

Preface

In almost all of the areas of gene expression control except one, plant research has lagged considerably behind studies in yeast, insects and vertebrates. Advances in animal gene expression control have also benefited plant research, as we continue to find that much of the machinery and mechanisms controlling gene expression have been preserved in all eukaryotes. However, there are some interesting differences in gene structure and regulation between plants and animals. First, vertebrate genes can be quite large, often spanning tens of thousands of base pairs and usually separated by numerous large introns, whereas plant genes tend to be much smaller (averaging between 1–2 kb (kilobases) with fewer and smaller introns. Second, as we shall see in the following chapters, plant transcripts retain introns more often than do animal transcripts (30% of all genes in the model plant, *Arabidopsis*, compared to 10% in humans). Unfortunately, at this time we have only a few plant models for gene regulation, and only *Arabidopsis*, rice and poplar have been fully sequenced. Since *Arabidopsis* was the first plant genome to be fully sequenced, most of our information has come from studies of its transcriptome, and it is not known to what extent it truly represents other members of the plant kingdom. In addition, as our knowledge of factors influencing gene expression increases, so too, does our recognition that the current annotations in the gene databases will need to be updated to reflect new information as it appears in the literature. Finally, compared to animals, plants have evolved different signaling mechanisms, partly because plant hormones do not exactly function as do those in animals, and partly because plants must cope with environmental changes differently than animals, since they cannot physically escape their environments except possibly through reproduction. Therefore, plants have evolved very complex, interacting signaling pathways in response to developmental signals and biotic/abiotic stresses. All of these observations ultimately reflect some of the differences plants display in regulating gene expression compared to yeasts, insects and vertebrates.

Although we have touched upon some of the differences between animal and plant control of gene expression here, it is equally important to recognize and appreciate the common mechanisms they share. For example, the basic

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transcriptional machinery *via* DNA-dependent RNA Polymerase II is virtually the same in plants and animals. Furthermore, some transcription factors, like *myb* and *myc* factors are similar in structure and function in both plants and animals. Plants and animals contain introns separating the coding regions of most genes and again, they utilize similar machinery to process the introns and form mature mRNAs. Since translation in all eukaryotes is basically the same, we see more similarities between plants and animals in this process, than differences. These mechanisms relate to mRNA structure, including sequences in the 5' leader region and those in the 3' untranslated region which influence the efficiency and selectivity of translation. It is hoped that the following chapters will expose the reader to some of the most recent, novel and fascinating examples of transcriptional and posttranscriptional control of gene expression in plants and, where appropriate, provide comparison to notable examples of animal gene regulation.

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