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Nota di contenuto	Regulation of Transcription in Plants; Contents; Contributors; Preface; 1 General transcription factors and the core promoter: ancient roots; 1.1 Introduction; 1.2 Origins of the eukaryotic promoter; 1.3 Organization of the eukaryotic promoter; 1.3.1 TATA-less promoters; 1.4 Transcription factor IID; 1.5 Role of TFIID in development; 1.6 Mediator; 1.6.1 Tail module; 1.6.2 Middle complex; 1.6.3 Head module; 1.6.4 CDK8/Srb8-11 module; 1.6.5 Mediator subunits unique to metazoans and plants; 1.7 Transcription factor IIB; 1.8 Summary; References 2 Transcription factors of Arabidopsis and rice: a genomic perspective2.1 Introduction; 2.2 Arabidopsis and rice genomes: the angiosperm complement of transcription factors; 2.2.1 General considerations for genome-wide analyses; 2.2.2 Arabidopsis transcription factors; 2.2.3 Rice transcription factors: a comparison to Arabidopsis; 2.2.4 Gene duplications, functional redundancy, and the transcription factor phenome; 2.3 Plant promoters; References; 3 Chromatin-associated architectural HMGA and HMGB proteins assist transcription factor function; 3.1 Introduction; 3.2 HMGA proteins

3.2.1 Structure and expression; 3.2.2 DNA and chromatin interactions; 3.3 HMGB proteins; 3.3.1 Structure and expression; 3.3.2 DNA and chromatin interactions; 3.4 Dynamic interaction of histone H1 and HMG proteins with chromatin; 3.5 HMGA and HMGB proteins as architectural assistant factors; Acknowledgements; References; 4 Histone modifications and transcription in plants; 4.1 Introduction; 4.2 Histone acetylation and transcriptional activation; 4.2.1 Plant histone acetyltransferases; 4.2.1.1 GNAT/MYST family; 4.2.1.2 TAFII 250 family; 4.2.1.3 P300/CBP family; 4.2.2 Bromodomain proteins 4.2.2.1 Bromodomain extra-terminal proteins 4.2.2.2 Plant bromodomain proteins; 4.2.3 Plant histone deacetylases; 4.2.3.1 RPD3/HDA1 family; 4.2.3.2 HD2 family; 4.2.3.3 SIR2 family; 4.2.4 Histone acetylation/deacetylation and environmental adaptation; 4.3 Histone methylation; 4.3.1 Plant SET-domain proteins; 4.3.1.1 E(Z)- and Trithorax-type HMTases; 4.3.1.2 Su(var)3-9-type HMTases; 4.3.1.3 ASH1-type and plant-specific HMTases; 4.3.2 Histone demethylase; 4.4 Interplay between histone acetylation and methylation in transcriptional regulation; 4.5 Conclusions; References

5 Chromatin remodeling and histone variants in transcriptional regulation and in maintaining DNA methylation 5.1 Introduction; 5.2 ATP-dependent chromatin remodeling; 5.2.1 SWI/SNF-like complexes in plants; 5.2.2 Other ATPases of the SNF2 family that control plant development; 5.3 Chromatin remodeling and DNA methylation; 5.3.1 The effects of ddm1 mutation differ from those caused by met1; 5.3.2 The model of DDM1 action; 5.3.3 DDM1 and methylation of histone H3; 5.3.4 Models of DDM1 targeting; 5.3.5 DRD1 - another SNF2 family protein involved in control of DNA methylation

5.4 Histone variants in the regulation of chromatin functions

Sommario/riassunto

Regulation of transcription represents a major, controlling step in plant gene expression, as it determines the tissue-specific and developmental stage-specific activity of many genes. Changes in gene expression have been shown to underlie the responses to environmental cues and stresses, the response against pathogens, the regulation of metabolic pathways, and the regulation of photosynthesis, for example. Regulation by transcription factors is an integral part of a highly complex network. In recent years, research on the regulation of transcription has made impressive progress.<b

2. Record Nr.	UNINA9910794341003321
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