Functional analysis of Arabidopsis chromatin modification and remodeling regulators (CHR5 and JMJ15) in gene expression
Yuan Shen

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Institut de Biologie des Plantes

DISCIPLINE : BIOLOGIE

THÈSE DE DOCTORAT

Soutenance prévue le 28/05/2014

par

Yuan SHEN

Functional analysis of Arabidopsis chromatin modification and remodeling regulators (CHR5 and JMJ15) in gene expression

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# ABBREVIATIONS

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
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<tbody>
<tr>
<td>ABI3</td>
<td>Abscisic acid Insensitive3</td>
</tr>
<tr>
<td>ARP</td>
<td>Actin-Related Protein</td>
</tr>
<tr>
<td>BAH</td>
<td>Bromo-Adjacent Homology</td>
</tr>
<tr>
<td>CBP</td>
<td>CREB-Binding Protein</td>
</tr>
<tr>
<td>CLF</td>
<td>Curly Leaf</td>
</tr>
<tr>
<td>CHD</td>
<td>Chromodomain Helicase DNA binding domain</td>
</tr>
<tr>
<td>ChIP</td>
<td>Chromatin ImmunoPrecipitation</td>
</tr>
<tr>
<td>CMT</td>
<td>Chromomethylase</td>
</tr>
<tr>
<td>CRC</td>
<td>Cruciferin C</td>
</tr>
<tr>
<td>DCL3</td>
<td>Dicer-like3</td>
</tr>
<tr>
<td>DDM1</td>
<td>Decreased in DNA Methylation 1</td>
</tr>
<tr>
<td>DME</td>
<td>DEMETER</td>
</tr>
<tr>
<td>DML2, 3</td>
<td>DEMETER like 2, 3</td>
</tr>
<tr>
<td>DNA</td>
<td>DeoxyriboNucleic Acid</td>
</tr>
<tr>
<td>DNMT1</td>
<td>DNA Methyltransferase 1</td>
</tr>
<tr>
<td>DRM2</td>
<td>Domains Rearranged Methyltransferase2</td>
</tr>
<tr>
<td>ES</td>
<td>Embryonic Stem</td>
</tr>
<tr>
<td>E(z)</td>
<td>Enhancer of zeste</td>
</tr>
<tr>
<td>EMF</td>
<td>Embryonic Flower</td>
</tr>
<tr>
<td>FAD</td>
<td>Flavin Adenine Dinucleotide</td>
</tr>
<tr>
<td>FIE</td>
<td>Fertilization Independent Endosperm</td>
</tr>
<tr>
<td>FIS2</td>
<td>Fertilization Independent Seed 2</td>
</tr>
<tr>
<td>FLC</td>
<td>Flowering Locus C</td>
</tr>
<tr>
<td>FT</td>
<td>Flowering Locus T</td>
</tr>
<tr>
<td>GNAT</td>
<td>Gcn5-related N-terminal Acetyltransferase</td>
</tr>
<tr>
<td>GUS</td>
<td>β-Glucoronidase</td>
</tr>
<tr>
<td>HAT</td>
<td>Histone Acetyltransferase</td>
</tr>
<tr>
<td>HDAC</td>
<td>Histone Deacetylase</td>
</tr>
<tr>
<td>HIS</td>
<td>High-level expression of Sugar-Inducible gene</td>
</tr>
<tr>
<td>HMT</td>
<td>Histone Methyltransferase</td>
</tr>
<tr>
<td>HR</td>
<td>Homologous Recombination</td>
</tr>
<tr>
<td>IBM1</td>
<td>Increased in BONSAI Methylation 1</td>
</tr>
<tr>
<td>JMJ</td>
<td>Jumonji domain containing protein</td>
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<tr>
<td>KYP</td>
<td>KRYPTONITE</td>
</tr>
<tr>
<td>LEA</td>
<td>Late Embryogenesis Abundant</td>
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<td>Leafy Cotyledon1, 2</td>
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<td>Abbreviation</td>
<td>Description</td>
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<tr>
<td>LHP1</td>
<td>Like Heterochromatin Protein 1</td>
</tr>
<tr>
<td>LSD1</td>
<td>Lysine Specific Demethylase1</td>
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<tr>
<td>MBD</td>
<td>Methyl CpG-Binding Domain</td>
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<td>MEA</td>
<td>MEDEA</td>
</tr>
<tr>
<td>MEE27</td>
<td>Maternal Effector Embryo arrest 27</td>
</tr>
<tr>
<td>MET1</td>
<td>Methyltransferase1</td>
</tr>
<tr>
<td>MSI1-5</td>
<td>Multicopy Suppressor of IRA 1-5</td>
</tr>
<tr>
<td>NFR</td>
<td>Nucleosome Free Region</td>
</tr>
<tr>
<td>NuRD</td>
<td>Nucleosome Remodeling and Deacetylase</td>
</tr>
<tr>
<td>PHD</td>
<td>Plant Homeodomain</td>
</tr>
<tr>
<td>PIC</td>
<td>Pre-initiation complex</td>
</tr>
<tr>
<td>PIE1</td>
<td>Photoperiod-Independent Early flowering1</td>
</tr>
<tr>
<td>PKL</td>
<td>PICKLE</td>
</tr>
<tr>
<td>POL</td>
<td>Polymerase</td>
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<tr>
<td>PRC1, 2</td>
<td>Polycomb Repressive Complex1, 2</td>
</tr>
<tr>
<td>PTGS</td>
<td>PostTranscriptional Gene Silencing</td>
</tr>
<tr>
<td>PTM</td>
<td>PostTranslational Modification</td>
</tr>
<tr>
<td>RdDM</td>
<td>RNA-directed DNA Methylation</td>
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<tr>
<td>RDR2</td>
<td>RNA-Dependent RNA Polymerase 2</td>
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<tr>
<td>REF6</td>
<td>Relative Early Flowering 6</td>
</tr>
<tr>
<td>RNA</td>
<td>Ribonucleic Acid</td>
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<tr>
<td>ROS1</td>
<td>Repressor of Silencing 1</td>
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<td>RPD3</td>
<td>Reduced Potassium Dependency 3</td>
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<td>Shoot Apical Meristem</td>
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<td>SET</td>
<td>Su(var)3-9 E(z) TRX</td>
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<td>SIR2</td>
<td>Silent Information Regulator 2</td>
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<td>SSP</td>
<td>Seed Storage Protein</td>
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<tr>
<td>SWI/SNF2</td>
<td>Switch/Sucrose Non-Fermenting</td>
</tr>
<tr>
<td>SWN</td>
<td>SWINGER</td>
</tr>
<tr>
<td>Su(var)3-9</td>
<td>Suppressor of variegation</td>
</tr>
<tr>
<td>TE</td>
<td>Transposable Elements</td>
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<tr>
<td>TF</td>
<td>Transcription Factors</td>
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<td>TRX</td>
<td>Trithorax</td>
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<tr>
<td>TSS</td>
<td>Transcription Start Site</td>
</tr>
<tr>
<td>UBP</td>
<td>Ubiquitin Protease</td>
</tr>
<tr>
<td>VRN</td>
<td>Vernalization</td>
</tr>
</tbody>
</table>
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2.3.3 Antagonistic function between CHR5 and PKL in seed maturation gene expression
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Chapter 3 Functional characterization of a histone demethylase JMJ15 in Arabidopsis
Over-expression of Histone H3K4 Demethylase Gene JMJ15 Enhances Stress Tolerance in Arabidopsis

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3.2 Introduction

3.3 Materials and methods

3.4 Results
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3.4.2 JMJ15 displayed a highly tissue-specific expression pattern
3.4.3 JMJ15 gain-of-function mutations showed a reduced plant height phenotype
3.4.4 Over-expression of JMJ15 preferentially repressed genes marked by H3K4 methylation
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CHAPTER 4 General discussion and perspectives
4.1 Function of CHR5 in plant gene expression
4.2 The function of JMJ15 in plant development

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Appendix
CHAPTER 1

GENERAL INTRODUCTION
**Epigenetics and epigenetic regulation**

The term "epigenetics" (epi meaning over or above) was coined by C. H. Waddington in 1942 as a portmanteau of the words epigenesis and genetics. He used it as a conceptual model of how genes might interact with their surroundings to produce a phenotype. Then Robin Holliday defined "epigenetics" as "the study of the mechanisms of temporal and spatial control of gene activity during the development of complex organisms". Thus epigenetic can be used to describe anything other than DNA sequence that influences the development of an organism. Recently, a consensus definition of the epigenetic trait, "stably heritable phenotype resulting from changes in a chromosome without alterations in the DNA sequence", was made at a Cold Spring Harbor meeting (Berger et al., 2009). In general, epigenetics is a fascinating new field in the genetic sciences and a brief history of major discoveries in epigenetics is shown in Figure 1.

![Figure 1. Timeline of epigenetics study](http://www.epigenetic.us/disco.htm)
Epigenetic regulation is the process by which a gene’s activity is modulated through covalent modifications to the DNA, the histones around which it wraps, or the physical packaging of the chromatin in which it is embedded. Mechanisms of epigenetic regulation are likely to have originated as a defense against parasitic DNAs, such as transposons and viruses, but they are also used to control the expression of many genes essential for development or environmental responses. In this chapter, I will focus on the mechanism and role of epigenetic regulation in plant gene expression and development.

1.1 Chromatin organization

Chromatin is the combination or complex of DNA and its associated proteins, which makes up the contents of the nucleus in eukaryotes. The basic unit of chromatin is the nucleosome, constituted of 147 bp of double stranded super helical DNA wrapped around an octamer formed by two copies each of four basic proteins called histones (H2A, H2B, H3, H4) (Figure 2) (Richmond and Davey, 2003). Repeating nucleosomes with intervening "linker" DNA are packed into a higher-order structure of 30 nm filaments. The 30 nm fiber is arranged into loops along a central protein scaffold to form chromosome (Figure 2).

Figure 2. Nucleosome structure. Left: The crystal structure of the nucleosome core particle consisting of H2A (yellow), H2B (red), H3 (blue) and H4 (green) core histones and DNA. Right: The major structure in DNA compaction: nucleosome, 30 nm fiber and chromosome.
Chromatin can be roughly divided into two states: (i) active or open state called euchromatin and (ii) silent or condensed chromatin state called heterochromatin. Euchromatin is generally gene rich, transcriptionally active and contains only few repetitive elements. Constitutively expressed genes in plants and other organisms typically reside within euchromatic regions and often have nucleosome free regions within their promoters (Rando and Ahmad, 2007; Zhang et al., 2007b). On the other hand, constitutive heterochromatin is rich in repetitive DNA, such as transposons and other duplicated sequences, permanently condensed, generally capable of silencing genes (Elgin and Grewal, 2003).

