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We have previously showed that the mRNA abundance of a few rice CONSTANS-like genes (OsCOL) was under circadian control. One OsCOL mRNA level oscillates in quite different phase, as compared to that of the Hd1 mRNA, rice CONSTANS homolog. This OsCOL gene was interrupted by about 15 kb-long intron which contains other predicted genes, including putative non-LTR retroelement reverse transcriptase. The pre-mRNA for this gene was detectable using RT-PCR and also under circadian control in the same phase as its mRNA. This suggests that the circadian regulation of the OsCOL mRNA abundance is mostly done at the transcriptional level. In order to elucidate the function of this gene, we have constructed transgenic rice lines expressing its cDNA in sense or antisense orientation under the maize ubiquitin promoter. The T1 segregating lines of both the transgenic rice showed similar heading date (flowering) to that of the non-transgenic lines under natural condition which is more likely long day condition. Under short day condition, however, the anti-sense transgenic lines showed later flowering than non-transgenic lines. In order to get insight into mechanism how the OsCOL gene controls heading date in rice, we performed a yeast two hybrid screening for possible protein-protein interaction partner for it. Since the OsCOL protein itself has transcription activation activity, we tried to screen the library with a number of truncated proteins. We found some putative candidates for interaction partners.