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Malting quality improvement using SAGE

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MALTING QUALITY IMPROVEMENT USING SAGE

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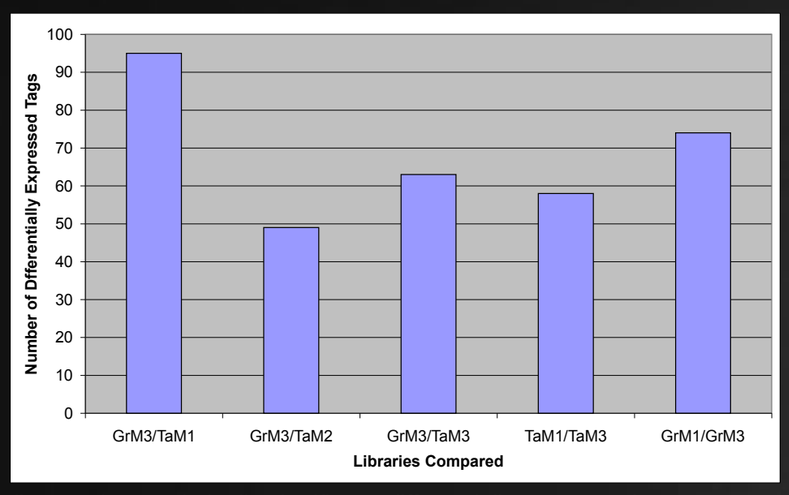
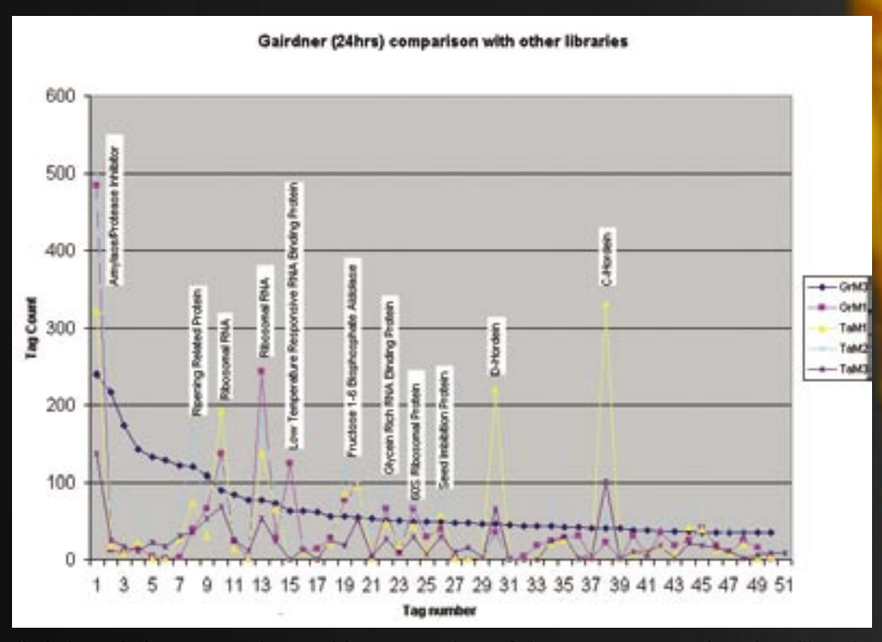
Understanding the gene expression profile of the seed is important to fully understand the physiological interactions occurring within. Although a vast amount of knowledge has been accumulated on seed dormancy and germination, many of the processes involved remain a mystery. By examining the types of transcripts expressed at any time in the cell and the level of expression, it is possible to determine which genes and their related proteins are being expressed at that moment in time.



Comparing statistically significant differentially expressed tags between libraries. Gairner at 24 hours (GrM3)and Tallon at 12 hours (TaM2) have the lowest number of these tags therefore these two libraries are the most similar.

SAGE (Serial Analysis of Gene Expression) is a technique that allows rapid, detailed analysis of thousands of transcripts in a cell. The process of SAGE relies on two principles. Firstly, a small sequence of nucleotides from the transcript, called a "tag" can effectively identify the original transcript from whence it came. Secondly, linking these tags allows rapid sequencing analysis of multiple transcripts. Genes for improved malting quality can be identified and examined using SAGE and ultimately used for commercial improvement.



Gairdner 24hr comparison with expression of the same genes in other libraries. Peak expression points are labelled.

In this study the gene expression profile of germinating (malting) barley is being examined at eight intervals over a time course of 120 hours post steeping. Libraries were constructed from mature unsteeped seed and seed from malted grain at specific time points after imbibition (0, 12, 24, 48, 72, 96 and 120 hours) from the Barley variety Tallon. Two libraries were constructed from two corresponding time points (0 and 24 hours post steeping) in the variety Gairdner, which varies considerably in its malting qualities.

Analysis has revealed 197 333 tags corresponding to around 50 000 unique transcripts. An average of 95% of all tags matched to an annotation within the database. Therefore 5% of all tags were novel, having no identifiable match.

Comparisons were made between the Tallon and Gairdner libraries to examine the similarities in gene expression. It could be seen that there were fewer significantly differentially expressed transcripts between the Gairdner 24 hour library and the Tallon 12 hour library than any other comparisons.

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