1.2 Nucleosome positioning

Nucleosome positioning is a dynamic process. Owing to the rapid progress of high-throughput array and sequencing techniques, it is possible to detect the global nucleosome positioning map in diverse organisms and identify the positions of individual nucleosomes at a specific time. For instance, the genome-wide nucleosome positioning maps of some model organisms including yeast, worms, flies and humans have been completed (Yuan et al., 2005; Lee et al., 2007; Mavrich et al., 2008; Schones et al., 2008; Valouev et al., 2008; Li et al., 2011). These results show that although most genomic DNA is occupied by nucleosomes, some functional regions, such as promoters, enhancers and terminators, are depleted of nucleosomes. In addition, nucleosomes at most genes are organized in basically the same pattern: a nucleosome free region (NFR) near the transcriptional start site (TSS), flanked by two well-positioned nucleosomes (the -1 and +1 nucleosomes) and followed by a nucleosomal array that packages the gene (Figure 3). The -1 nucleosome located upstream of TSS covers a region from -300 to -150 which regulates the accessibility of promoter regulatory elements in that region. The -1 nucleosome will process changes during transcription such as histone replacement, acetylation and methylation, as well as transcription repositioning and ultimately eviction after pre-initiation complex (PIC) formation (Li et al., 2011). The +1 nucleosome displays the strongest
positioning which often includes histone variants (H2A.Z and H3.3) and histone modifications such as methylation and acetylation. During transcription the +1 nucleosome might be evicted for PIC assembly. Nucleosomes at the 5’end of the gene are generally better localized than those in the middle. It is reported that nucleosome positioning is mainly determined by the intrinsic DNA sequence, while the NFR is determined mainly by the binding of transcription factors (TF) (Ozonov and van Nimwegen, 2013; Struhl and Segal, 2013).

![Figure 3. Nucleosomal landscape of yeast genes.](image)

Figure 3. Nucleosomal landscape of yeast genes. The distribution of nucleosomes in a gene is shown. The peaks and valleys represent similar positioning relative to TSS. The green shading represents high H2A.Z levels and histone modification (Jiang and Pugh, 2009).

Nucleosome positioning plays both positive and negative roles in transcription via modulating accessibility of DNA to proteins. To initiate the transcription, the transcription start site must be made available to the transcription machinery. During elongation, RNA polymerase II (Pol II) must overcome the transcriptional barriers imposed by nucleosomes in chromatin. Therefore, nucleosomes positioned at promoter region influence the initiation of transcription, and relocation of nucleosomes has a dramatic effect on transcription rates (Parthasarthy and Gopinathan, 2006; Choi et al., 2009; Hodges et al., 2009).
1.3 Histone modification

Histones are small alkaline proteins (11 to 21.5 kDa), which are highly conserved from yeast to humans. Histones are composed of a globular carboxyl (C)-terminal domain and a protruding amino (N)-terminal “tails” that are mainly targeted by numerous posttranslational modifications (PTM). These modifications are usually limited to several amino acids, for example lysine acetylation, lysine and arginine methylation, serine and threonine phosphorylation, and lysine ubiquitination and sumoylation. Histone modifications can be abbreviated as the histone name, the position of the mark, and the nature and number of the marks. For example, H3K4me3 is a trimethylation of Histone H3 Lysine 4 (K4) of. At least eight types of histone modifications have been characterized to date (Table 1) (Kouzarides, 2007).

<table>
<thead>
<tr>
<th>Chromatin Modifications</th>
<th>Residues Modified</th>
<th>Functions Regulated</th>
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<tbody>
<tr>
<td>Acetylation</td>
<td>K-ac</td>
<td>Transcription, Repair, Replication, Condensation</td>
</tr>
<tr>
<td>Methylation (lysines)</td>
<td>K-me1 K-me2 K-me3</td>
<td>Transcription, Repair</td>
</tr>
<tr>
<td>Methylation (arginines)</td>
<td>K-me1 K-me2a K-me2s</td>
<td>Transcription</td>
</tr>
<tr>
<td>Phosphorylation</td>
<td>S-ph T-ph</td>
<td>Transcription, Repair, Condensation</td>
</tr>
<tr>
<td>Ubiquitylation</td>
<td>K-ub</td>
<td>Transcription, Repair</td>
</tr>
<tr>
<td>Sumoylation</td>
<td>K-su</td>
<td>Transcription</td>
</tr>
<tr>
<td>ADP ribosylation</td>
<td>E-er</td>
<td>Transcription</td>
</tr>
<tr>
<td>Deimination</td>
<td>R&gt;Cit</td>
<td>Transcription</td>
</tr>
<tr>
<td>Proline Isomerization</td>
<td>P-cis&gt;P-trans</td>
<td>Transcription</td>
</tr>
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</table>

Table 1. Overview of different classes of modification identified on histones (Kouzarides, 2007).

Histone modifications at many sites are conserved in plants, however there also exist a few unique histone modification sites in *Arabidopsis* (Zhang et al., 2007a). For example, acetylated H4K20, H2BK6, H2BK11, H2BK27, H2BK32, and H2AK144 and monoubiquinated H2BK143 are found in *Arabidopsis* but not in human or yeast cells, whereas H3K79me, highly conserved and functioning in telomeric silencing in non-plant systems, is not modified in *Arabidopsis* (Zhang et al., 2007a). Although most of the known histone modifications occur on the N-terminal tails of histones, exceptions include monoubiquitination of the C-terminal tails of
H2A and H2B and acetylation of H2AK144. Figure 4 shows the main known histone acetylation (ac), methylation (me) and ubiquitination (ub) sites in *Arabidopsis*.

**Figure 4.** Major histone modification in *Arabidopsis*. Left: Histone acetylation (ac), methylation (me) and ubiquitination (ub) sites on core histones are shown. Green is generally associated with transcriptional activation. Red is often related to transcriptional repression. Right: Genome wide distribution pattern of histone modifications from a transcription perspective (Lauria and Rossi, 2011)

Genome wide analyses show that histone modifications particularly on H3 are related to gene expression (Figure 4). In *Arabidopsis* it is found that H3K9ac and H3K27ac are almost exclusively located within genes and invariably correlate with transcriptional activation, with both marks being enriched towards 5’ end of genes and peaking around transcriptional start site (TSS) (Charron et al., 2009; Zhou et al., 2010). The distribution of H3K56ac is similar to that of H3K9ac and H3K27ac, but it is not correlated with active transcription and seems to be a mark of transcriptional competence (Tanurdzic et al., 2008). Histone methylation is more complicated, as it can either activate or repress gene expression depending on the location of the lysine and the number of methyl groups added. Here below I will discuss the role of histone acetylation/deacetylation, histone methylation/demethylation and histone ubiquitination/deubiquitination function in plant gene expression.
1.3.1 Histone acetylation and deacetylation

Among these post-transcriptional modifications, histone acetylation was first reported and most well characterized. Histone acetylation is a dynamic, reversible process that is highly conserved among eukaryotes. It involves the transfer of an acetyl group from acetyl-CoA to ε-amino group of lysine residues in all core histones, mainly at the tails but also at a few residues within the globular domain (Berger, 2007). The lysine acetylation neutralizes the positive charge of histone and therefore decreases their affinity for negatively charged DNA. Histone acetylation can also be recognized by histone modifications readers such as bromo-domain proteins (Filippakopoulos and Knapp, 2012), which promote the recruitment of additional ATP-dependent chromatin remodelers and chromatin modifier complexes, establishing a relaxed chromatin that facilitates the recruitment of RNA polymerases and gene expression (Bannister and Kouzarides, 2011). Histone acetylation which relaxes chromatin structure is often associated with active gene transcription. On the other hand, histone deacetylation which induces chromatin compaction is related to gene repression (Berger, 2007). The level of histone acetylation is catalyzed by the activity of both histone acetyltransferases (HATs) and histone deacetylases (HDACs).

1.3.1.1 Plant histone acetyltransferases (HATs)

Based on primary homology with their yeast and mammalian counterparts, plant HATs are classified into four types, the GCN5-RELATED N-TERMINAL ACETYLTRANSFERASES (GNAT), MOZE YBF2/SAS3 SAS2 TIP60 (MYST), CREB-BINDING PROTEIN (CBP/P300), and TATA-BINDING PROTEIN-ASSOCIATED FACTOR II 250 (TAFII250) types (Pandey et al., 2002). The *Arabidopsis* genome is predicted to encode 12 histone acetyltransferases, including three GNAT family genes (*HAG1/AtGCN5, HAG3/ELP3*, and *HAG2*, respectively), two MYST family genes (*HAG4 and HAG5*), five p300/CBP family genes (*HAC1, HAC2, HAC4, HAC5 and HAC12*), and two TAF1 genes (*HAF1 and HAF2*). AtGCN5 is shown to have a histone H3 acetyltransferase activity *in vitro*.
(Earley et al., 2007) and the global H3 acetylation is reduced in Atgcn5 mutants by Western blot (Bertrand et al., 2003). In vivo AtGCN5 is found to affect the acetylation of H3K9, H3K14, H3K27, and H4K12 on the target promoters (Benhamed et al., 2006). AtGCN5 is involved in many plant development pathways such as meristem function, leaf cell differentiation, leaf and floral organogenesis, and responses to environmental conditions such as light and cold (Bertrand et al., 2003; Benhamed et al., 2006; Kim et al., 2009; Kornet and Scheres, 2009; Servet et al., 2010), in accordance with the fact that AtGCN5 is required for both long-term developmental gene and short-term inducible gene expression (Benhamed et al., 2008). AtELP3/ELO3/HAG3 as a component of the Elongator complex is reported to interact with MINIYO (IYO) to activate RNA polymerase II (RNAPII) transcriptional elongation (Nelissen et al., 2010; Sanmartin et al., 2011). AtELP3 is found to be involved in auxin-related process by regulating H3K14 acetylation of auxin activated genes (Nelissen et al., 2010). The Arabidopsis MYST-family HAM1 and HAM2 proteins were proved to specifically acetylate H4K5 in vitro (Earley et al., 2007) and to function redundantly to regulate gametophyte development and flowering transition in vivo (Latrasse et al., 2008; Xiao et al., 2013). Arabidopsis CBP/p300-like protein AtHAC1/PCAT2 is found to possess a HAT activity on core histones in vitro (Bordoli et al., 2001) and to be implicated in the control of flowering time and ethylene signaling pathway (Deng et al., 2007; Han et al., 2007; Li et al., 2014). Finally, TAF1 is found to participate in light signal by regulating H3 and/or H4 acetylation at some light-responsive loci (Bertrand et al., 2005).

