

Expression Profiling of Natural Antisense Transcripts in *Agaricus bisporus*

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Our view of the role of RNA has changed from being a passive intermediary of genetic information to acting as a regulator of gene expression in the form of short-interfering RNA, micro RNA, riboswitches and natural antisense. Long length natural antisense transcripts (NATs) have been identified for genes which are up-regulated after harvest in the fruitbody of the mushroom *Agaricus bisporus*. These NATs therefore are likely to be involved in the regulation of postharvest events such as development and senescence. A novel quantitative reverse transcriptase PCR technique has been developed. The data have been statistically analysed to produce expression profiles of NATs for six postharvest genes. The average antisense/sense ratios varied by three orders of magnitude, from 8.0 for *shs13* to 6×10^{-3} for cruciform DNA binding protein. The expression profiles were found to be highly specific for individual genes, to be dynamic over time and highly variable between neighbouring tissues. This latter characteristic has led to the speculation that NATs may be involved in tissue differentiation. Sequence information of natural antisense transcripts from *A. bisporus* suggests that they are synthesized from messenger (sense) RNA by RNA-dependent RNA-polymerase. Evidence will be presented that to support the hypothesis that the level of antisense may be controlled by the 3' processing of sense RNA.