



International Rice Research Institute (IRRI)

About IRRI and SNP-Seek

IRRI's Mission: Through our work and partnerships, we aim to improve the health and welfare of rice farmers and consumers; promote environmental sustainability in a world challenged by climate change; and support the empowerment of women and the youth in the rice industry.

In partnership with the Chinese Academy of Agricultural Sciences and BGI Shenzhen, IRRI re-sequenced 3024 types of rice (3K Rice Genomes Project, 3K RGP). This data was released to the public in 2014 (3K RGP, *GigaScience* 3:7). IRRI developed the [SNP-Seek database](#) using ZK and other tools to house genomic variants from this and other projects. Our target customers are global rice researchers involved in genetics, genomics and breeding.

“Certain ZK features (BigListBox, charts) were especially helpful since building them independently would have taken a lot of time.”

ZK x IRRI

ZK powers the user interface of the [SNP-Seek database](#), a web resource providing access to the largest collection of variant calls for Asian rice with display and analysis tools. SNP-Seek development is open-source and is available from https://bitbucket.org/irridev/iric_portal/src/master/.

It is extensively used by rice researchers and breeders around the world. We average approximately 2000 sessions per month for several hundred users with 60% returning visitors. The project started in 2014, with a first version running in 2015. The database was the main subject of publications by Alexandrov et al. (2015, *Nucleic Acids Res* 43:D1023-D1027), Mansueto et al. (2016, *Curr Plant Biol* 7:16-25), and Mansueto et al. (2017, *Nucleic Acids Res* 45:D1075-D1081). SNP-Seek development is ongoing, and the database is regularly updated with new features and datasets.

The Challenge

This project handles a very large amount of data that needs to be displayed, and be made available for downloads by users. Aside

from data display, this project also provides ways of presenting data like charts or graphs needed for analyses.

Other technicalities are the need to use other JavaScript libraries for large embedded applications that entail using JSP to prevent library version conflicts and using CSS to change the styles for display and page layouts.

Why ZK

Familiarity with coding in Java Swing and similarity to coding a desktop GUI were factors in choosing ZK. We have used ZK from the beginning of API development for SNP-Seek.

We chose ZK since:

- It is easy to use for Java developers, without needing Javascript for many tasks.
- ZK offers a rich functionality especially in data visualization. We liked the community contributed tool for displaying large tables (BigListBox). Using this tool is one of the crucial parts in the app architecture, and we could not find a feature of similar power in other frameworks.



Figure1. BigListBox is used to display large SNP data.

Best of ZK

The ZK chart library provides excellent presentation of data and supports downloading of data points. The BigListBox component also shows how it handles displaying of large data.

As stated above, a big part of the reason why we use ZK is the BigListBox component which we use to display big data. In this case, displaying SNPs.

The Result

SNP-Seek provides an easy and flexible way to query a large genomic variation dataset.

ZK allowed us to build the user interface faster and efficiently. Certain ZK features were especially helpful since building them independently would have taken a lot of time.

There is ongoing, continuous development for this project. We will be releasing a new version of the project shortly using the latest versions of ZK that improves the user interface, adds visualizations, and other new features to support the research community.

The screenshot shows the Rice SNP-Seek Database interface. At the top, there's a navigation bar with the IR&C logo and 'Rice SNP-Seek Database' title. Below it, a search bar and navigation links (Home, Search, Browse, My Lists, Order Seeds, Download, Help) are visible. The main content area is divided into search filters and a results table.

Search Filters:

- Variety set: 3k
- SNP set: 3k filtered
- Subpopulation: all varieties
- My Variety List: [dropdown]
- Chromosome: CHR1 (ex. chr01)
- Start: 16292
- End: 20323
- Gene locus: LOC_OS01G011040 (ex. loc_os01g011010)
- SNP List: [dropdown]
- Locus List: [dropdown]
- Options: Variant (Include indels, Show phenotype, Legacy, CO Terms, Mismatch only)
- Advance options: Include SNPs (All, All highlight Nonsynonymous, Non-synonymous only, Missing allele ignore in count)

SNP QUERY Instructions:

- Select two varieties to compare; OR Compare All Varieties, members of a Subpopulation or Variety List, with the Reference
- Specify region(chromosome, start and end) OR Gene LOC_Os (MSU locus name)
- Set options and click action button

Results Table:

Nipponbare positions	Variety	Assay	Accession	Subpopulation	Dataset	Mismatch	16349	16474	16544	16737	17263	18505	18780	18849	19267	19346	19375	19595	19722	19837	19919	20171
Nipponbare							T	T	A	G	A	T	C	A	G	A	C	G	T	A	C	T
AI ZI HUNG:IRGC 51255-1	AI ZH	IRIS	IRGC	nd14	3k	8.0	C	G	G	G	A	T	C	A	A	G	A	G	T	T	C	C
BA SHI ZAO:IRGC 67903-1	BA SH	IRIS	IRGC	nd14	3k	8.0	C	G	G	G	A	T	C	A	A	G	A	G	T	T	C	C
SSANGDUJO:IRGC 55632-1	SSAN	IRIS	IRGC	nd14	3k	8.0	C	G	G	G	A	T	C	A	A	G	A	G	T	T	C	C
DA NUO (ZHAN):IRGC 72025-1	DA N	IRIS	IRGC	nd14	3k	8.0	C	G	G	G	A	T	C	A	A	G	A	G	T	T	C	C
MIN KE ZHAN:IRGC 72230-1	MIN H	IRIS	IRGC	nd14	3k	8.0	C	G	G	G	A	T	C	A	A	G	A	G	T	T	C	C

```

<tabpanel id="tabpanelTableLarge">
  <biglistbox id="biglistboxArrayLarge"
    class="z-biglistbox-two" height="800px" sclass="mylist"
    visible="false" width="90%" hflex="0" vflex="0" xmlns:w="client"
    w:onScroll="jq('$tip').fadeOut();" />
</tabpanel>

<tabpanel id="tabpanelSnpef"
  <listbox id="listboxSnpef"
    pageSize="100" size="1000"
    <listhead sizale="1000">
      // biglistboxArray.invalidate();
      biglistboxArrayLarge.setSortAscending(matricmpproviderAsc);
      biglistboxArrayLarge.setSortDescending(matricmpproviderDesc);
      biglistboxArrayLarge.setWidth("1100px");
      biglistboxArrayLarge.setRowHeight("10px");
      biglistboxArrayLarge.setColWidth("10px");
      biglistboxArrayLarge.setStyle("font-size:6px");

      biglistboxArrayLarge.setMatrixRenderer(biglistboxArray.getMatrixRenderer());
      biglistboxArrayLarge.setModel(biglistboxArray.getModel());
      biglistboxArrayLarge.setVisible(true);
    </listhead>
  </listbox>
</tabpanel>