1.3.1.2 Plant histone deacetylases (HDACs)

Similar to HATs, the HDACs in Arabidopsis are encoded by 18 genes and can be classed into three types, including Reduced Potassium Dependency 3/Histone DeAcetylase 1 (RPD3/HDA1), Silent Information Regulator 2 (SIR2) and the plant-specific Histone Deacetylase 2 (HD2) (Pandey et al., 2002). There are 12 RPD3/HDA1 genes, many of which have been characterized. For instance,
CHAPTER 1—GENERAL INTRODUCTION

HDA19/HD1 down-regulation or overexpression results in a significant change of H3 and H4 acetylation (Tian et al., 2003; Zhou et al., 2005; Fong et al., 2006). Similarly, HDA6 is also found to deacetylate multiple lysines on H3 and H4 \textit{in vitro}, however the total level of histone acetylation is only slightly affected in \textit{hda6} mutants (Probst et al., 2004; Earley et al., 2006). HDA19 and HDA6 play redundant roles in embryonic and flower development, responses to environmental conditions such as JA/ethylene-mediated defense, ABA-mediated responses to drought or salinity (Zhou et al., 2005; Tanaka et al., 2008; Chen and Wu, 2010). Recently, several lines of evidence suggest that HDA6 and HDA19, like their counterparts in other eukaryotes, operate histone deacetylation within a large muti-protein complex (Perrella et al., 2013). HDA18 is found to have \textit{in vitro} histone deacetylase activity and to be implicated in root epidermal patterning (Xu et al., 2005; Alinsug et al., 2012; Liu et al., 2013a). HDA15 negatively regulates chlorophyll biosynthetic and photosynthetic genes in dark by decreasing histone acetylation and RNAPII-associated transcription (Liu et al., 2013b). HDA14 is shown to deacetylate α-tubulin and partially retained on GTP/taxol-stabilized microtubules by direct association with the PP2A-A2 phosphatase (Tran et al., 2012). The SIR2 family contains two members (\textit{SRT1} and \textit{SRT2}) in \textit{Arabidopsis} genome, which catalyze deacetylation via a reaction depending on NAD+ (Dali-Youcef et al., 2007). SRT2 is a negative regulator of basal defense (Wang et al., 2010) and functions in mitochondrial energy metabolism by deacetylazing organellar proteins (Konig et al., 2014). The HD2 family proteins are found exclusively in plants. AtHD2A, AtHD2B and AtHD2C are proposed to function in transcriptional gene repression during seed development, plant defense, and response to abiotic and biotic stresses (Sridha and Wu, 2006; Bourque et al., 2011; Colville et al., 2011; Luo et al., 2012; Grandperret et al., 2013; Yano et al., 2013). The main function and sublocalization of \textit{Arabidopsis} HDACs is shown in Table 2.
1.3.2 Histone methylation and demethylation

Histone methylation mainly occurs on lysines and arginines residues of histone N-terminal tails. Histone lysines can be mono-, di- or tri-methylated and arginines can be mono- or di-methylated, where the two methyl groups can be added to one (asymmetrical) or the two (symmetrical) amine groups of aginine (Bedford and Clarke, 2009; Black et al., 2012). Histone methylation has important roles in many biological processes, such as transcription, cell cycle, DNA repair, stress response, and heterochromatin formation (Mosammaparast and Shi, 2010). In Arabidopsis, histone H3 methylation at K4, K9, K27 and K36 have been well characterized in recent years.

Table 2. Summary of HDAC proteins characterized in plants (modified from Grandperret et al., 2013).

<table>
<thead>
<tr>
<th>Name</th>
<th>Accession</th>
<th>Localization</th>
<th>Function</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>RPD3/HDA1</td>
<td></td>
<td></td>
<td>embryo and flower development, stress response,</td>
<td>(Chou et al., 2005; Behrens, M., 2014)</td>
</tr>
<tr>
<td>HDA1</td>
<td>AT4G38150</td>
<td>Nucleus</td>
<td>light response and basal defense</td>
<td>(Tanaka et al., 2009; Choi et al., 2012)</td>
</tr>
<tr>
<td>HDA2</td>
<td>AT5G58040</td>
<td>Nucleus?</td>
<td>Unknown</td>
<td>(Alinaeg et al., 2012)</td>
</tr>
<tr>
<td>HDA5</td>
<td>AT5G81060</td>
<td>Cytoplasm, Nucleus, ER</td>
<td>Binds 14-3-3 proteins; involved in light response.</td>
<td>(Alinaeg et al., 2012)</td>
</tr>
<tr>
<td>HDA6</td>
<td>AT5G83110</td>
<td>Nucleus, Chloroplast envelope</td>
<td>Embryonic and flower development, Jasmonate and salt signaling, silencing RNA genes, repression transgenes and transposable elements.</td>
<td>(Prest et al., 2006; (Kumar et al., 2010)</td>
</tr>
<tr>
<td>HDA7</td>
<td>AT5G35600</td>
<td>Nucleus</td>
<td>Unknown</td>
<td>(Alinaeg et al., 2009)</td>
</tr>
<tr>
<td>HDA8</td>
<td>AT1G09460</td>
<td>Cytoplasm</td>
<td>Unknown</td>
<td>(Alinaeg et al., 2009)</td>
</tr>
<tr>
<td>HDA9</td>
<td>AT5G46680</td>
<td>Nucleus</td>
<td>Flowering</td>
<td>(Kim et al., 2012)</td>
</tr>
<tr>
<td>HDA10</td>
<td>AT8G46660</td>
<td>Nucleus</td>
<td>Unknown</td>
<td></td>
</tr>
<tr>
<td>HDA14</td>
<td>AT4G33470</td>
<td>Mitochondria, Cytosol</td>
<td>Association with PP2A-A2 phosphatase and microtubules</td>
<td>(Alinaeg et al., 2012; Tran et al., 2012)</td>
</tr>
<tr>
<td>HDA15</td>
<td>AT5G18520</td>
<td>Nucleus, Cytosol</td>
<td>Negative control of chlorophyll synthesis</td>
<td>(Alinaeg et al., 2012; Crauford and Galvani, 2007; Lu et al., 2012)</td>
</tr>
<tr>
<td>HDA17</td>
<td>AT3G44940</td>
<td>Nucleus</td>
<td>Enhances Agrobacterium transformation</td>
<td></td>
</tr>
<tr>
<td>HDA18</td>
<td>AT5G81070</td>
<td>Nucleus, Cytosol</td>
<td>Differentiation of hair and non-hair cells in the root epidermis</td>
<td>(Ku et al., 2005; (Alinaeg et al., 2012; Li et al., 2013)</td>
</tr>
<tr>
<td>SIR2</td>
<td>AT5G35760</td>
<td>Nucleus</td>
<td>Plant defense, mitochondrial energy metabolism</td>
<td>(Wang et al., 2010; Koestl AC et al., 2014)</td>
</tr>
<tr>
<td>SIR1</td>
<td>AT5G09230</td>
<td>Nucleus</td>
<td>Unknown</td>
<td></td>
</tr>
<tr>
<td>HDZ1</td>
<td>AT1G44750</td>
<td>Nucleus</td>
<td>Seed dormancy</td>
<td>(Calville et al., 2013; (Chou et al., 2004)</td>
</tr>
<tr>
<td>HDZ3</td>
<td>AT5G23650</td>
<td>Nucleus</td>
<td>Seed dormancy</td>
<td>(Yano et al., 2013)</td>
</tr>
<tr>
<td>HDZ4</td>
<td>AT5G27840</td>
<td>Nucleus</td>
<td>ABA and salt stress signaling, Seed dormancy</td>
<td>(Shade and Wu, 2008; (Calville et al., 2011)</td>
</tr>
<tr>
<td>HDZ4</td>
<td>AT5G27840</td>
<td>Nucleus</td>
<td>ABA and salt stress signaling, Seed dormancy</td>
<td>(Luo et al., 2012)</td>
</tr>
</tbody>
</table>

Arabidopsis, histone H3 methylation at K4, K9, K27 and K36 have been well characterized in recent years.
In *Arabidopsis*, H3K4 methylation is associated exclusively with genes and promoters (two thirds of all genes) and is absent from heterochromatic regions (Zhang et al., 2009). H3K4me1 is abundant in the body of genes, while H3K4me2 and H3K4me3 are enriched in promoter and 5’end regions, with H3K4me3 being further upstream of H3K4me2 (Zhang et al., 2009). Only H3K4me3 is associated with active gene transcription while H3K4me1 and H3K4me2 are not well correlated with gene transcription (Zhang et al., 2009). H3K4me3 promotes transcription through interaction with effectors including transcription factors to recruit RNAPII to target genes (Lauberth et al., 2013).

H3K27 methylation is a repressive mark. In plant, H3K27me1 is enriched at constitutive heterochromatin, while H3K27me3 is preferentially localized to the transcribed regions of genes, with an increase towards the 5’ end (Zhang et al., 2007c; Roudier et al., 2011). About 17% of coding genes show H3K27me3, indicating that H3K27me3 is a major repressive mark for gene expression in *Arabidopsis* (Zhang et al., 2007c). Several well-known *Arabidopsis* developmental genes, including flower timing gene *FLOWERING LOCUS C* (*FLC*), floral organ patterning gene *AGAMOUS* (*AG*), homeobox gene *SHOOT MERISTEMLESS* (*STM*), imprinted genes *MEDEA* (*MEA*) and *PHERES1* (*PHE1*) and embryo identity genes *LEAFY COTYLEDON1* (*LEC1*), *LEAFY COTYLEDON 2* (*LEC2*), *ABSCISIC ACID-INSENSITIVE 3* (*ABI3*), *FUSCA3* (*FUS3*) have been reported to be repressed by H3K27me3 (Schubert et al., 2006; Turck et al., 2007; Bouyer et al., 2011; Lafos et al., 2011). The expression level of H3K27me3-marked genes is very low suggesting transcription repression by H3K27me3 is alleviated only in the place where their expression is needed (Zhang et al., 2007c).

Histone H3K9 methylation in *Arabidopsis* predominantly occurs at H3K9me1 and H3K9me2, while some H3K9me3 can be detected mainly located in genes peaking at 5’ and 3’ ends as a mild activating transcription mark (Charron et al., 2009). H3K9me2 is abundant in pericentromeric heterochromatin as well as in transposons and repeated sequence region, consistent with its role in repression of
transposon elements (Bernatavichute et al., 2008). It is found that H3K9me2 and DNA methylation form a self-reinforcing loop in the maintenance of genome-wide transcriptional gene silencing and genome stability in *Arabidopsis* (Bernatavichute et al., 2008; Zhou et al., 2010; Du et al., 2012; Stroud et al., 2014).

