The Evolution of COP9 Signalosome in Unicellular and Multicellular Organisms.

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Abstract

The COP9 Signalosome is a highly conserved protein complex, recently being crystallized for human. In mammals and plants the COP9 complex consists of 9 subunits, CSN 1-8 and CSNAP. The COP9 signalosome regulates the activity of culling ring E3 ubiquitin and plays central roles in pleiotropy, cell cycle and defense of pathogens. Despite the interesting and essential functions, a thorough analyses of the COP9 signalosome subunits in evolutionary comparative perspective is missing. Here we compared 61 eukaryotic genomes including plants, animals and yeasts genomes and show that the most conserved subunits of eukaryotes among the 9 subunits are CSN2 and CSN5. This may indicate a strong evolutionary selection for these two subunits. Despite the strong conservation of the protein sequence, the genomic structures of the intron/exon boundaries indicate no conservation at genomic level. This suggests that the gene structure is exposed to a much less selection compared to the protein sequence. We also show the conservation of

important active domains, such as PCI and MPN. We identified novel exons and alternative splicing variants for all CSN subunits. This indicates another level of complexity of the COP9 signalosome. Notably, most COP9 subunits were identified in all multicellular and unicellular eukaryotic organisms analyzed, but not in prokaryotes or archaeas. Thus, genes encoding CSN subunits present in all analyzed eukaryotes indicate the invention of the signalosome at the root of eukaryotes. The identification of alternative splice variants indicates possible 'mini-complexes' or COP9 complexes with independent subunits containing potentially novel and not yet identified functions.

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