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HMG-CoA reductases of *Mucor circinelloides*

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Mucor circinelloides is a carotene producing zygomycete, which is used as a model organism in the study of carotenoid biosynthesis. Carotenoids and other important isoprenoids of the fungal cell (such as ergosterol and the prenyl group of certain proteins) are synthesized in the acetate-mevalonate pathway. The central step in the pathway is the conversion of the 3-hydroxy-3-methylglutaryl coenzyme A (HMG-CoA) to mevalonic acid catalysed by the HMG-CoA reductase enzyme.

The *M. circinelloides* genome contains three different HMG-CoA reductase genes (named as *hmgR1*, *hmgR2* and *hmgR3*), which were cloned using the sequence data available in the genome database of the fungus (http://genome.jgi-psf.org/Mucci2/Mucci2.home.html). We used the genes in gene expression studies to investigate their function. Relative transcription levels of the three genes during the life cycle and under different cultivation conditions (aerobic/anaerobic growth, different carbon sources, different temperature and salt stress) were analyzed by quantitative real-time PCR (qPCR). In these studies, *hmgR1* showed low relative transcription levels under all conditions, while *hmgR2* showed high transcription levels under all aerobic conditions. Under anaerobic condition, transcription of *hmgR3* increased significantly.

We built three different expression vectors (pNG1, pNG2 and pNG3 containing the genes *hmgR1*, *hmgR2* and *hmgR3*, respectively) and used PEG mediated protoplast transformation to elevate the copy number of the genes. The carotenoid production and the sensitivity of statins changed after elevating the copy number of the genes. Enhanced expression of *hmgR2* increased the amount of the ergosterol in the transformants. Elevated copy number of *hmgR3* affected the carotene production and the sensitivity of statins in the highest degree among the different types of transformants.

We used antisens RNA (asRNA) mediated gene silencing to investigate other function of each gene. Three different vectors (pAS1, pAS2 and pAS3) were built containing antisense DNA fragments of *hmgR1*, *hmgR2* and *hmgR3*, respectively between the promoter and terminal region of glyceraldehyde-3-phosphate dehydrogenase. After PEG mediated protoplast transformation, transformants were isolated (MS12-pAS1, MS12-pAS2 and MS12-pAS3). Macro- and micromorphology, carotene and ergosterol content and the growth rate were examined in the resulting transformants. Growth rate, germination of spores and ergosterol content decreased in the transformants MS12-pAS3. Moreover, transformants showed altered morphology with swollen, frequently branching hyphae indicating a possible role of *hmgR3* in the mycelial development. In the MS12-pAS2 transformants, ergosterol content also decreased, but the morphology did not change.

Our results suggest that *hmgR2* may play an important role in the general isoprenoid metabolism and highly expresses under aerobic conditions. According to the transformation and qPCR studies, *hmgR3* seems to have role in the mycelial development, carotene biosynthesis and may be necessary for the sensing of the oxygen concentration of the environment. Moreover *hmgR3* may necessary to the germination of sporangiospores and apoptotic processes.

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TAF10 proteins indicate structural and functional links between histone acetyltransferase and basal transcription factor complexes

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TATA-binding protein associated factors (TAFs) have been identified as subunits of the TFIID basal transcription factor complex required for RNA polymerase II initiation. More recent studies indicate that TAFs are also present in histone acetyl transferase complexes, which regulate transcription initiation and the organization of the chromatin structure. This observation raises the possibility of complex „trans-mutation" by which due to changes in subunit composition one type of multiprotein complex is converted to an other type as transcription initiation is progressing.

Of the two *Drosophila* GCN5 histone acetyltransferase (HAT)-containing complexes SAGA and ATAC, TAF10 subunits are present in the former while they are missing from the latter. Despite that we found that the gene expression alterations in *taf10* mutants are very similar to those observed in ATAC subunit (Ada2a, Ada3) mutants. First, we aimed to find out whether only *taf10* mutants have similar gene expression alterations to ATAC mutants or other TAFs mutants also show the ATAC specific gene expression patterns. For this we studied the gene expression pattern of *Drosophila* stocks in which *taf5*, *taf10* or *taf8* was downregulated by RNAi.

We have recently shown that *Halloween* genes, which are expressed in the prothoracic gland and regulate ecdysone synthesis are