H3K36me3 peaks in the first half of the coding region in *Arabidopsis*, in contrast to the 3’ end localization reported in mammals (Wang et al., 2008; Roudier et al., 2011). In fact, H3K36me3 distribution in *Arabidopsis* is similar to that of H3K79me3 in other organisms (Wang et al., 2009; Zhou et al., 2011). In addition *Arabidopsis* lacks H3K79me3 modification and the H3K79 methyltransferase, it is possible that H3K36me3 in plants functions equivalently to H3K79me3 in mammals. Furthermore, H3K36me2 in *Arabidopsis* peaks at the 3’ end of expressed genes, suggesting it could play a role similar to that attributed to H3K36me3 in other organisms (Oh et al., 2008; Roudier et al., 2011).

### 1.3.2.1 Plant histone methyltransferases (HMTs)

The homeostasis of the histone methylation is maintained by histone methyltransferases (HMTs) (Liu et al., 2010). HMTs usually contain a SET domain, named after the three *Drosophila* proteins: Suppressor of variegation (Su(var)3-9), Enhancer of Zeste (E(z)) and Trithorax (TRX). In *Arabidopsis*, 49 genes encoding putative SET domain-containing proteins have been identified and are divided into five categories (www.chromDB.org) (Ng et al., 2007a; Gendler et al., 2008; Thorstensen et al., 2011). Different classes of SET domain proteins, their histone methyltransferase specificity, interaction partners, and interacting domains are showed in Table 3.
### Table 3. Plant SET domain-containing proteins (modified from Thorstensen et al., 2011).

<table>
<thead>
<tr>
<th>Class</th>
<th>Name (Arabidopsis)</th>
<th>SDG number (Arabidopsis)</th>
<th>ATGID</th>
<th>HMThase specificity</th>
<th>Method*</th>
<th>Interacts with</th>
<th>Interacting domain</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>IV</td>
<td>ATXR5</td>
<td>SDG15</td>
<td>Atg15</td>
<td>H2K12me3</td>
<td>P, ChIP</td>
<td>PCNA</td>
<td></td>
<td>뷔길호 et al., 2009</td>
</tr>
<tr>
<td></td>
<td>ATXR6</td>
<td>SDG14</td>
<td>Atg14</td>
<td>H2K12me1</td>
<td>FR, ChIP</td>
<td>PCNA</td>
<td></td>
<td>뷔길호 et al., 2009</td>
</tr>
<tr>
<td>V-SU(YR)</td>
<td>3-9</td>
<td>SUH1</td>
<td>SDG3</td>
<td>Atg2</td>
<td>CG, methylated</td>
<td>VDS1RA</td>
<td></td>
<td>존슨에등., 2008, (Naccarato et al., 2001), (Ay et al., 2009)</td>
</tr>
<tr>
<td></td>
<td>SUVH2</td>
<td>SDG7</td>
<td>Atg22/240</td>
<td>H2K12me1</td>
<td>CH1, CH2, CH3</td>
<td>VDS1RA</td>
<td></td>
<td>(Wang et al., 2000), (Elbs and Bender, 2006)</td>
</tr>
<tr>
<td></td>
<td>SUVH3</td>
<td>SDG10</td>
<td>Atg3</td>
<td>H2K12me2</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Elbs and Bender, 2006), (Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVH6</td>
<td>SDG23</td>
<td>Atg227</td>
<td>H2K9me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Johnston et al., 2008) (Wang et al., 2006), (Elbs and Bender, 2006)</td>
</tr>
<tr>
<td></td>
<td>SUVH7</td>
<td>SDG17</td>
<td>Atg17</td>
<td>H2K12me1</td>
<td>CH1, ChIP, CH2, CH3</td>
<td>VDS1RA</td>
<td></td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVH8</td>
<td>SDG21</td>
<td>Atg21</td>
<td>H2K12me1</td>
<td>CH1, ChIP</td>
<td>VDS1RA</td>
<td></td>
<td>(Wang et al., 2000), (Elbs and Bender, 2006)</td>
</tr>
<tr>
<td></td>
<td>SUVH9</td>
<td>SDG22</td>
<td>Atg13</td>
<td>H2K9me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVR1</td>
<td>SDG13</td>
<td>Atg13</td>
<td>H2K9me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVR2</td>
<td>SDG18</td>
<td>Atg18</td>
<td>H2K12me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVR3</td>
<td>SDG20</td>
<td>Atg20</td>
<td>H2K9me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVR4</td>
<td>SDG21</td>
<td>Atg21</td>
<td>H2K12me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
<tr>
<td></td>
<td>SUVR5</td>
<td>SDG23</td>
<td>Atg23</td>
<td>H2K12me3</td>
<td>ChIP</td>
<td>CHB</td>
<td>VDS1RA</td>
<td>(Rajakaruna et al., 2011)</td>
</tr>
</tbody>
</table>
Like animal homologs, plant E(z) proteins are part of Polycomb Repressive Complex 2 (PRC2) that suppresses genes by mediating H3K27 trimethylation. PRC2 core complex in *Drosophila* is composed of four components (Figure 5): E(z), Su(z)12, a DNA/Protein binding C2H2 Zn-finger protein; Extra Sex Combs (ESC), a protein with a WD40 beta-propeller; Nucleosome remodeling factor 55 (N55), a WD40 domain protein (Schwartz and Pirrotta, 2007). In *Arabidopsis*, the PRC2 proteins are conserved in small families, which associate in different compositions to target different loci (Pien and Grossniklaus, 2007; Hennig and Derkacheva, 2009). The homologs of E(z) are *CURLY LEAF (CLF)*, *SWINGER (SWN)* and *MEDEA (MEA)* while *EMBRYONIC FLOWER 2 (EMF2)*, *REDUCED VERNALIZATION RESPONSE 2 (VRN2)* and *FERTILIZATION INDEPENDENT SEED 2 (FIS2)* are related to Su(z)12 (Luo et al., 1999; Gendall et al., 2001; Chanvivattana et al., 2004). The WD-40 protein ESC is encoded by *FERTILIZATION INDEPENDENT ENDOSPERM (FIE)* (Ohad et al., 1999). N55 has 5 homologs named *MULTICOPY SUPPRESSOR OF IRA 1 to 5 (MSI1-5)* (Kohler et al., 2003; Guitton and Berger, 2005).

![Figure 5. PRC2 complex core components in *Drosophila* and *Arabidopsis*.](image)

According to the Su(z)12 components, there are three distinct *Arabidopsis* PRC2 complexes PRC2-FIS, PRC2-EMF and PRC2-VRN. Mutations of the PRC2-FIS partners *MEA, FIS2, FIE* and *MSII* lead to autonomous endosperm development, and the complex is thought to control embryonic development by repressing central seed development regulators (Ohad et al., 1999; Kohler et al., 2003; Weinhofer et al., 2010). The PRC2-EMF complex contains CLF/SWN and functions in floral transition, floral organ development and vegetative growth (Aichinger et al.,...
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2009; Hennig and Derkacheva, 2009; Bouyer et al., 2011). PRC2-VRN complex also contains CLF/SWN which regulates flowering time mediated by vernalization (Wood et al., 2006; De Lucia et al., 2008). clf mutant induces early flowering and pleiotropic phenotypes, while swn mutant shows a wild type like phenotype. However, the clf swn double mutant is severely impaired and develops to a callus-like structure, and H3K27me3 is probably globally mitigated (Chanvivattana et al., 2004; Aichinger et al., 2009), suggesting that CLF and SWN have partial redundant functions in plant development.

In the Arabidopsis ASH1 class, four ASH1 HOMOLOG (ASHH) and three ASH1 RELATED (ASHR) members are identified (Baumbusch et al., 2001). ASHH1/SDG26 can methylate H3 and H4 in vitro and ashh1 mutant shows a delayed flowering phenotype (Xu et al., 2008; Berr et al., 2009). ASHH2 is considered as a major H3K36me2/me3 HMT in Arabidopsis (Zhao et al., 2005; Xu et al., 2008), and ashh2 mutant results in a pleiotropic phenotype (Dong et al., 2008; Cazzonelli et al., 2009; Grini et al., 2009; Berr et al., 2010a; Tang et al., 2012). The TRX class of SET domain proteins in Arabidopsis consists of two subgroups: ARABIDOPSIS TRITHORAX (ATX1-5) and ARABIDOPSIS TRITHORAX RELATED (ATXR1-7) (Baumbusch et al., 2001). It is shown that ATX1 mediates H3K4 trimethylation and ATX2 mediates H3K4 dimethylation on a few loci. atx1 mutants display an early flowering phenotype and alter leaf morphogenesis. ATXR3/SDG2 functions in many processes including gametophyte development, flowering time, leaf and root growth (Berr et al., 2010b; Guo et al., 2010; Yun et al., 2012; Yao et al., 2013). In sdg2 mutants, there is a global genome-wide reduction in H3K4me3, suggesting it is a major H3K4 trimethyltransferase in Arabidopsis (Berr et al., 2010b; Guo et al., 2010) ATXR5 and ATXR6 have an H3K27 monomethyltransferase activity. The double mutations atxr5 atxr6 show partial heterochromatin decondensation and transcriptional activation of repressed heterochromatic elements, accompanied with decreasing H3K27me1 in vivo (Jacob et al., 2009). The SU(VAR)3-9 class contain 14 proteins in Arabidopsis which are divided into two subgroups: the SU(VAR)3–9
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Homologs SUVH1-9 and the SU(VAR)3–9 Related proteins (SUVR) SUVR1-5 (Baumbusch et al., 2001). In general, members of this class have a H3K9 methyltransferase activity and are associated with inactive genes and highly condensed constitutive heterochromatin. KRYPTONITE (KYP/SUVR4) is the earliest and best studied member of this class. It is found in two independent genetic screens which are relative to reactivation of loci that were transcriptionally silenced by DNA methylation (Jackson et al., 2002; Malagnac et al., 2002). Mutations in KYP lead to a major decrease of heterochromatic H3K9me2 but not significant effect on H3K9me1, revealing that KYP is a major H3K9me2 methyltransferase in Arabidopsis (Jackson et al., 2004). SUVH5 and SUVH6, two close KYP/SUVH4 homologs, were demonstrated to methylate H3K9 in vitro and are partially redundant with KYP (Ebbs et al., 2005; Ebbs and Bender, 2006). SUVH2 and SUVH9 function in RNA-directed DNA methylation (RdDM) pathway, in which SUVH2 and SUVH9 bind to methylated DNA and facilitate the recruitment of Pol V to RdDM loci (Johnson et al., 2008; Johnson et al., 2014; Liu et al., 2014). SUVR4 requires the H3K9me1 peptide as substrate in vitro, whereas its two close homologs SUVR1 and SUVR2 do not have detectable HMTase activity (Thorstensen et al., 2006). SUVR4 as well as H3K27 monomethyltransferase ATXR5 and ATXR6 are found to involve in rRNA metabolism (Pontvianne et al., 2012).

