



ABSTRACT

***“Perfectly Prepared RNA:
getting transcripts ready for translation”***

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Organelle gene expression involves a series of more or less coupled processes from transcription through transcript processing to translation. Many of the events that occur during these processes require sequence recognition by RNA processing factors. It has become abundantly clear over the last decade that in plants, pentatricopeptide repeat (PPR) proteins are the most numerous of these factors, with a bewildering array of 450+ family members in most angiosperms studied to date.

The development of screens for RNA processing defects has enabled the identification of the functions of some of these proteins by reverse genetics; several other PPR genes have been singled out by forward genetic screens for phenotypes that involve defects in organelle function. The RNA targets and molecular functions for over 40 PPR proteins have been characterised, allowing the first generalisations to be drawn concerning their modes of action.

Although the functions of over 90% of the PPR family are still to be worked out, it is becoming clear that certain subclasses of the family have a strong tendency to be associated with particular molecular processes such as transcription, splicing or RNA editing.

Progress is being made at modelling the structure of PPR proteins and understanding how they recognise specific RNA sequences, offering hope that they could form the basis for a new way of designing custom-made RNA binding proteins for biotechnology.