

## SL203

### Posttranscriptional Mechanisms that Affect Chloroplast Gene Expression

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Most chloroplast genes are cotranscribed as members of polycistronic transcription units. Multiple transcripts have been observed for most chloroplast gene clusters. These may be generated by multiple transcriptional initiation, by complex RNA processing of the primary transcripts, or multipletranscriptional termination. During spinach chloroplast development, most chloroplast genes have been found to be constitutivelytranscribed, although significant changes were noticed in the steady-state level of transcripts. This suggests thatposttranscriptional processing of primary transcripts may play an important roll in the control of gene expression.

Among posttranscriptional processes, intron splicing and translational regulation were investigated. The in vivo branch points of atpF and petD introns were found to be eight bases upstream of their respective 3' intron/exon boundaries. In constrast, no splicing intermeadiates could be detected by primer extention analysis of petB and rpoCl. Nothern and primerextention expriments demonstrated that although intron lariats form during the in vivo splicing of all four of these introns, the quantity of intron/3' exon splicing intermediates presents in the rpoCl and petB compare to aptF and petD. When the steady-state distribution of ribosomes on translating mRNAs of the large ATP synthase gene cluster were examined, several ribosomal pause sites were detected in in the coding regions of the gene cluster. Significance of this result will be discussed.