Zbrowse: An interactive GWAS results browser

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http://sviridis.org/
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Project Goals: “A Systems-Level Analysis of Drought and Density Response in the Model C4 Grass Setaria viridis”. The specific aims of the proposal are to: 1) Identify QTL for the effect of drought and density on biomass and seed yield components of Setaria. 2) Conduct in-depth physiological profiles in roots and leaves of a subset of selected lines 3) Integrate datasets and develop metabolic and gene networks for Setaria 4) Develop transformation technologies for Setaria viridis 5) Functionally examine the role of candidate genes deduced by network models; and 6) Develop protocols and best practices for monitoring gene flow in transgenic Setaria. To achieve these aims we will produce one of the most extensive molecular characterizations of plant growth in the field to date, generating several million data points that will be collected from physiological and molecular genetic studies. We will develop novel informatics models and network tools that will guide future molecular characterization in S. viridis and guide breeding efforts in major feedstock targets.

We have developed an interactive GWAS results viewer that is an extension of the classic GWAS Manhattan Plot. Zbrowse runs on a personal computer, but is displayed in a web browser and allows for the rapid graphical comparison of GWAS experiments performed on complex traits such as multiple phenotypes measured in multiple locations. The manhattan plots are fully interactive. The browser allows zooming by dragging. Clicking a point in a genome or chromosome-wide view quickly zooms in close enough to see genes under the point. Results can be filtered to only display overlapping QTL between experiments. In addition, results with base pair ranges, such as joint linkage support intervals, can be viewed on the same plot as the GWAS results to quickly visualize overlaps. The browser allows for easy and interactive navigation between plots displaying the entire genome, down to a plot less than a mega base wide displaying gene tracks. Genes under peaks can be clicked to open a browser tab with more information about the gene and all genes under a peak can be viewed in table form in the browser or exported as a comma-separated table.

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