113 Conservation of proteasome structure and activity between plants and other eukaryotes

AHMAD R. BAHRAMI AND JULIE E. GRAY

Department of Molecular Biology and Biotechnology, University of Sheffield, Sheffield, S10 2UH, UK.

Protein degradation is currently considered to be one of the major methods of post transcriptional control of gene expression and proteolytic regulatory systems are emerging as an important events in controlling the passage of cells through different developmental stages. It is known that the level of various short lived regulatory proteins can determine the fate of a cell, and the levels of these proteins are in turn controlled by synthesis and degradation. This degradation must be selective andcontrolled temporally and spatially to avoid damage to other cellular processes. The ubiquitin-26S proteasome proteolysis pathway, with the proteasome as the catalytic core, is conserved throughout eukaryotes and is well suited to this purpose. Electron microscopic studies have shown that proteasomes are very similar in all eukaryotes and sequence data has revealed certain proteasome subunits to be more than 70% identical across a wide range of species [1].

We have identified a tobacco flower cDNA, NtPSAl [accession number Y16644], with extensive homology to alpha type proteasome subunits. Sequence analysis shows great similarity with those reported from human, 63.4% (see figure 1), and yeast, 50.3%. This high level of conservation adds support to the idea that proteasomes play an important role in cell growth and development in all eukaryotes including plants.

In animals and yeast it has been demonstrated that the ubiquitin dependent proteolysis pathway controls the level of many short-lived proteins that are involved in various regulatory processes, including signal transduction, homeosis, cell division, and transcription. Among these crucial proteins are transcription factors, c-Jun, and c-Fos, the p53 tumour suppressor, and components of NFkB [2]. Proteasome activity has also been shown to be important in responding to environmental changes. For example, in response to extracellular signals NFkB components are disassociated and IKB is degraded by proteasomes to allow NFkB to induce the transcription of related genes [2]. In plants, rapid degradation of the unstable form of phytochrome A (Pfr), a light receptor protein, is believed to be brought about by proteasome action [3]. We have found mRNA transcripts homologous to the NtPSAl tobacco sequence at higher levels in actively dividing cells suggesting a possible role for proteasomes in cell division in plants.

Proteasomes implement their vast range of regulatory activities by changing their subcellular locations. Specific sequence domains such as nuclear localization signals that have been found in alpha proteasome subunits from many eukaryotes appear to be necessary for translocation from the cytoplasm to the nucleus [4, 5]. The NtPSAl predicted peptide sequence also contains a well conserved nuclear localization signal.

These results suggest a similar role for proteasomes in the regulation of cellular events by degradation of crucial short-lived proteins in plants as in other eukaryotic organisms. Although our knowledge of plant regulatory proteins is far from complete there is already evidence of short-lived proteins being involved in the response to phytohormones. For example, a family of short-lived proteins are thought to be involved in the auxin response pathway [6], that may be modulated by proteolysis, and there is data indicating similarity between an auxin responsive gene and a ubiquitin activating enzyme [7].


Figure 1. Alignment of NtPSAl (indicated by B) deduced protein with the reported alpha proteasome subunits from human PRC1 human (indicated by A). The shadowed boxes show the conserved sequences. The underlined and italic amino acids indicate the proteasome alpha type subunit signature and a putative nuclear localization signal respectively. This alignment was made by the PILEUP tool of the GCG program of Daresbury computer service.