1.3.2.2 Plant histone demethylases (HDMs)

Histone methylation was considered as irreversible until the discovery of Lysine Specific Demethylase 1 (LSD1), which was shown to remove methyl groups from H3K4 (Shi et al., 2004). Histone demethylases can be divided into two classes housing distinct mechanisms: amine oxidation by LSD1 and hydroxylation by Jumonji C (JmjC) domain–containing proteins (Liu et al., 2010). LSD1 family proteins need flavin adenine dinucleotide (FAD) and only acts on mono- or di-methylated but not tri-methylated lysines. The Arabidopsis genome encodes 4 Lysine-Specific Demethylase 1 (LSD1) homologs: LSD1-LIKE 1(LDL1), LDL2, LDL3
and FLOWERING LOCUS D (FLD). FLD, LDL1 and LDL2 are involved in transition from vegetative to reproductive phase with partial redundancy by repressing FLC expression (Jiang et al., 2007). In ldl1ldl2 and ldl1 fld double mutants, H3K4me2 on FLC locus is elevated suggesting an H3K4 demethylases activity of the proteins (Jiang et al., 2007). FLD is shown to interact with the HDA6 in flowing control (Yu et al., 2011), indicating the crosstalk between H3K4 demethylation and histone deacetylation in transcription repression.

1.3.2.3 JmjC proteins and their functions in plant development

The jumonji (jmj) gene was first identified in mouse by gene trap approach and was named after the morphology of the neural plates in mutant mice, which looks like a cruciform or “jumonji” in Japanese (Takeuchi et al., 1995). Structure analysis indicates that Jumonji proteins contain a conserved domain, named JmjC domain, consist of conserved 2-oxoglutarate-Fe (II)-binding site found in the dioxygenase super family (Clissold and Ponting, 2001). In recent years, a number of JmjC domain-containing demethylases have been identified in animals, which remove mono-, di- and trimethylated lysines in the presence of Fe (II) and α-ketoglutarate as cofactors (Tsukada et al., 2006; Couture et al., 2007; Ng et al., 2007b). JmjC proteins can also demethylate arginine residues, and other protein substrates or nucleotides (Chang et al., 2007). Phylogenetic analyses of sequences from mammalians show that JmjC proteins can be divided into several subfamilies, including JARID/KDM5, JMJD1/JHDM2/KDM3, JMJD2/KDM4, JMJD3/UTX/KDM6, JHDM1/FBX/KDM2 and the JmjC domain-only group. Arabidopsis genome encodes 21 JmjC domain-containing proteins which show both conservation and divergence with animal homologs in evolution (Figure 6) (Sun and Zhou, 2008). For example, JARID/KDM5, JMJD1/JHDM2/KDM3, JMJD2/KDM4 and JmjC domain-only subfamilies are conserved among plant and animals, while JMJD3/UTX/KDM6 and JHDM1/FBX/KDM2 groups have not been found in Arabidopsis and plants contain a special group of JmjC proteins with additional protein modules (Lu et al., 2008).
Figure 6. Phylogenetic relationship and structure of jmjC domain-containing proteins. *Arabidopsis* JmjC proteins are labeled in yellow (adapted from Sun and Zhou 2008).
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JMJD2/KDM4 group

The JMJD2/KDM4 subfamily is the first reported JmjC proteins in animals, which consist of three ~130 kDa proteins (KDM4A-C) and KDM4D, a half size protein lacking double PHD and Tudor domains (Klose and Zhang, 2007). JMJD2/KDM4 proteins are demethylases which of di- and trimethylated H3K9 and H3K36 as well as trimethylated H1.4K26 (Berry and Janknecht, 2013). In Arabidopsis, Early Flowering 6 (ELF6/JMJ11), its close homolog Relative of Early Flowering 6 (REF6/JMJ12) and JMJ13 belong to this group (Sun and Zhou, 2008). ELF6 and REF6 play divergent roles in the control of flowering time, as mutations in ELF6 show an early flowering phenotype and ref6 mutants display a late flowering phenotype (Noh et al., 2004). The function of ELF6 as a floral repressor is related to FT repression (Jeong et al., 2009). The activity of SDG8 (a specific H3K4/H3K36 HMT) on FLC can be balanced by REF6, indicating REF6 may be involved in H3K36 demethylation (Ko et al., 2010). Interestingly, ELF6 and REF6 can change H3K9 methylation status on some brassinosteroid related genes, suggesting that ELF6 and REF6 may act as H3K9 demethylases (Yu et al., 2008). Recently REF6 is found to specifically demethylate H3K27me3 and H3K27me2 on hundreds of genes involved in plant development (Lu et al., 2011a), probably reflecting the effect of different potential co-factors on substrate specificity of the enzyme.

JMJD1/JHDM2/KDM3 group

JMJD1/JHDM2/KDM3 subfamily contains JHDM2A, JHDM2B, JHDM2C and HR in mammals, which possess JmjC and modified zinc-finger domain and have the ability to demethylate mono- and dimethylated H3K9 (Mosammaparast and Shi, 2010). In Arabidopsis, JMJ24, JMJ25, JMJ26, JMJ27, JMJ28 and JMJ29 belong to this group (Lu et al., 2008; Sun and Zhou, 2008). JMJ25 is also named as IBM1 (Increased in BONSAI Methylation 1), as mutation of IBM1 displays ectopic H3K9 methylation at the BONSAI locus, leading to non-CG DNA hypermethylation and gene silencing (Saize et al., 2008b). Loss of function of IBM1 causes multiple
developmental defects, including small and narrow leaves, pollen grain abortion, floral organ and embryo abnormalities and decreased reproduction (Saze et al., 2008b). Genome-wide profiling has revealed that \textit{ibm1} mutation displays ectopic CHG DNA methylation and H3K9me2 accumulation in thousands of genes, especially at long transcribed genes, whereas transposable elements (TEs) are unaffected (Miura et al., 2009; Inagaki et al., 2010). These results suggest that \textit{IBM1} protects protein coding genes from repression via H3K9 and non-CG DNA methylation (Saze et al., 2008b; Miura et al., 2009; Inagaki et al., 2010). In addition, aberrant phenotypes in \textit{ibm1} mutants in both DNA methylation and plant development can be suppressed by mutations in the H3K9 HMTase KYP/ SUVH4 and the CHG methylase CMT3, showing the interplay between H3K9 methylation and DNA methylation in regulating gene expression (Saze et al., 2008b). The relationship between H3K9me2 and DNA methylation will be discussed in 1.5. Furthermore, it is found that \textit{IBM1} not only protects genes from silencing via the direct association to prevent the coupling of histone and DNA methylation, but also targets components of RdDM pathway, \textit{RNA-DEPENDENT RNAPOLYMERASE 2 (RDR2)} and \textit{DICER-LIKE 3 (DCL3)}, hence indirectly participating in RdDM-directed repression (Fan et al., 2012).

\textit{JmjC domain-only group}

This group contains several JmjC domain-containing proteins that, apart from the JmjC domain, contain no other recognizable protein domains. This group establishes its own branch based on homology within the JmjC domain. It is proposed that the proteins in this group might have been diverged in eukaryotes to carry out functions that are independent of histone demethylation (Klose and Zhang, 2007). For instance, JMJD6 was initially suggested to demethylate both asymmetrically and symmetrically dimethylated H3 arginine 2 (H3R2me2) and H4 arginine 3 (H4R3me2) (Chang et al., 2007), however the activity was challenged by another study showing that JMJD6 has lysyl hydroxylation activity (Webby et al., 2009). JMJD5 (also called KDM8) has
been reported to demethylate H3K36me2 to regulate genes that control cell cycle and circadian rhythm (Hsia et al., 2010; Jones et al., 2010; Ishimura et al., 2012). Similarly, the activity of JMJD5 on histone demethylation is also questioned considering the biochemical assays in vitro and main function as a protein hydroxylase in vivo (Del Rizzo et al., 2012; Youn et al., 2012).

In Arabidopsis, JMJ20, JMJ21, JMJ22, JMJ23, JMJ30 and JMJ31 belong to this group. JMJ20 and JMJ22 are found to act as histone arginine demethylases that play redundantly positive roles in seed germination (Cho et al., 2012). In vitro, JMJ20 could demethylate H3R2me2, H4R3me1, and H4R3me2s. In vivo, JMJ20/JMJ22 are induced upon phytochrome B activation, and JMJ20/JMJ22 promote the expression of gibberellin anabolic genes GA3ox1/GA3ox2 by direct binding to and reducing repressive H4R3me2s levels on these genes (Cho et al., 2012).

Similarly to the homolog of JMJD5, JMJ30 is involved in the pace of circadian clock by regulating the center oscillators CCA1, LHY and TOC1 expression via a potential negative feedback loop between CCA1/LHY and JMJ30 (Lu et al., 2011b). Interestingly, human JMJD5 is able to rescue the circadian phenotype of jmj30 mutants and vice versa, suggesting that this gene has conserved function in both Arabidopsis and humans in circadian clock (Jones et al., 2010). However, the histone demethylase activity of JMJ30 in Arabidopsis still remains to be determined.

JARID/KDM5 group

KDM5 proteins contain five conserved domains: JmjN, AT-rich, JmjC, PHD and C5HC2-zinc-finger (Figure 6). This group catalyzes the demethylation of H3K4me3 and H3K4me2, and is constituted by KDM5A, KDM5B, KDM5C, KDM5D and JARID2 in mammalian cells (Blair et al., 2011). However, Arabidopsis genome only encodes one member JMJ17 whose molecular activity and biological function remains to be discovered (Sun and Zhou, 2008).
Plant specific JmjC proteins

