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A comparison between selected subunits of the 26S Proteasome and the CSN complex in *Arabidopsis thaliana*

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The 26S proteasome is the major non-lysosomal protease complex that selectively destroys proteins in eukaryotic cells *via* the ubiquitin / proteasome pathway. The COP9 signalosome complex (CSN complex) that was initially defined as a repressor of photomorphogenesis in *Arabidopsis* is a conserved nuclear protein complex found in eukaryotes, and it is now implicated in diverse cellular and developmental processes. The COP9 signalosome is closely related to the lid sub-complex of the 26S proteasome in structural composition and probably shares a common evolutionary ancestor. This study is a comparison between the subunits of the 26S proteasome lid and the CSN complex in sequence level and structure level, solely using bioinformatics tools. First the corresponding subunits were compared at the DNA and protein sequence levels, using multiple sequence alignment algorithms. According to the pair-wise DNA sequence comparison of the coding sequences showed sequence identities around 50%. BLASTP tool was used to identify similar sequences from databases for the selected subunit proteins. According to the results it can be proposed that the selected subunits may be involved in meiosis regulation, apoptosis, programmed cell death and differentiation process. Since the protein structures for any of these subunits have not yet been determined experimentally, the 3-D structures of subunits were computationally predicted. Homology modeling approach failed due to unavailability of homologous sequences with experimentally determined structures. Secondary structure prediction was carried out using PSIPRED web server and the transmembrane (TM) regions were predicted by MEMSAT web tool. The sequence based fold recognition was performed by the Phyre web server, to predict the 3D structures. According to the results the secondary structures of corresponding subunit proteins were almost similar. Although the MEMSAT prediction indicated weak TM helices for some subunits, it is unlikely that they are actually TM proteins, because they are localized in the nucleus and cytoplasm by forming complexes. The Phyre server predicted several 3D models for the subunit proteins based on template structures. According to the fold similarities to the template structures, it can be proposed that the selected subunits may be involved in de-ubiquitination, electron transfer reactions, pre-mRNA splicing and transcriptional regulation.

Keywords: 26S Proteasome, CSN, sequence, structure, bioinformatics

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