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The mature cereal seed transcriptome

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The Mature Cereal Seed Transcriptome

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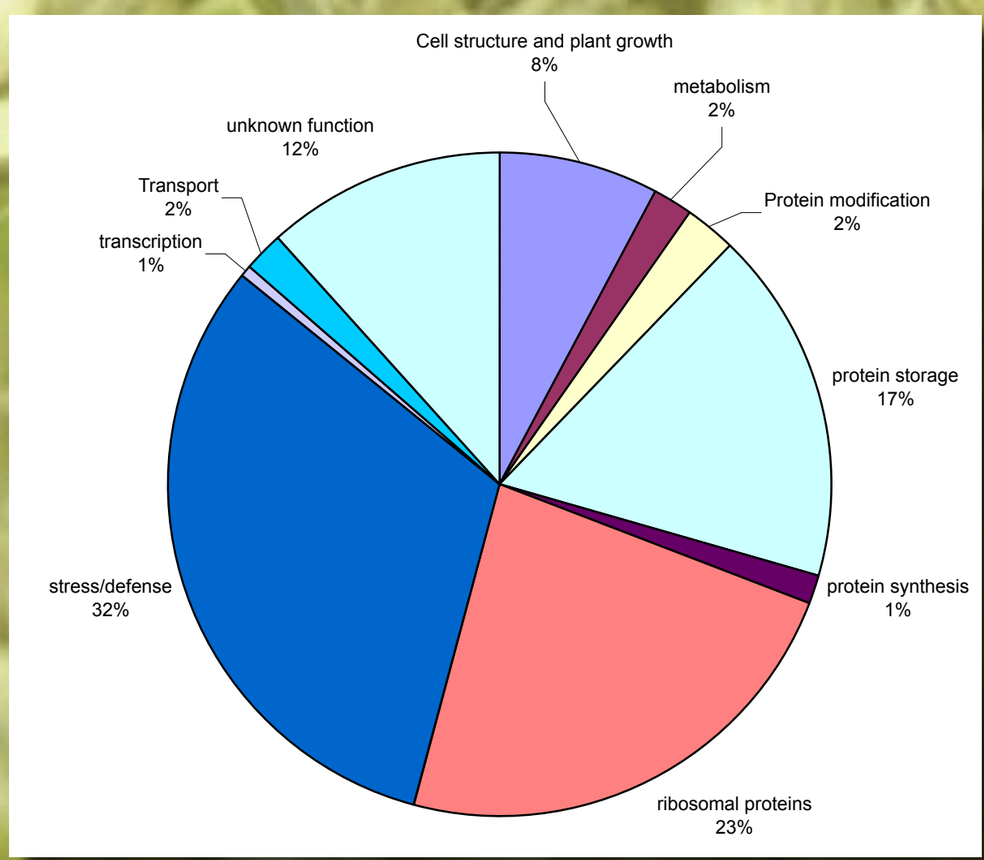
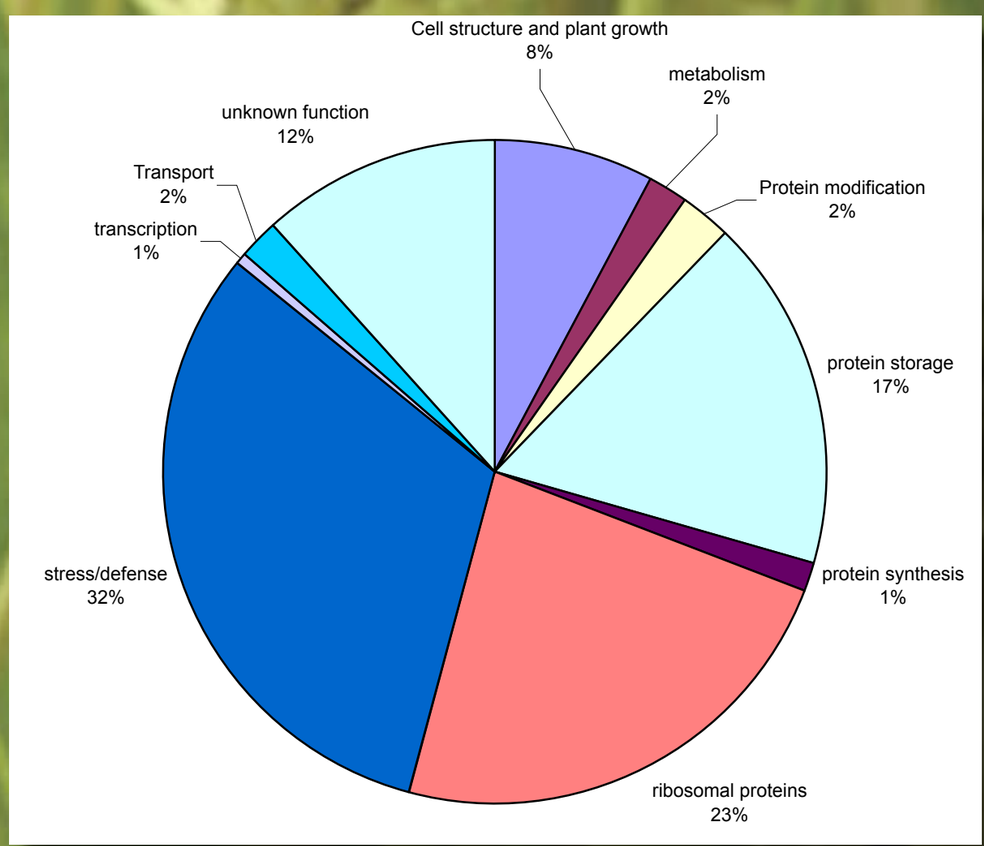
Time point	Total tags analysed	Unique tags	Relative Aundance range (%)	Relative Abundance range (%)	Tags occurring ≥ 10 (gene count)	Tags occurring ≥ 2 (gene count)	Tags occurring once (gene count)
Barley							
Mature seed HvTaM0	18,725	8,396	0.0056 – 1.7730	1 – 332	37% (223)	65% (1,913)	35% (6,483)
Wheat							
40 days post anthesis TaBaGD40	21,710	10,022	0.0046 – 4.7305	1 – 1027	36% (191)	63% (2,096)	37% (7,926)

Table showing statistical summary of wheat and barley dry seed libraries.



Barley top 100 transcripts divided into functional groups.



Wheat top 100 transcripts divided into functional groups

Understanding the gene expression profile of the dry seed of both barley and wheat is important to fully understand the physiological interactions occurring within the seed. 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. 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.

We have examined tags from dry seed of each of the barley and the wheat transcriptomes. There are considerable differences between them, particularly in the most highly expressed tags.

A total of 18725 tags in Barley dry seed library and 21710 in the wheat dry seed library were sequenced. This accounts for 8493 unique tags in the barley and 10022 in the wheat. When comparing the tags from these libraries it was found that of the total number of tags there were only 450 tags (2.4%) in common between the two libraries. A majority of these were identified by BLAST search to be ribosomal RNA proteins or match to a cDNA clone which has yet to be assigned a function. As well as taking a snapshot of the activity within the seed this stands to reinforce the idea that divergent evolution has occurred within the seed due to many years of human selection.

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