This group contains JmjN, JmjC, a C5HC2-zinc-finger, and FYRN/FYRC domains at their C-termini (Figure 6). Interestingly, FYRN/FYRC domains are usually found together in the H3K4 methyltransferase Trithorax and its homologs. In Arabidopsis, JMJ14, JMJ15, JMJ16, JMJ18 and JMJ19 belong to this group. In vitro JMJ14 effectively demethylates H3K4me3 and to a lesser extent H3K4me2 and H3K4me1 (Jeong et al., 2009; Lu et al., 2010; Yang et al., 2010). This demethylase activity is confirmed by in vivo assay in Nicotiana benthamiana (Lu et al., 2010). In Arabidopsis, JMJ14 is shown to demethylate H3K4me3 and H3K4me2 at the FT locus, which is consistent with the fact that jmj14 mutants display a lower level of FT expression and an earlier flowering time (Jeong et al., 2009; Lu et al., 2010). JMJ14 is also required for DRM2-mediated RdDM pathway (Deleris et al., 2010). Mutation of JMJ14 causes reduced DNA methylation in non-CG contexts at RdDM targets such as MEA-ISR, FWA, AtSN1, but not Ta3 which is methylated by CMT3. Accompanied with reduced DNA methylation, there is an increase in H3K4me3 at RdDM targets in jmj14 mutants. However, JMJ14 does not impact de novo DNA methylation (Deleris et al., 2010). Furthermore, genome-wide DNA methylation analyses reveal that JMJ14 and LSD1 genes LDL1 and LDL2 cooperate to maintain RdDM pattern by counteracting H3K4 methylation (Greenberg et al., 2013). Another study searching for components of RNA silencing shows that JMJ14 participates in silencing sequences targeted by RdDM (Searle et al., 2010). Although in jmj14 mutants target sequences show significant increases of RNA transcripts and decreases of non-CG DNA methylation, endogenous small RNA abundance is not affected in jmj14 mutants. Further analysis indicates that JMJ14 acts downstream from Argonaute effector complex in RdDM (Searle et al., 2010). Similarly, JMJ14 is also identified in a screen for mutants defective in posttranscriptional gene silencing (PTGS) (Le Masson et al., 2012). jmj14 mutants release transgene PTGS that is correlated with an increase in promoter methylation and retardation of transcription (Le Masson et al., 2012).
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JMJ18 is found to be involved in the control of flowing time (Yang et al., 2012b). Mutations in JMJ18 resulted in a weak late-flowering, while JMJ18 overexpressors exhibited an obvious early-flowering phenotype (Yang et al., 2012b). In vitro, JMJ18 displays demethylase activity toward H3K4me3 and H3K4me2. In Arabidopsis, JMJ18 directly represses FLC expression by demethylating H3K4 methylation on FLC loci, thereby promoting the expression of downstream flowering activator FT to stimulate flowering (Yang et al., 2012b).

JMJ15 has been first identified as MEE27 (Maternal Effecter Embryo arrest 27) in a screen for mutants defective in the female gametophyte development (Pagnussat et al., 2005), suggesting it may play a role in reproductive development. In tobacco cells, JMJ15 is capable of demethylating H3K4me3, H3K4me2 and H3K4me1 (Liu et al., 2010). Similarly, JMJ15 is also proved to be a histone demethylase of H3K4me3 by MALDI-TOF mass spectrometry in vitro (Yang et al., 2012a).

1.3.3 Histone ubiquitination and deubiquitination

In addition to acetylation and methylation, histones can also be modified through ubiquitination (Jason et al., 2002). Although core histones, linker histones and several histone variants have been reported to be ubiquitinated (Hicke, 2001), most studies are so far focused on H2A and H2B monoubiquitination (Zhang, 2003; Weake and Workman, 2008). Similar to animals, H2A monoubiquitination (H2Aub1) in plant is mediated by Polycomb Repressive Complex1 (PRC1) and is required for the repression of genes when they are not necessary in a specific differentiation status (Bratzel et al., 2010; Molitor and Shen, 2013; Feng and Shen, 2014). In contrast to H2Aub1 for gene silencing, H2B monoubiquitination (H2Bub1) is mainly associated with gene activation (Zhang, 2003; Weake and Workman, 2008). The E2 enzyme Rad6 and E3 enzyme Bre1 and their homologs of the ubiquitination system are responsible for H2Bub1 in different eukaryotic organisms. In Arabidopsis, there are two Bre1 homologs, named HUB1 and HUB2, and three Rad6 homologs named ATUBC1,
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ATUBC2 and ATUBC3. Histone ubiquitination is also a reversible process. Deubiquitination enzymes or ubiquitin proteases (UBPs) specially cleave the peptide bond between the ubiquitin and substrate. In *Arabidopsis*, from over 27 putative proteins encoding UBPs (Liu et al., 2008), only UBP26/SUP32 has so far been reported to participate in H2B deubiquitination (Sridhar et al., 2007).

1.4 DNA methylation

Unlike the situation in mammals, where methylation in differentiated cells is found almost exclusively in CG dinucleotides, cytosine methylation in plants often occurs in three sequence contexts: CG, CHG and CHH (where H is either T, A or C) (Henderson and Jacobsen, 2007; Zilberman et al., 2007). Bisulfite sequencing of the *Arabidopsis* genome shows that approximately 5% of all cytosines are methylated, with 55% of that methylation in CG, 23% in CHG and 22% in CHH contexts, respectively (Cokus et al., 2008; Lister et al., 2008). Depending on the location in the genome, DNA methylation can be broadly classified as either genic or non-genic. The genic pattern is methylation in the transcribed region or gene body (excluded from both ends and assuming a bell-like shap with a slight bias toward the 3’ end) (Feng and Jacobsen, 2011). This genic methylation is found in ~1/3 of all protein coding genes in *Arabidopsis* and takes place predominantly in the CG context (Zhang et al., 2006; Cokus et al., 2008; Lister et al., 2008). It is found that genic methylation somewhat positively correlates with gene transcription, with the highest methylation level observed in genes with moderate transcription activities (Tran et al., 2005; Zilberman et al., 2007). The non-genic pattern is methylation on transposable elements (TEs) and other repetitive DNA, which are mostly found in pericentromeric heterochromatic regions but also exist in small patches between genes in the euchromatic arms (Feng and Jacobsen, 2011). Non-genic methylation happens in all three contexts and is generally associated with transcriptional repression (Zhang et al., 2006; Cokus et al., 2008; Lister et al., 2008). Some studies have shown that non-genic
DNA methylation represses protein-coding gene transcription when the mark is present in the gene’s regulatory regions or promoters (Chan et al., 2005)

In *Arabidopsis*, methylation at CG dinucleotides is catalyzed by DNA Methyltransferase 1 (*MET1*), the ortholog of mammalian DNA Methyltransferase 1 (*DNMT1*) (Kankel et al., 2003). The CG site is symmetrical on the opposite strand and MET1 can bind to the methylation strand and methylated the newly synthesized strand to maintain the DNA methylation pattern. Methylation at CHG is mediated mainly by CHROMOMETHYLASE3 (*CMT3*) (Lindroth et al., 2001). This site is also symmetrical and can potentially be regenerated by a semi-conservative mechanism. Methylation in the non-symmetric CHH context is maintained mainly by DOMAINS REARRANGED METHYLTRANSFERASE 2 (*DRM2*) and CHROMOMETHYLASE2 (*CMT2*) (Cao and Jacobsen, 2002a; Stroud et al., 2014). In addition to these well-characterized context preferences, there is a degree of redundancy for maintenance of non-CG methylation between CMT3 and DRM2 (Cao and Jacobsen, 2002b; Stroud et al., 2013), as well as CMT2 at some loci (Zemach et al., 2013; Stroud et al., 2014). Among all the methyltransferase, only DRM2 is required for *de novo* DNA methylation in all three contexts (Cao and Jacobsen, 2002a).

There also exist mechanisms to remove cytosine methylation. DNA demethylation can be achieved either passively or actively. Passive demethylation takes place during DNA replication by replacing methylated cytosines with unmethylated ones (Saze et al., 2008a), whereas active demethylation occurs in a base excision repair pathway initiated by DNA glycosylases. Four DNA glycosylases are known in *Arabidopsis*: REPRESSOR OF SILENCING 1 (*ROS1*), DEMETER (*DME*), DEMETER-LIKE2 (*DML2*) and DML3 (Gong et al., 2002; Penterman et al., 2007b; Ortega-Galisteo et al., 2008; Zhu, 2009). *ROS1* is a DNA repair protein shown to repress DNA methylation at numerous endogenous loci including many transposons (Gong et al., 2002; Penterman et al., 2007a; Zhu et al., 2007). *DME* is required for genomic imprinting during female gametophyte development, in the fertilized egg cell
and during endosperm formation (Gehring et al., 2006; Morales-Ruiz et al., 2006; Schoft et al., 2011). The two Demeter-like genes DML2 and DML3 are also required for appropriate distribution of DNA methylation marks within the genome (Ortega-Galisteo et al., 2008).

### 1.5 The link between DNA methylation and histone modification

In *Arabidopsis*, DNA methylation is correlated with specific histone modifications that vary depending on the context and genomic location of the DNA methylation. For instance, genic DNA methylation is largely co-incident with H3K4me1 (Zhang et al., 2009). In contrast, non-genic DNA methylation is negatively correlated with H3K4me2/me3 (Greenberg et al., 2013).

The relationship between H3K9me2 and CHG DNA methylation is established by the CMT3 pathway: CMT3 binds to H3K9me2 through its eponymous chromodomain, as well as bromo-adjacent homology (BAH) domain (Lindroth et al., 2004; Rajakumara et al., 2011). Loss of CHG methylation in *kyp suvh5 suvh6* (three major H3K9 methyltransferases) triple mutants mimics the loss of CHG methylation in *cmt3* mutants genome-wide (Stroud et al., 2013), suggesting that KYP, SUVH5 and SUVH6 repress transcription by directing CHG methylation via CMT3 DNA methyltransferase. The H3K9 demethylase gene *ibml* mutations display ectopic CHG DNA methylation and aberrant DNA methylation in *ibml* mutants can be suppressed by mutants in *KYP* or *CMT3* (Saże et al., 2008b). All of these illustrate the tight correlation between H3K9me2 and DNA methylation. In addition, DRM2 maintains CHH methylation through a small interfering RNA (siRNA)-driven signal in a process known as RNA-directed DNA methylation (RdDM) (Law et al., 2010). DRM2-dependent RdDM relies on two plant specific RNA polymerases: RNA Polymerase IV and V (Pol IV and V). It is found that Pol IV occupancy requires a factor, *SAWADEE HOMEODOMAIN HOMOLOG1 (SHHI)*, which is a dual histone modification sensor, preferentially binding to histones containing H3K9 methylation.
as well as lacking in H3K4me2/me3 (Law et al., 2011; Law et al., 2013). On the other hand, mutations of *JMJ14*, *LDL1* and *LDL2* (three H3K4 demethylases) reduce non-CG DNA methylation at RdDM targets accompanied by an increase in H3K4 methylation (Deleris et al., 2010; Greenberg et al., 2013), suggesting that H3K4 methylation antagonizes DNA methylation.

### 1.6 Chromatin remodeling

ATP-dependent chromatin remodeling is an essential aspect of chromatin dynamics that leads to conformational changes in nucleosome assembly and positioning (Figure 7). Chromatin remodeling process is mediated by a large family of SWI/SNF related enzymes in an energy-dependent manner. The term SWI/SNF stems from the two independent screening in yeast that characterize the genes affecting the mating-type switching (SWI) and sucrose fermentation (Sucrose Non-Fermenting, SNF) pathway (Neigeborn and Carlson, 1984; Stern et al., 1984). There are four main conserved classes of SWI/SNF chromatin remodelers that utilize ATP hydrolysis to alter histone-DNA contacts and share a conserved ATPase domain. The ATPase domain is comprised of two parts, the DExx and HELICc regions, which are separated by a linker. The four classes are distinguished according to the unique domains outside the ATPase motif and their specific associated subunits (Figure 7).

