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# The mature cereal seed transcriptome

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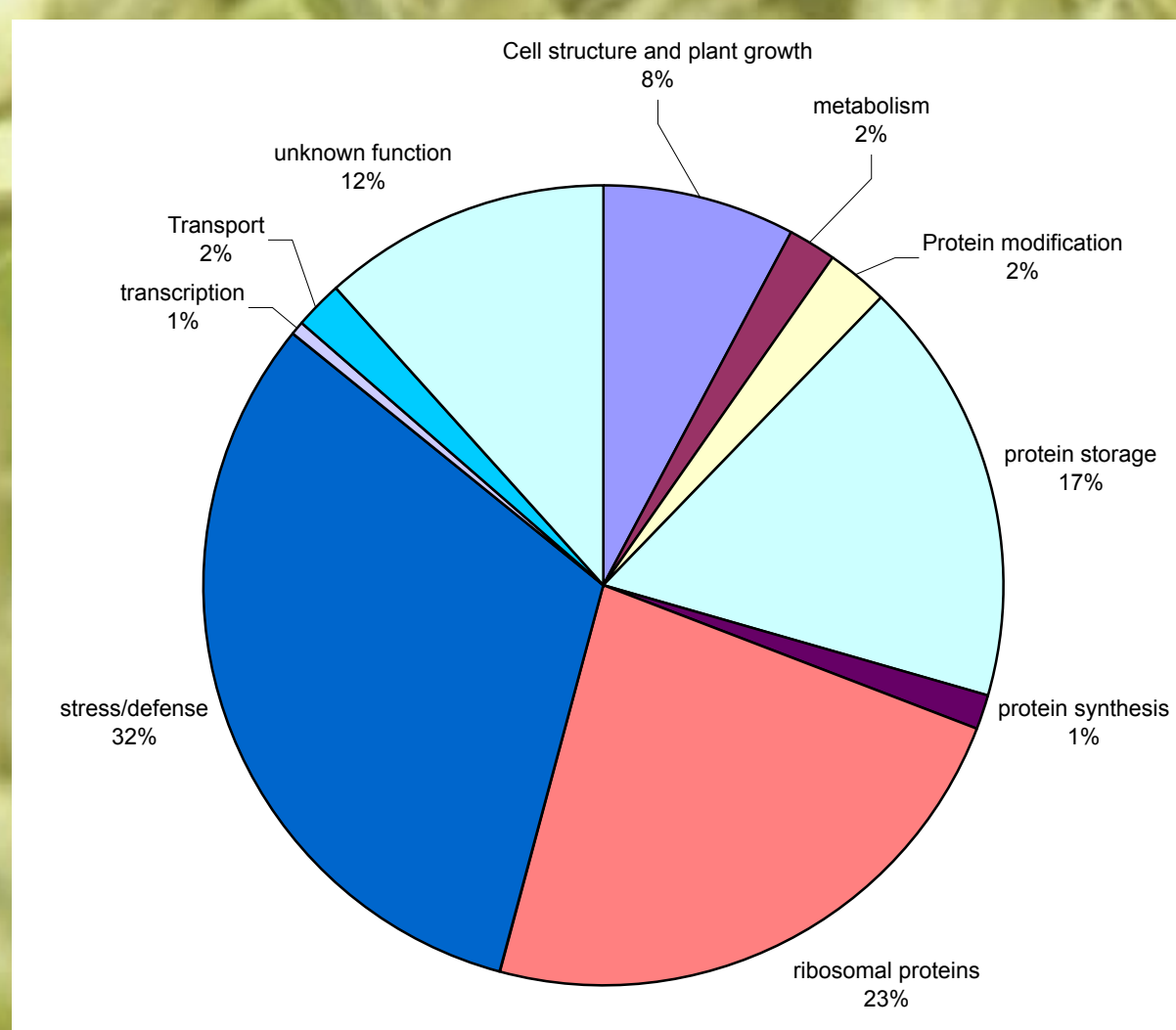


