Control of mRNA stability in higher plants

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Abstract

The degradation rates of different mRNAs in higher plants can vary over a broad range and are regulated by a variety of endogenous and exogenous stimuli. During the past several years, efforts to better understand the control of mRNA stability in plants have increased considerably and this has led to improved methodologies and important mechanistic insights. In this review, we highlight some of the most interesting examples of plant transcripts that are controlled at the level of mRNA decay and discuss what has been learned from their study. Experiments that implicate or demonstrate the involvement of particular cis- and trans-acting factors in mRNA decay pathways are a major focus, as are those experiments that have led to mechanistic models. Emphasis is also placed on studies that address the relationship between translation and mRNA stability. Our current knowledge indicates that some of the determinants and pathways for mRNA decay may differ in plants compared to other eukaryotes, whereas others appear to be similar. This knowledge, coupled with the availability of biochemical, molecular and genetic approaches to elucidate plant mRNA decay mechanisms, should continue to lead to findings of novel and general significance.
Introduction

The control of mRNA stability is one of the most prominent forms of post-transcriptional gene regulation in eukaryotic cells. Although, historically, mRNA degradation has received less attention than mRNA synthesis, clearly both processes act together to establish the steady-state levels of different mRNAs and determine how fast those levels can change. Because mRNA degradation is the downstream process, its control can enhance, diminish or override regulation (or the lack thereof) exerted at the transcriptional level. Available data indicate that the average mRNA in plants and vertebrates survives and often continues to be translated for several hours before it is degraded [6, 74, 80]. However, mRNAs that degrade in a matter of minutes [33, 52, 57, 80] or remain intact for days or even weeks [6] are known to exist in higher eukaryotes. A range of mRNA stability has also been reported for bacteria and lower eukaryotes such as yeast, but in these organisms, the average transcripts degrade more rapidly than in higher eukaryotes. This feature makes it easier for microorganisms to quickly adapt to changing environmental conditions.

As sessile organisms, plants might benefit considerably from control at the level of mRNA stability, particularly when rapid responses to exogenous or endogenous stimuli are required. For example, if the optimal response to an environmental stimulus is to rapidly shut down the synthesis of a given protein, then having the protein encoded by a very unstable mRNA will be a big advantage. Conversely, for proteins that are needed at relatively constant levels, the buffering capacity of stable mRNAs would be the most beneficial. By differentially modulating the stability of individual transcripts in response to various signals, a further level of regulation can be achieved.

Interest in the control of inherent and regulated mRNA stability in higher plants has grown appreciably in recent years for several reasons. First, research continues to reveal genes that are apparently regulated at the level of mRNA stability [24, 76]. Second, the methodologies and model systems that are available for measuring mRNA stability have improved, and it is apparent that plants may provide opportunities to study unique mechanisms or to apply unique approaches. Finally, the study of mRNA stability in plants can have applied as well as basic significance because in some cases limitations at the level of mRNA stability can hinder the expression of foreign genes introduced into plants for crop improvement [17]. In this chapter, our discussion focuses on the stability of nuclear-encoded transcripts in higher plants. Our goal is not to present a comprehensive review, but rather to concentrate on the recent molecular analyses that provide the greatest mechanistic insights and a few less developed examples with high future potential. In addition to the progress made in plants, marked advances have resulted from studies of mRNA stability in yeast and animal systems, as highlighted in several recent reviews [14, 63, 66, 77]. We do not include investigations probing the role of mRNA stability in gene silencing because this topic is dealt with elsewhere in this volume (chapter by Baulcombe). Readers are also encouraged to see other chapters in this volume for discussions on mRNA stability in Chlamydomonas and in plant organelles (chapters by Rochaix and Sugita and Sugiura, respectively).

Measuring mRNA stability

A number of methods have been used to measure and compare the stability of different mRNAs. Some approaches directly measure mRNA half-lives, whereas others rely on the measurement of other parameters to evaluate mRNA stability. Each method has its strengths and limitations, factors which must be considered when selecting a method to evaluate mRNA stability and when comparing data obtained with different methods. Therefore, we begin with descriptions of several methods used to investigate mRNA stability and briefly discuss their strengths and possible limitations.

Nuclear run-on transcription

The most common method of finding evidence for regulation at the level of mRNA stability is to carry out nuclear run-on transcription experiments. During this procedure, isolated nuclei are allowed to continue transcription (i.e. run-on) in the presence of a labeled nucleotide. The amount of label incorporated into RNAs transcribed from the gene of interest is quantitated by hybridization and considered to represent the transcriptional activity at the time the nuclei were harvested. Generally, these experiments are used to compare multiple genes under the same condition or the same gene under different conditions. Large differences in transcript accumulation that cannot be accounted for by similar differences in transcriptional activity in run-on assays are generally attributed to differences in mRNA