RNA Editing in Plant Mitochondria

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Abstract RNA editing in plant mitochondria alters more than 400 cytidines to uridines in flowering plants. In other plants such as ferns and mosses, the reverse reaction is observed at almost equal frequency. In the last few years, the development of transfection systems with isolated mitochondria and of in vitro systems with mitochondrial extracts has considerably improved our understanding of the parameters of site recognition. However, the biochemistry and the enzymes involved are still open questions. We here summarize our present knowledge of RNA editing as an essential part of RNA maturation in flowering plant mitochondria.

“All our science, measured against reality, is primitive and childlike – and yet it is the most precious thing we have.”

Albert Einstein

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1 Introduction

In mitochondria and plastids of almost all the land plants examined, the sequences of many transcripts are altered by posttranscriptional conversion of C to U and U to C (Covello and Gray 1989; Gualberto et al. 1989; Hiesel et al. 1989). In plastids, including chloroplasts of flowering plants, in total only about 35 Cs are found to be deaminated to Us, details of which are described in the chapter by Masahiro Sugiura (this volume).

In mitochondria, by extrapolation from the RNAs analysed to date, about 400–500 C to U changes are expected. In Arabidopsis thaliana, Brassica napus and Oryza sativa, the entire set of editing sites in protein-coding regions has been investigated, amounting to 441, 427 and 491 editing sites per mitochondrial transcriptome in these species respectively (Giegé and Brennicke 1999; Notsu et al. 2002; Handa 2003). The total number of C to U changes will be somewhat higher, since several events have been documented in non-protein-coding regions such as tRNAs and introns, as well as in leader and trailer regions. However, these are comparatively few editing sites; by extrapolation, about 20–50 can be expected in a given transcriptome.

RNA editing is required for gene expression in many of the systems discussed in this volume. Often, the genomic information encoding an open reading frame or a tRNA is cryptic or incomplete, and will not yield a functional product. Thus, the corresponding genetic system is dependent on RNA editing for its biological optimization and eventually for survival. In the plant mitochondrial systems, this process is likewise essential for the synthesis of functional proteins which, after editing, exhibit closer sequence conservation with their homologs in other systems. In addition, RNA editing in plant mitochondria ensures that several affected tRNAs can fold correctly and become functional (Marchfelder and Binder 2004). Thus, RNA editing in plant mitochondria is an essential step of RNA maturation without which no working respiratory chain and no functional mitochondria can be produced and maintained in the cell.

In this overview, we will first summarize the observations of RNA editing in plant mitochondria in the steady-state RNA population, and the consequences of editing. In the second part, we will look at recent approaches trying to characterize the biochemistry involved and to identify the parameters of site recognition.

2 C to U and U to C Changes and Their Distribution in the Plant Kingdom

RNA editing sites in flowering plant mitochondria involve almost exclusively C to U changes, in which the C in the pre-mRNA is deaminated to a U moiety (Fig. 1). The more than 400 RNA editing sites are found largely in the coding regions of mRNAs and occur less frequently in introns and other non-translated regions. In some cases, RNA editing in tRNA molecules restores essential base-pairings. In