eight categories of information on cultivars, including crop variety number, uses, area of production, description, pictures, breeders or organizations, and references (Figure 2B). A total of fifty P. ginseng cultivars are recorded in PanaxGDB, including 19 from China, 30 from Korea, and one from Japan, as well as two cultivars of P. quinquefolius, one of P. japonicus, and nine of P. notoginseng from China.

Genetic Information
PanaxGDB provides viewing of the latest assemblies of Panax genomes (P. ginseng and P. notoginseng). Genome assembly files of P. notoginseng are open to the public for research for the first time. For convenience and practicality, genome assemblies were re-annotated and uploaded. On the Gene page, users can enter a TF, GO, and KEGG orthology identifiers (IDs), Pfam domain, InterPro domain, or gene ID in different search boxes to obtain detailed corresponding information, such as structural and functional annotation of genes of interest. For each gene, 22 categories of information are provided, such as gene locus, length, and downloadable sequence, among others, which can be displayed using the “Operate” option in the upper-right of the display list (Figure 2C). Users can also access the ginseng genome databases from the Home page. In the gene expression module, one or more genes can be selected according to specific needs, and gene expression levels of different groups or treatments can be visualized from a heat map of ticking, related genes. Heat maps provide information on data accession numbers and associated reference (Figure 2C).

On the Tool page, JBrowse and Blast can help users visualize Panax genomes and sequence alignments. Currently, P. ginseng and P. notoginseng genomes, gene annotations, and information on Panax variants can be imported into JBrowse. Sets of genomes, gene and density information on SNP/300 kb, and allele frequency can be explored in PanaxGDB in JBrowse (Figure 2D). The Blast tool is provided for sequence alignment with Sequence coding for amino acids in protein (CDS) and protein sequences of P. ginseng and P. notoginseng and uses the input of a similar sequence (Figure 2E). The final Blast result can be downloaded in HTML format.

Metabolites of Panax
Secondary metabolites in Panax are pharmacologically active. Therefore, a metabolites page was provided with an interface (Compounds page) to retrieve, visualize, and investigate metabolite distribution in 12 Panax species (Figure 2F). The page includes 587 compounds of Panax, of which 492 are saponins. Damarane-type saponins accounted for 76.8% (451) of the known compounds. More than 200 saponins have been detected in P. ginseng and P. notoginseng according to the available phytochemical and pharmacological literature. In the Statistics modules, the proportion, quantity, and distribution of different types of compounds across different species can be visualized. In the list of chemical compounds, users can find ginsenoside Rh1, Rb2, Rc, Rd, Rb3, Re, Rg1, 20(S)-Rg2, Rh1, Rf, and Ro, notoginsenoside R1, and gypenoside XVII in at least eight Panax species. More than two Panax species contain 148 types of saponins. However, some characteristic saponins, such as quinquenoside I, II, III, IV, and V, are found only in P. quinquefolium (Yoshikawa et al., 1998). According to statistics, characteristic saponins are found in P. ginseng, P. notoginseng, P. quinquefolius, P. japonicus, P. japonicus var. major, P. vietnamensis, P. stipuleanatus, and P. bipinnatifidus. However, the list might be incomplete because of insufficient detection depth. To search for additional information, users can search by entering the name of a specific compound, compound
type, or species origin. Users can click on a metabolite to link the metabolite information subpage and complete metabolite information, including biochemistry, biosynthesis pathway, and its species origin. Another hidden effect of this page is to help understand validated biosynthetic pathways of compounds, especially saponins, and validated genes in those pathways.

