

Barley SNP Databases and GVT

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SCRI Barley SNP Database

http://bioinf.scri.sari.ac.uk/barley_snpsdb/

The screenshot shows the Barley SNP Database website. The top section displays the DNA sequence of contig ABC00076. Below this, there is a BLAST search interface with a text input field and a search button. The search results show a list of SNP positions and their corresponding reference sequences.

This screenshot provides a detailed view of SNP positions across several contigs. It shows a grid of SNP positions with their coordinates and reference sequences. The contigs are labeled as Contig001 through Contig007. The SNP positions are listed in columns, with their coordinates and reference sequences shown in rows.

The Barley SNP database supports the SNP development component of a high throughput SNP genotyping project in Barley. It currently contains background data on SNP assays and resequencing and links this information with Barley EST assemblies, map information, comparative information from the rice genome and expression data from the Barley1 Affymetrix GeneChip. The actual genotype information will be stored in the Germinate data. Currently we are exploring a variety of modes of data transfer between the databases and a range of analytical and visualisation tools such as GVT (below) and TASSEL. Currently we are investigating webservice methodologies.

The Genotype Visualisation Tool (GVT)

The Genotype Visualisation Tool (GVT) is a Java application designed for the visualisation and analysis of plant genotype data in the form of graphical genotypes. It has been designed to support a range of genotyping technologies, including SSRs, SNPs, AFLPs and RBIPs. We anticipate that it should be extendable to other technologies.

The screenshot shows the Genotype Visualisation Tool (GVT) interface. The main window displays a graphical genotype with a grid of colored bands representing different genotyping markers. The interface includes a menu bar, a toolbar, and a sidebar with various options for data loading and visualization.

Data can be loaded into the GVT platform through the GERMINATE database or similar GDCP enabled databases or from a local Excel spreadsheet based on a supplied template. GVT is a Java 1.5 application and currently we are working to develop additional analysis tools as well as the visualisation of genotypes in both pedigree and clustering contexts into the GVT framework.

This screenshot provides a detailed view of a graphical genotype in the GVT interface. It shows a large grid of colored bands representing different genotyping markers across multiple samples. The interface includes a sidebar with various options for data loading and visualization, and a zoom control at the bottom.