

# **5<sup>th</sup> Annual Joint Bioinformatics Workshop**

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by

**Jacob Nelson**  
Iowa State University

## ***Predicting promoter Sequences Using Genes that are Expressed Similarly***

### ***ABSTRACT***

Wise laboratory has identified using microarray analysis of the barley1 gene chip, two hundred and eight genes in barley that are differentially expressed in compatible versus incompatible reactions when infected by a mildew pathogen. To find out the cause of these similar expression results we will examine the promoter regions of these genes. The barley genome is not sequenced yet, so we are using a comparative approach and examined the corresponding promoter regions in the rice genome.

The sequences from the differentially expressed barley genes were compared to the TIGR rice gene predictions. We then obtained one kilobase upstream sequences from each rice gene that was obtained. The sequences were then examined using Ab-initio motif detection programs such as GLAM and MotifSampler to identify over expressed regions.

The data and current findings will be presented on the poster.