**Population Structure**

The resequencing database was set for *Panax* breeding and germplasm resource management. Data from *P. notoginseng* were collected on the Population page, and 200 3-year-old *P. notoginseng* samples from Yunnan, China, with nine important agricultural traits were randomly selected for resequencing. The average sequencing size of each sample was 28.83 Gb. Results were visualized and uploaded to the Population page with three modules which included Statistics (Figure 3A), Analysis (Figure 3B), and Variations (Figure 3C). Statistical results of the resequencing can be seen on the Statistics subpage. On the Analysis subpage, the phylogenetic tree was derived from the SNP data, and the tree shows *P. notoginseng* of Wenshan and can be divided into five subgroups. In the GWAS module, there were 192 highly significant peaks on 12 pseudochromosomes associated with traits (root weight and leaf width) related to saponin yield. Those SNPs can be found on the Variations pages, and 22 occurred in CDSs (Supplementary Table 1), which can be found on the Gene page. Those genes were...
annotated as proteins associated with cell metabolism and growth, including peptidyl-prolyl cis-trans isomerase, aminotransferase, oxoglutarate dioxygenase, 2-isopropylmalate synthase, WD40-repeat protein, AMP-dependent synthetase, and phosphatidylinositol N-acetylglucosaminyltransferase, protein kinases, or as plant stress-related proteins, including heat shock protein (Supplementary Table 1).

**Omics Data Acquisition and Upload**

To make it more convenient to use Panax omics data, all publicly available data were gathered and classified. The Download page contains information and links to all available public Panax omics data, and long-read sequencing and resequencing data were published for the first time in PanaxGDB (Figure 3D). Downloadable content in this module includes 405 transcriptome sequencings, two genomes, 21 metagenomes, and 67 chloroplast genomes. The visual data can help users to summarize information. Because the database is an open platform, prospective ginseng omics data are welcomed and can be included in the database by contacting the authors through the Data Submission page.

**DISCUSSION**

An early ginseng genome database was limited to the genome and transcriptome of *P. ginseng*, and it was not possible to visually compare expression levels of more than two genes (Jayakodi et al., 2018). In PanaxGDB, additional transcriptome data from different tissues and experiments were re-assembled, and information on those data, including sources and references, can be intuitively visualized, including comparisons of expression levels of different genes. PanaxGDB provides the most comprehensive overview of the omics, metabolome, and germplasm resources of *Panax* and forms a user-friendly interface. In addition, the most complete analysis of resequencing and annotation results of the 5th version of the *P. notoginseng* genome and the full-length RNA-seq of *P. notoginseng*, as well as Panax cultivars, are fully displayed.

PanaxGDB is introduced as a comprehensive database with the first highly integrated multidirectional research results of the *Panax* genus to improve the practical use of data. PanaxGDB can be an important resource for those working with *Panax* in comparative studies of major cultivars, in the development of pharmacological value, and in heterogeneous biosynthetic research on saponins. As an open platform, advanced users are welcome to submit data related to *Panax* species to regularly update the database. Thus, PanaxGDB can continuously serve as a central portal to boost research on the biology and chemistry of Panax.

**DATA AVAILABILITY STATEMENT**

All data of this study are available through the PanaxGDB database website (http://panaxGDB.ynau.edu.cn).

**AUTHOR CONTRIBUTIONS**

XuL and SY: conception and design of the study. YLiu, YLi, ZY, GX, YLu, QZ, XueL, GL, and BH: acquisition of data or analysis and interpretation of data. YLin, XuL, YD, GZ, and QY: database construction and visualization. YLin, BH, XuL, and SY: drafting of the article or revising it critically for important intellectual content. YLin, BH, YLu, YLi, YD, ZY, GX, GL, XueL, QZ, QY, GZ, SY, and XuL: final approval of the version to be published.

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**SUPPLEMENTARY MATERIAL**

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fpls.2022.883818/full#supplementary-material

**REFERENCES**

Alexander, D. H., Novembre, J., and Lange, K. (2009). Fast model-based estimation of ancestry in unrelated individuals. *Genome Res.* 19, 1655–1664. doi: 10.1101/gr.094052.109

Beedata (2020). Report on Data Analysis of China’s Sanqi Industries in 2020. Available online at: https://finance.sina.com.cn/money/future/agri/2020-10-16/doc-iiznezxr6369582.shtml (accessed December 24, 2021).