```

Figure 2. BigListBox implementation and example code.

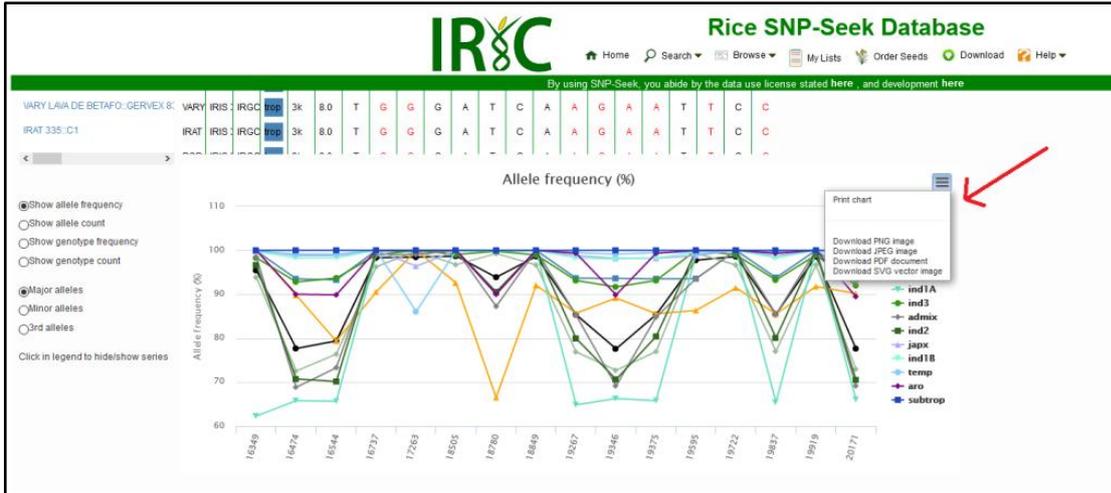
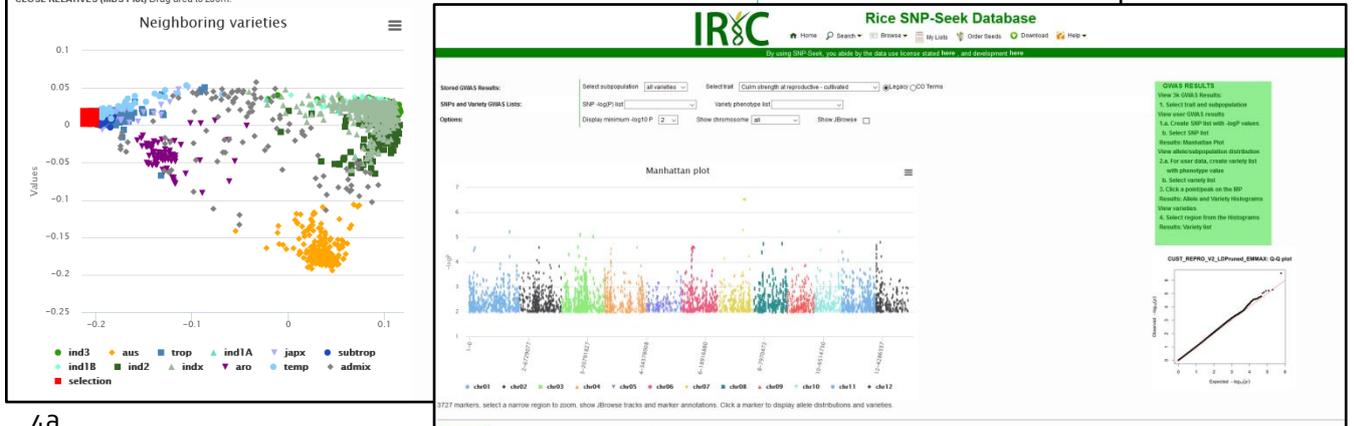


Figure 3. Downloading of data points.



4a

4b

Figure 4a. Interactive MDS plot of selected varieties showing their groupings.
Figure 4b. Manhattan Interactive Plot for displaying curated GWAS results.

About ZK

ZK is the leading enterprise Java Web framework with more than 1,500,000 downloads. ZK is deployed by a large number of Fortune Global 500 companies, including Barclays, Swiss RE, Roche, Deutsche Bank, Sony, Sun Microsystems, and Toyota, providing them with the ability to rapidly create rich Ajax enterprise level applications.

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