Cloning and characterization of HAT and HDAC recruiting factors from *Brassica napus*

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In eukaryotes, gene expression requires that appropriate transcription factors gain access to regulatory regions located mainly at the 5'-upstream region of the gene. Accessibility to regulatory regions is determined by local chromatin structure, which is controlled, to a large extent, by the acetylation state of histones governed by the actions of histone acetyltransferases (HATs) and histone deacetylases (HDACs). In general, acetylation and deacetylation of histones are associated with activation and repression, respectively, of gene expression. Therefore, recruitment of HAT and HDAC to specific promoters to control the acetylation state of histones in turn influences gene expression. Isolation of nuclear proteins that interact with HAT and HDAC is a direct approach to identify factors that recruit HAT and HDAC to target chromosomal sites. To identify proteins that interact with HDAC in *Brassica napus*, we screened a yeast two-hybrid library using HDAC of the related species *Arabidopsis thaliana* as bait. A number of positive clones were obtained and two of them were partially characterized. A kinase inducible domain (KID)-containing protein, bnKCP1, was found to respond to low temperature, and a SCARECROW-like factor, bnSCR1, was expressed mainly in root tissues. Both proteins interact with HDAC *in vitro*, and have putative functional motifs typically present in transcription factors. Moreover, when tested in yeast, bnKCP1 and bnSCR1 activated the expression of the *Lac*Z reporter gene. We conclude that bnKCP1 and bnSCR1 are two potential transcription regulators that function as recruiting factors for HDAC in *B. napus*.