The fission yeast COP9/signalosome is involved in cullin modification by ubiquitin-related Ned8p

ABSTRACT

Our data indicates that CSN is a worldwide facilitator of Ned8p modification of various cullins and may include other proteins involved in regulating cellular processes.

INTRODUCTION

The fission yeast COP9/signalosome is involved in cullin modification by ubiquitin-related Ned8p. The authors propose that the fission yeast COP9/signalosome is involved in the expression of NnA2 by a specific NnA2-related gene, Ned8p. This gene is expressed on the surface of the cells of the blood–brain barrier, and is activated by both NAD and NADH. By binding to NAD, Ned8p activates the ubiquitin-related gene, Ned8p, which, in turn, activates the gene encoding the fission yeast COP9/signalosome. This gene is involved in the expression of NnA2 by a specific NnA2-related gene Among the cullin/RING family of ubiquitin ligases, the SCF complexes are the most well-known. These enzymes play a dual function as regulators of the stability and activity of cell cycle regulator (CUL1), transcription factor, and RING domain proteins, but also act as binding agents for other substrates. At least five cullins, namely CUL1, are present in the human genome, with S. pombe encoding pcu3 and cubiquity 4 (which have no direct correlations in budding yeast) and 5 other culling factors: Pcu1p and PCU4p are neddylated, essential for their function in vivo. While it is evident to some that neddylation has an effect on the activity of cullin/RING complexes, mechanisms controlling this modification are only recently developed. In particular, Lyapina et al. have identified new connections between the COP9/signalosome (CSN), a multiprotein complex composed of eight subunits that play varying roles in regulatory processes such as cell cycle control, signal transduction, transcriptional activation, and plant photomorphogenesis, but have not found any specific biochemical The accumulation of Pcu1p in the neddylated state is due to disruption of S. pombe CSN subunit 1 (caa1/csn1), as demonstrated by Lyapina et al. It was not immediately clear whether this reflected the global control of multiple cullins by Csm1d as part of the entire CSP or simply the disruption effect of several other CSE subdomains.

CONCLUSION

Remarkable conclusions According to our findings, the control of Ned8p's cullin modification by the S. pombe CSN complex is generalized. Although not specific in any particular way, CSP may regulate the activity of various culling-related ubiquitin ligases by counterbalancing their stimulatory Neldelsäure (Ned8) modification pathways. Future research will determine whether some of the other functions of CSO involve post-translational modification of regulatory proteins by corresponding ukulium-like modifiers.