# The Mature Cereal Seed Transcriptome

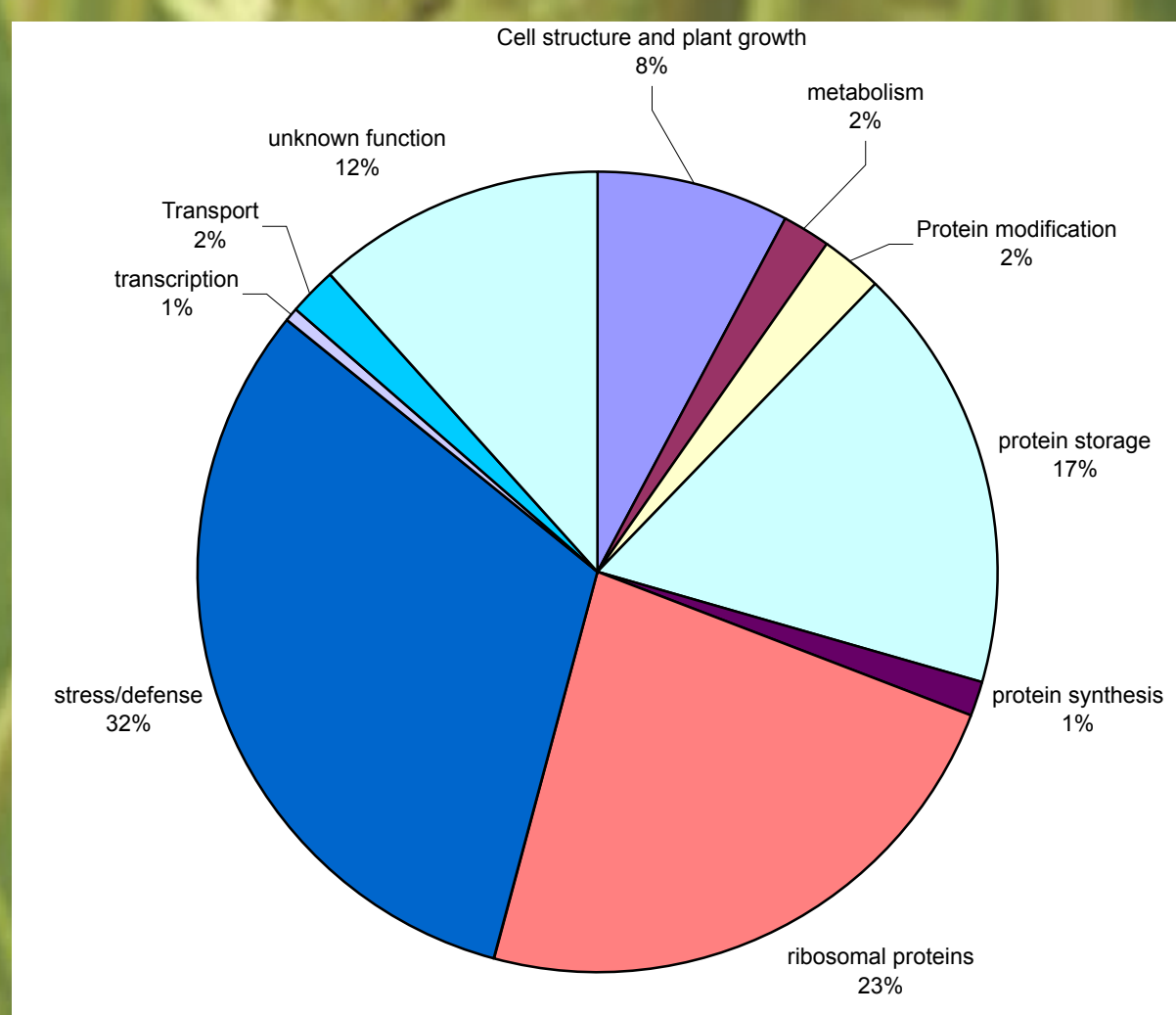
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Time point	Total tags analysed	Unique tags	Relative Abundance range (%)	Relative Abundance range (%)	Tags occurring $\geq 10$ (gene count)	Tags occurring $\geq 2$ (gene count)	Tags occurring once (gene count)
<b>Barley</b> Mature seed HvTaM0	18,725	8,396	0.0056 – 1.7730	1 – 332	37% (223)	65% (1,913)	35% (6,483)
<b>Wheat</b> 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.