![Figure 7. The chromatin remodeling families and chromatin remodeling functions](Clapier and Cairns, 2009). Left: Chromatin remodeler families. All remodeler families contain a SWI2/SNF2-family ATPase subunit. The differences among each family are the unique
domains residing within, or adjacent to, the ATPase domain. Right: The different outcomes of ATP-dependent chromatin remodeling. Remodelers can assist in chromatin assembly generating room for additional deposition (a). Remodeler action on a nucleosome array results in two categories: (b) site exposure, in which a site (red) for a DNA-binding protein (DBP) becomes accessible by nucleosomal sliding (repositioning), or nucleosomal eviction (ejection) or localized unwrapping, and (c) altered composition, in which the nucleosome content is modified by dimer replacement or through dimer eviction.

SWI/SNF chromatin remodelers have been mostly conserved through evolution across yeast, animals and plants kingdoms (Flaus et al., 2006; Narlikar et al., 2013). Based on the presence of ATPase/helicase domain, there are 42 potential SWI/SNF2 chromatin remodelers (http://www.chromdb.org/index.html) in Arabidopsis. Those that have been studied are indicated in Figure 8.

Figure 8. Phylogenetic relationship and domain structure of the major SNF2 family members in Arabidopsis (Gentry and Hennig, 2014).

1.6.1 SWI/SNF class—SYD, BRM and MINU1/2 in Arabidopsis

The SWI/SNF class contains a bromodomain at the C-terminal, that binds to acetylated N-terminal histone region, besides a helicase-SANT (SWI3, ADA2, NcoR, TFIIIB) domain and an ATPase domain (Hassan et al., 2002; Martens and Winston, 2003). This is consistent with the fact that HAT complexes stabilize SWI/SNF nucleosome binding at the promoter region (Hassan et al., 2001). This family has many activities, for instance it slides and evicts nucleosome at many loci but lacks
roles in chromatin assembly (Clapier and Cairns, 2009). Proteins in this class include
SMARCA4 (BRG1) and SMARCA2 (BRM) in human, Brahma in Drosophila and
Swi2/Snf2 and Sth1 in S. cervisiae. These proteins are mostly identified as
transcriptional activators and several studies reveal the sequential recruitment of HAT
and SWI/SNF complexes to promote transcription (Yudkovsky et al., 1999; Dilworth
et al., 2000). However, there is also evidence showing that SWI/SNF complex directly
repress transcription of some genes (Martens and Winston, 2003).

Arabidopsis SPLAYED (SYD/CHR3), BRAHMA (BRM/CHR2),
MINU1/CHR12 and MINU2/CHR23 belong to the SWI/SNF class. SYD and BRM
(3574 and 2193 amino acids, respectively) are large proteins; MINU2 and MINU3
(1132 and 1054 amino acids, respectively) are significantly smaller. Only BRM has a
C-terminal region that resembles a bromodomain domain, which is found to target
remodeling complexes to hyperacetylated chromatin in yeast (Kasten et al., 2004;
Jerzmanowski, 2007).

Loss of function alleles of SYD were first identified by genetic screening for
mutants that enhanced the lfy phenotype (Wagner and Meyerowitz, 2002). LEAFY
(LFY) is a meristem identity gene that is required for switching from vegetative to
reproductive development (Weigel et al., 1992). syd null mutants exhibit pleiotropic
developmental defects including stem cell maintenance, patterning (alteration of leaf
polarity, flower morphogenesis and ovule development), developmental transitions
(precocious onset of reproductive development) and growth (small stature, slow
growth and reduced apical dominance) (Wagner and Meyerowitz, 2002). SYD represses
LFY activity prior to the floral transition, whereas it functions as a
co-activator with LFY in the transcriptional regulation of class B and C floral
homeotic genes (Wagner and Meyerowitz, 2002). SYD is required for reproductive
shoot apical meristem (SAM) by directly regulating the expression of WUS (Kwon et
al., 2005).
BRM was originally identified by a genetic screen for mutants that exacerbated the defect of cotyledon separation in cuc2 (Kwon et al., 2006). syd and brm null mutants exhibit both similar and distinct developmental defects, indicating partially functional redundancy. For example, both single mutants share short stature and delayed growth. The double mutant syd brm reveals embryo lethality but the single not (Bezhani et al., 2007). Although both are required for flower patterning and cotyledon separation, BRM and SYD may control different molecular events. During the formation of cotyledon separation, BRM upregulates the transcription of all three CUC genes, whereas SYD only upregulates the expression of CUC2 (Kwon et al., 2006). During the initiation of flower patterning, the temporal recruitment of SYD to AP3 and AG is similar to LFY, whereas the temporal binding of BRM is different (Wu et al., 2012). In addition, BRM has also some specific role. For example, brm mutants strongly inhibit the primary root elongation and promote more lateral roots and secondary root branches. Some studies reveal that the phenotype of brm mutant is similar to that of swi3c, suggesting that they may work in the same complex, which is confirmed by yeast two hybrid assays (Farrona et al., 2004; Sarnowski et al., 2005; Hurtado et al., 2006; Archacki et al., 2009).

MINU1 and MINU2, other two SNF2/SWI smaller members, also have redundant roles in plant development. No significant phenotype has yet been characterized in single mutant, however, the double mutants show embryonic lethality which is associated with increased expression of WUSCHEL and WOX5 (Sang et al., 2012).

1.6.2 ISWI class—CHR11 and CHR17 in Arabidopsis

The ISWI class takes its name from the Drosophila ISWI (Imitation Switch). In Drosophila, this unique member can belong to three different complexes: NURF (nucleosome-remodeling factor), CHRAC (chromatin-accessibility complex) and ACF (ATP-dependent chromatin assembly and remodeling factor) (Tsukiyama and Wu, 1995; Ito et al., 1997). All have chromatin remodeling activities and participate
in transcription regulation (Corona and Tamkun, 2004). The ISWI members possess a SANT adjunct to a SLIDE domain (SANT-like ISWI) at the C-terminus, both of which together form a nucleosome recognition module that binds to an unmodified histone tail and DNA component of nucleosomal substrates (Boyer et al., 2004). Many ISWI complexes (ACF, CHRAC) optimize nucleosome spacing to promote chromatin assembly and repress the gene transcription. However, certain complexes (NURF) can randomize spacing, which can assist in RNAPII transcription (Clapier and Cairns, 2009, 2012).

\textbf{CHR 11} and \textbf{CHR17} encode two ISWI proteins in \textit{Arabidopsis}. Both have conserved domains, HAND, SANT and SLIDE in the C-terminal. CHR11 is highly expressed in sporophytic and gametophytic tissues during reproductive development (Huanca-Mamani et al., 2005). Therefore, CHR11 is shown to be required for haploid nuclear proliferation during megagametogenesis and cell expansion during the sporophytic phase (Huanca-Mamani et al., 2005). One study shows that CHR11 and CHR17 physically interact with RLT1 and RLT2, two plant-specific DDT-domain containing proteins, together in preventing vegetative-to-reproductive transition by regulating several key genes such as \textit{FT}, \textit{SEP3} (Li et al., 2012). It is also found that the SLIDE domain of CHR11 and the DDT domain of RLT1 together with an adjacent sequence are responsible for the interaction (Dong et al., 2013).

\textbf{1.6.3 INO80 class —INO80 and PIE1 in Arabidopsis}

INO80 class of chromatin remodelers was first identified from \textit{S. cerevisiae} which is required for growth in absence of inositol (Ebbert et al., 1999). There are two INO80 members \textit{Ino80} and \textit{Swr1} in yeast, and three homologous genes \textit{INO80}, \textit{SRCAP} (SNF2-related CREB-activator protein) and \textit{p400} in humans. One of the structural characteristics of this class is a large insertion in the middle of ATPase domain, to which the helicase-related (AAA-ATPase) Rvb1/2 proteins and one actin-related protein (ARP) bind. INO80 complex has different functions including transcription activation and DNA repair (Shen et al., 2000). Although SWR1 is highly related to
INO80, it is unique in reorganizing nucleosome by recruitment and exchange of H2A.Z variant (Krogan et al., 2003; Mizuguchi et al., 2004).

*Arabidopsis* encodes one homolog of Ino80 protein. Ino80 mutant reduces the homologous recombination (HR) frequency to 15% of that in wild type. However it does not seem to affect other DNA repair pathways (Fritsch et al., 2004). This is unlike the situation of yeast Ino80 that is involved in both HR and non-HR DNA repair events. Like yeast Ino80, *Arabidopsis* INO80 regulates a subset of genes not functionally related to HR, suggesting its dual role in transcription and DNA repair (Fritsch et al., 2004). *Swr1* is required for replacement of histone H2A with the H2A.Z variant in yeast. PIE1 (*PHOTOPERIOD-INDEPENDENT EARLY FLOWERING 1*) encodes the single representative of SWR1 gene in *Arabidopsis*. pie is originally identified as a suppressor of FRIGIDA-dependent late flowering (Noh and Amasino, 2003). Similar to homolog in yeast, PIE1 as part of SWR complex is responsible for deposition of H2A.Z at multiple loci (Choi et al., 2007; March-Diaz et al., 2008). It is also found that PIE1 plays important roles in somatic DNA repair and during meiosis (Rosa et al., 2013). *Arabidopsis* characterized SWI/SNF2 remodelers are summarized in Table 4.

