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Project title: A genomic approach to understanding and improving mushroom compost utilisation.

The overall objective from this research is to identify potential means of improving mushroom yields, particularly in the third flush through improved compost utilisation and strain selection. The ability of *Agaricus bisporus* (common button mushroom) to colonise compost is due to the specific adaptation in terms of the enzymes it produces to utilise the substrate. Many genes and enzymes have been identified to have critical roles in this utilisation in order to facilitate the development of the mushroom fruit body. However, it is not known which of these are critical in controlling yields and these enzymes are likely to change dynamically in phase with the flush. While ultimately dependent on such enzymes, the yield is also affected by other factors.

The aims of the research

1. Examination of the genes and enzymes associated with nutrition will be carried out using microarray analysis of the *A. bisporus* genome to identify gene transcripts which are differentially expressed at the specific time points in the cropping cycle.
2. Genes identified as such may potentially be involved in yield control or flushing patterns. A promoter analysis of these genes, which are dynamically expressed, will then be carried out to identify potential regulatory mechanisms. Expression analysis of these genes will also be carried out in *A. bisporus* strains with different yielding properties.
3. Promoter analysis will be conducted on the genes with the most promising expression profiles being characterised by heterologous/homologous expression systems to determine substrate specificity, conditions which induce expression and gene down-regulation to determine any phenotypic effect.
4. To evaluate factors limiting yields, cropping experiments will be carried out. Yield parameters and gene expression of genes previously identified will also be measured.

