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Impact of deletion of a catabolite repressor Mig1 on hyphal morphology and cellulase expression in *Penicillium funiculosum* NCIM1228

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Abstract

Carbon catabolite repression (CCR) is a regulatory mechanism which negatively regulates genes of for ancillary carbon source utilization. It is mediated by Mig1 orthologues, which are Zn finger transcriptional repressors. We studied the effect of CCR disruption in *Penicillium funiculosum* NCIM1228, a hypercelluloytic ascomycete. Upon phylogenetic analysis of fungal genomes, Mig1 presence across all taxa of kingdom fungi revealed its conserved role in catabolite repression. Also it was found to constitute distinct clade from industrially important cellulase producing fungi like *Trichoderma reesei* and *Aspergillus sp.* It shared the clade with other highly evolved fungi *T. cellulolyticus* and *P. marneffei* and represented more recent radiations of evolutionary conserved catabolite repressor Mig1. Genotypic analysis showed that NCIM1228 harbors a truncated yet functional allele of Mig1. Mig1 orthologue of NCIM1228 has a non-sense mutation at 134th amino acid position, making a large C-terminal portion of Mig1 (415aa) dispensable for carbon repression. NCIM1228 was grown in presence of allyl alcohol to check the phenotypic effect. NCIM1228 showed sensitivity to allyl alcohol as compared to *Penicillium funiculosum (Pf).* Deleting active Zn finger domain made NCIM1228 completely sensitive to allyl alcohol. Surprisingly, the deletion showed small and compact colonies with compromised filamentous proliferation while the dry mycelial weight didn't change when grown on 0.5% glucose supplemented with 2% avicel. Using microscopy, we unraveled that *PfΔMig1* showed reduced aerial hyphae and profuse branching pattern in terminal hyphae resulting in compact colonies. We further observed more than two-fold (7.6 FPU/ml) higher FPU in production media than NCIM1228 under similar condition.

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