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Isolation and Characterization of Mouse CHD1 ATPase Homolog Gene in Yeast

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The *hrp2+* gene was cloned by polymerase chain reaction amplification using degenerative primers from conserved SNF2 motifs within the *ERCC6* gene, which encodes a protein involved in DNA excision repair. Like other SNF2/SW12 family proteins, the deduced amino acid sequence of Hrp2 contains DNA-dependent ATPase/7 helicase domains as well as the chromodomain and the DNA binding domain. Sequence analysis of *hrp2+* gene showed striking evolutionary conservation among the SNF2 family of proteins. The transcript of *hrp2+* gene was found to be a 4.7 kb as identified by Northern hybridization. In order to investigate the inducibility of *hrp2+* gene, transcript levels were examined after treating the cells to various DNA damaging agents. The transcripts of *hrp2+* were induced by UV-irradiation. But the transcripts were not induced by treatment of 0.25% Methylmethane sulfonate (MMS). These results implied that the effects of damaging agents are complex and different regulatory pathways exist for the induction of this gene. To determine the steady-state level of *hrp2+* transcripts during growth, cells were cultured in medium and collected at every 2hr to prepare total RNAs. The northern blot analysis showed that the level of *hrp2+* transcripts reached its maximum before the cells entered the exponential growth phase and then decreased gradually. This result implies that Hrp2 may be required at early stages of cell growth.