Chen, R. J., Chung, T.-Y., Li, F.-Y., Lin, N.-H., and Tzen, J. T. (2009). Effect of sugar positions in ginsenosides and their inhibitory potency on Na+/K+-ATPase activity. *Acta Pharmacol. Sin.* 30, 61–69. doi: 10.1038/aps.2008.6

Chen, W., Balan, P., and Popovich, D. G. (2019). Review of ginseng anti-diabetic studies. *Molecules* 24:4501. doi: 10.3390/molecules24244501

De Sena Brandine, G., and Smith, A. D. (2019). Falco: high-speed FastQC emulation for quality control of sequencing data. *F1000Res.* 8:1874. doi: 10.12688/f1000research.21142.1

Ding, S., Wang, M., Fang, S., Xu, H., Fan, H., Tian, Y., et al. (2018). D-dencichine regulates thrombopoiesis by promoting megakaryocyte...
adhesion, migration and platelet formation. Front. Pharmacol. 9:297.
doi: 10.3389/fphar.2018.00297
Ibaoga (2021). Report of Produce Sale Demand and Investment Forecast on
China Ginseng Industry (2021-2026) [Preprint]. Available online at: https://bg.
qianzhan.com/report/detail/300/200731-fb56d43.html (accessed December
28, 2021).
Jayakodi, M., Choi, B. S., Lee, S. C., Kim, N. H., Park, J. Y., Jang, W., et al. (2018).
Ginseng Genome Database: an open-access platform for genomics of Panax
ginseng. BMC Plant Biol. 18:62. doi: 10.1186/s12870-018-1282-9
Jiang, Z., Tu, L., Yang, W., Zhang, Y., Hu, T., Ma, B., et al. (2021). The chromosome-level reference genome assembly for Panax notoginseng
and insights into ginsenoside biosynthesis. Plant Commun. 2:100113.
doi: 10.1016/j.plcom.2020.100113
Kim, K., Lee, S. C., Lee, J., Lee, H. O., Jho, H. J., Kim, N. H., et al. (2015a). Comprehensive survey of genetic diversity in chloroplast genomes
and 45S rDNAs within Panax ginseng species. PLoS ONE. 10:e011759.
doi: 10.1371/journal.pone.011759
Kim, K., Lee, S. C., Lee, J., Yu, Y., Yang, K., Choi, B. S., et al. (2015b). Complete chloroplast and ribosomal sequences for 30 accessions elucidate evolution of
Oryza AA genome species. Sci. Rep. 5:15655. doi: 10.1038/srep15655
Layer, R. M., Chiang, C., Quinlan, A. R., and Hall, I. M. (2014). LUMPY: a
pipeline to construct a phylogenetic tree from huge SNP data. BMC Genomics.
15:162. doi: 10.1186/1471-2164-15-162
Li, H., and Durbin, R. (2009). Fast and accurate short read alignment
with Burrows-Wheeler transform. Bioinformatics. 25, 1754–1760.
doi: 10.1093/bioinformatics/btp324
Liu, L., Xu, F. R., and Wang, Y. Z. (2020). Traditional uses, chemical diversity and biological activities of Panax L. (Araliaceae): a review. J. Ethnopharmacol.
263:112792. doi: 10.1016/j.ympev.2020.106851
Liu, Y. Z., Li, M., and Hakonarson, H. (2010). ANNOVAR: functional annotation
of genetic variants from high-throughput sequencing data. Nucleic Acids Res.
38:e164. doi: 10.1093/nar/gkq603
Wang, L., Huang, Y., Yin, G., Wang, J., Wang, P., Chen, Z. Y., et al. (2020b).
Antimicrobial activities of Asian ginseng, American ginseng, and notoginseng.
Phyther. Res. 34, 1226–1236. doi: 10.1002/ptr.6605
Wang, P., Wei, Y., Fan, Y., Liu, Q., Wei, W., Yang, C., et al. (2015). Production of
