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**RCO1 and RCM1 of *Neurospora crassa* that are homologous to Tup1 and Ssn6 of *Saccharomyces cerevisiae***

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RCO1 of *N. crassa* shows overall 46.3% homology with *S. cerevisiae* Tup1 that contains WD40 repeats. RCO1 also contains seven WD40 repeats whose sequences show averaging 68% identity to those of Tup1. *rco-1* mutants are aconidial, female sterile, had reduced growth rates, and formed hypae that coiled in a counterclockwise direction. Analysis of the *N. crassa* genome data revealed at least 14 proteins that contain tetratricopeptide repeat (TPR) motifs. One of them [designated *rcm-1* (regulation of conidiation and morphology)] shows over 60% homology with Sup6 of *S. cerevisiae*. Sequence analysis of its cDNA shows that it encodes a putative 102kDa protein. Mutant strains generated by RIP (repeat induced point mutation) process show four distinctive patterns of vegetative growth at various rates. They are male-fertile, yet all female-sterile and produced little or no perithecium. Tup1-Sup6 complex in *S. cerevisiae* is a general transcription repressor that mediates transcriptional repression of genes concerned with a variety of cellular processes including growth rate, differentiation, oxygen-stress, and fertility. This repression system seems to be conserved among eukaryotes. Now, relationship between RCO1 and RCM1 is under investigation.