The cop9 signalosome, a multi-protein complex involved in protein degradation

Giovanna Serino [#], and Xing-Wang Deng*

Department of Molecular, Cellular & Developmental Biology, Yale University, New Haven, CT06520-8104, USA
Current address: GS: Dipartimento di Genetica e Biologia Molecolare-Universita" di Roma "La Sapienza", P.le A.Moro 5, 00185 Roma, Italy.
Email giovanna.serino@uniroma1.it
* To whom correspondence should be addressed:
Department of MCDB, Yale University,
Osborn Memorial Laboratories, Room 352A,
New Haven, CT 06520-8104
Phone (203)432-8908; Fax: (203)432-5726; Email: xingwang.deng@yale.edu

Keywords: *Arabidopsis*, The COP9 signalosome, protein degradation, ubiquitin, RUB1

The COP9 signalosome (CSN) is a nuclear-enriched, eight-subunits complex that has been initially identified through analysis of *constitutive photomorphogenic/ de-etiolated/fusca* (*cop/det/fus*) mutants of Arabidopsis (Schwechheimer and Deng, 2001). Arabidopsis wild-type seedlings can undergo two different developmental responses, photomorphogenesis in the light and skotomorphogenesis (or etiolation) in darkness (Kendrick et al., 1994). The *cop/det/fus* mutants display a constitutive photomorphogenic phenotype, both in the light and in the dark. This is reflected at the molecular level by the constitutive expression of light-inducible genes (Wei and Deng, 1996). Thus, the *COP/DET/FUS* genes can be regarded as negative regulators of photomorphogenesis, because their absence leads to the photomorphogenic development, even in darkness. A close analysis of the *cop/det/fus* phenotype revealed that the role of the COP9 signalosome goes beyond the control of photomorphogenesis. In fact, all severe *csn* mutations lead to lethality shortly after two weeks post-germination, indicating that other pathways might be mis-regulated in *csn* mutants. Its general role as a master controller of multiple aspects of development is further confirmed by the finding that the COP9 signalosome is evolutionary conserved from plants to animals (Wei et al., 1998). Indeed, the COP9 signalosome can be found in most eukaryotes, from *Saccharomyces pombe* to human, with the exception of *Saccharomyces cerevisiae*, which