bioactive ginsenosides Rh2 and Rg3 by metabolically engineered yeasts. Metab.
Eng. 29, 97–105. doi: 10.1016/j.ymben.2015.03.003
Wu, T. D., and Watanabe, K. C. (2005). GMAP: a genomic mapping and alignment
program for mRNA and EST sequences. Bioinformatics 21, 1859–1875.
doi: 10.1093/bioinformatics/bti310
Xu, C., Wang, W., Wang, B., Zhang, T., Cui, X., Pu, Y., et al. (2019). Analytical
methods and biological activities of Panax notoginseng saponins: recent trends. J. Ethnopharmacol. 236, 443–465. doi: 10.1016/j.jep.2019.02.035
Yang, J., Lee, S. H., Goddard, M. E., and Visscher, P. M. (2011). GCTA: a
tool for genome-wide complex trait analysis. Am. J. Hum. Genet. 88, 76–82.
doi: 10.1016/j.ajhg.2010.11.011
Yang, W. Z., Hu, Y., Wu, W. Y., Ye, M., and Guo, D. A. (2014). Saponins in the
genus Panax L.(Araliaceae): a systematic review of their chemical diversity.
Phytochemistry 106, 7–24. doi: 10.1016/j.phytochem.2014.07.012
Yang, Z., Liu, G., Zhang, G., Yan, J., Dong, Y., Lu, Y., et al. (2021). The
chromosome-scale high-quality genome assembly of Panax notoginseng provides insight into dencichine biosynthesis. Plant Biotechnol. J. 19, 869–871.
doi: 10.1111/pbi.13558
Yoshikawa, M., Murakami, T., Yashiro, K., Yamahara, J., Matsuda, S., Saijoh,
R., et al. (1998). Bioactive saponins and glycosides. XI. Structures of new
dammarane-type triterpene oligoglycosides, quingenosides I, II, III, IV, and
V, from American ginseng, the roots of Panax quinquefolium. L. Chem. Pharm.
Bull. 46, 647–654. doi: 10.1248/cpb.60.6467
Zhang, C., Dong, S. S., Xu, J. Y., He, W. M., and Yang, L. T. (2019).
PopLDecay: a fast and effective tool for linkage disequilibrium decay analysis based on variant call format files. Bioinformatics 35, 1788–1788.
doi: 10.1093/bioinformatics/btj875
Zhang, H., Abid, S., Ahn, J. C., Mathiyalagan, R., Kim, J. Y., Yang, D. C.,
et al. (2020). Characteristics of Panax ginseng Cultivars in Korea and China.
Molecules 25:2635. doi: 10.3390/molecules25112635
Zhang, Y., Park, C., Bennett, C., Thornton, M., and Kim, D. (2021). Rapid and
accurate alignment of nucleotide conversion sequencing reads with HISAT-2.
Genome Res. 31, 1290–1295. doi: 10.1101/gr.275193.120
Zhou, M., Yang, G., Sun, G., Guo, Z., Gong, X., and Pan, Y. (2020).
Resolving complicated relationships of the Panax bipinnatifidus complex in
southwestern China by RAD-seq data. Mol. Phylogenet. Evol. 149:106851.
doi: 10.1016/j.ympev.2020.106851
Zhu, S., Zhou, K., Fushimi, H., Cai, S., and Komatsu, K. (2004). Comparative study
on triterpene saponins of Ginseng drugs. Planta Med. 70, 666–677.
doi: 10.1055/s-2004-827192
Zuo, Y., J., Wei, J., and Zhou, S. L. (2017). Intercellular and intracellular biogeography of the eastern Asian - Eastern North American disjunct Panax (the ginseng genus, Araliaceae), emphasizing its diversification processes in eastern Asia. Mol. Phylogenet. Evol. 117, 60–74.
doi: 10.1016/j.ympev.2017.06.016

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