<table>
<thead>
<tr>
<th>Family</th>
<th>Protein</th>
<th>AGL code</th>
<th>Mutant phenotype</th>
<th>Aliases</th>
</tr>
</thead>
<tbody>
<tr>
<td>SNF2</td>
<td>SYD</td>
<td>A1g28330</td>
<td>Floral organ defects, loss of SAM, slow growth, ovule growth arrest</td>
<td>CHR3</td>
</tr>
<tr>
<td></td>
<td>BRM</td>
<td>A1g46020</td>
<td>Increased arrest in early development, slowed growth, delayed development</td>
<td>CHR2, CHA2</td>
</tr>
<tr>
<td></td>
<td>MINU1</td>
<td>A3g00610</td>
<td>Embryonic lethality, stem cell maintenance defects</td>
<td>CHR12</td>
</tr>
<tr>
<td></td>
<td>MINU2</td>
<td>A5g19310</td>
<td></td>
<td>CHR23</td>
</tr>
<tr>
<td>ISWI</td>
<td>CHR11</td>
<td>A3g06400</td>
<td>Reduced embryo size</td>
<td></td>
</tr>
<tr>
<td></td>
<td>CHR11, CHR17</td>
<td>A2g06400, A5g18620</td>
<td>Early flowering, reduced adult size</td>
<td>CHR13</td>
</tr>
<tr>
<td>SWR1</td>
<td>PIE1</td>
<td>A3g12810</td>
<td>Early flowering in short day</td>
<td></td>
</tr>
<tr>
<td>INO80</td>
<td>INO80</td>
<td>A3g57300</td>
<td>Reduced homologous recombination</td>
<td>CHD3, CHR5</td>
</tr>
<tr>
<td>CHD</td>
<td>PKR1</td>
<td>A2g25170</td>
<td>Thick opaque root, reduced apical dominance, shortened hypocotyl</td>
<td>CHD3, CHR5</td>
</tr>
<tr>
<td></td>
<td>PKR2</td>
<td>A4g21900</td>
<td>Exacerbate pld hypocotyl shortening</td>
<td>CHR4</td>
</tr>
<tr>
<td></td>
<td>CHR5</td>
<td>A2g13370</td>
<td>Exacerbate pld hypocotyl shortening and root phenotype</td>
<td>CHR7</td>
</tr>
</tbody>
</table>

Table 4. Summary of the major SWI/SNF2 chromatin remodelers and their mutant phenotypes in *Arabidopsis* (Gentry and Hennig, 2014).
1.6.4 CHD class

CHD chromatin remodeling proteins is named based on the three characteristic domains: an N-terminal pair of Chromodomains, a central Helicase-like ATPase motor, and a C-terminal DNA binding domain (Lusser and Kadonaga, 2003). The chromodomain is a well conserved ancient structural motif, since it can be found in a vast array of organisms as diverse as protists, plants, amphibians, and mammals (Eissenberg, 2001). Yeast has only one CHD protein (Chd1), whereas other high organisms such as fly, human and plants have several CHD proteins, some of which can be in large functional complex. Based on the structure and function, CHD proteins have been broadly divided into three separate subfamilies (Hall and Georgel, 2007). Subfamily I proteins (CHD1 and CHD2 in humans) are the prototypical examples of the family and do not contain additional identified functional domains. Subfamily II (CHD3 and CHD4) is characterized by the presence of plant homeodomain (PHD)-zinc-finger domain and in the absence of a clear DNA-binding domain (Hall and Georgel, 2007). Subfamily III (CHD 5-9 in humans) is less defined structurally and far less studied compared to the other two subgroups.

Besides CHD proteins, the chromodomain has also been identified in other chromatin associated proteins such as HP1 (Brasher et al., 2000) and Polycomb (Ingram et al., 1999; Brehm et al., 2004). The chromodomain of human CHD1 binds to H3K4me2 or me3 (Flanagan et al., 2005; Sims et al., 2005). In contrast, the chromodomain of Mi-2 (CHD3) seems to recognize DNA rather than methylated histone tails (Brehm et al., 2004). The ATPase domain is required for the remodeling of nucleosomes through histone displacement (Durr and Hopfner, 2006) or histone octamer sliding (Becker and Horz, 2002). The ATP hydrolysis energy is transduced into the conformational stress necessary to remodel chromatin (Pazin and Kadonaga, 1997). Thus the ATPase domain serves as a DNA-translocating motor to break histone-DNA contacts and release histones from nucleosomes (Durr and Hopfner, 2006). Of the 3 defined domains for CHD proteins, the DNA-binding domain is by far the least conserved. This domain is fairly well defined in CHD1, whereas CHD3/4, as
part of the Nucleosome remodeling and deacetylase (NuRD) complex, may also gain DNA binding ability through interactions with other subunits of the complex. Moreover, the PHD domains of CHD3/4 can bind histone H3 and affect interactions with nucleosomes (Bienz, 2006). Some CHD remodelers have the ability to slide or evict nucleosomes to promote transcription, however, others play repressive roles such as vertebrate Mi-2/NuRD complex, which contains histone deacetylases (HDAC1/2) and methyl CpG-binding domain (MBD) proteins (Hall and Georgel, 2007).

1.6.4.1 The function of CHD1 protein

The subfamily I member CHD1 was initially thought to be integral to transcriptional activity. As mentioned above, the chromodomain of human CHD1 was found to specially bind to H3K4me3. Presently, there is in vitro evidence both for (Pray-Grant et al., 2005) and against (Sims et al., 2005) Chd1 binding to H3K4me in budding yeast S. cerevisiae. The fission yeast S. pombe Chd1 orthologues Hrp1 and Hrp3 may interact and bind to H3K4me via the chromodomains of Hrp3, which have all the consensus residues required for methyl-lysine binding (Opel et al., 2007). In Drosophila melanogaster, the chromodomain of CHD1 is critical for chromatin remodeling activity but is less important for localization to chromatin (Morettini et al., 2011). The crystal structural and biochemical studies show an autoregulated domain organization of S. cerevisiae Chd1 (Narlikar et al., 2013). The chromodomain contacts the two lobes of ATPase domain and inhibits the ATPase motor (Hauk et al., 2010). In contrast, the DNA binding element, containing homology to SANT and SLIDE domains, contributes to positively regulate ATPase activity (McKnight et al., 2011). In vitro assays reveal that Chd1 has the ability to assemble, remodel, slide and promote regular spacing of nucleosomes (Lusser et al., 2005; Stockdale et al., 2006).

Chd1 plays important roles in transcription processes including initiation, elongation and termination (Alen et al., 2002; Simic et al., 2003; Biswas et al., 2007; Quan and Hartzog, 2010). It has been shown that human CHD1 associates with the pre-initiation transcription complex through interactions with Mediator in vitro (Lin et
Yeast Chd1 is found to be a factor required for remodeling the nucleosomal PHO5 promoter and for transcriptional activation of the gene (Ehrensberger and Kornberg, 2011). In fly and yeast, CHD1 is localized to a transcriptionally active gene and physically interacts with elongation factors and RNA Polymerase II (Simic et al., 2003; Srinivasan et al., 2005). Yeast Chd1 is also an essential factor for chromatin structure at the ends of genes at transcription, and transcriptional termination fails to occur in its absence (Alen et al., 2002).

CHD1 is a chromatin remodeler which participates in diverse biological processes. In Drosophila, although chd1-mutant zygotes are viable and display only a mild notched-wing phenotype, chd1-null male and female are sterile (McDaniel et al., 2008). In fact, maternal Chd1 in Drosophila is required for incorporation of H3.3 into the male pronucleus during early development after fertilization. Failure to incorporate H3.3 may render the paternal genome unable to participate in mitosis in the zygote, resulting in non-viable haploid embryos (Konev et al., 2007). In mice, Chd1 is essential for embryonic stem (ES) cell pluripotency and the formation of induced pluripotent stem cells (Gaspar-Maia et al., 2009). Chd1 mice mutants show an increase in the heterochromatic mark H3K9me3 and the ES cells display a tendency towards neuronal differentiation (Gaspar-Maia et al., 2009). CHD1 is also found to work as a tumor suppressor, as deletion or mutation of Chd1 is associated with prostate cancer, with cells displaying an increase in invasiveness (Huang et al., 2012).

Recent study points to a critical role for Chd1 in nucleosome positioning in vivo. As mentioned above, nucleosomes typically show a stereotypic organization over most genes: a nucleosome free region just upstream of the TSS followed by a regular nucleosomal array over the coding region. However, in the absence of S. cerevisiae Chd1, the nucleosome positioning is largely lost over gene bodies (Gkikopoulou et al., 2011). Specially, NFR and +1 nucleosome over the transcribed regions are minimally affected, but downstream nucleosomes (particularly those starting at the +3 nucleosome) were dramatically delocalized in chd1 mutants (Figure
9) (Gkikopoulos et al., 2011). This is consistent with in vitro data that Chd1 is able to space nucleosome arrays on plasmid DNA in vitro (Lusser et al., 2005). A similar situation is observed in S. pombe, as the deletion of Chd1 homologs, Hrp1 and Hrp3, interrupts nucleosome spacing (Figure 9) (Hennig et al., 2012; Pointner et al., 2012; Shim et al., 2012).

In S. cerevisiae, loss of Chd1 impairs nucleosome reassembly coupled with H2B monoubiquitination (Lee et al., 2012). Loss of Chd1 results in a substantial loss of H2Bub levels, and nucleosomal occupancy is reduced in gene bodies in both chd1 and h2b mutants, suggesting that Chd1 may positively regulate gene expression through promoting nucleosome reassembly coupled with H2B monoubiquitination (Lee et al., 2012). Consistent with a role for Chd1 in maintaining chromatin structure at active genes, Chd1 is also reported to prevent cryptic transcription within gene bodies in S. pombe, as the deletion of hrp1 and hrp3 causes strong, genome-wide accumulation of antisense transcripts (Hennig et al., 2012; Shim et al., 2012). Furthermore, Chd1 is also involved in histone exchange in gene body in Drosophila and yeast (Radman-Livaja et al., 2012; Smolle et al., 2012). It is possible that irregular spacing of nucleosomes in chd1 mutants renders it prone to dissociation as a result of collisions between and adjacent nucleosomes. Transient dissociation of histones provides an opportunity for exchange with the soluble pool of nascent histones (Radman-Livaja et al., 2012; Smolle et al., 2012; Narlikar et al., 2013).
CHAPTER 1—GENERAL INTRODUCTION

Genome-wide mapping of S. cerevisiae Chd1 binding on native chromatin shows that Chd1 is highly enriched in NFRs, although it acts in activated gene body (Gkikopoulos et al., 2011; Zentner et al., 2013). In light of these data, Chd1 plays essential roles in regulating nucleosome dynamics during transcription at different levels as shown in Figure 10.

**Figure 10. A model for Chd1 in regulating nucleosome dynamics during transcription.**

<table>
<thead>
<tr>
<th>5’ functions</th>
<th>Elongation functions</th>
<th>3’ functions</th>
</tr>
</thead>
<tbody>
<tr>
<td>Chd1 is localized at the 5’end of active genes.</td>
<td>Chd1 is colocalized with RNApolII via interaction with known transcription elongation factors.</td>
<td>Chd1 is enriched at the 3’NFR in S. cerevisiae.</td>
</tr>
<tr>
<td>Chd1 is recruited by H3K4me2/3 and mediator in mammals and by the PAF1 complex in yeast.</td>
<td>Loss of Chd1 interrupts nucleosome positioning in yeast. Chd1 prevents cryptic transcription within gene bodies in S. pombe. Chd1 regulates histone exchange at gene body in Drosophila and yeast. Also, loss of Chd1 reduces H2B monoubiquitination in yeast and human.</td>
<td>Chd1 is involved in the termination of RNAPIII transcription in yeast.</td>
</tr>
<tr>
<td>Chd1 may function in nucleosome disassembly at promoters.</td>
<td>Chd1 regulates nucleosome organization during transcription combined with repressing cryptic transcription and histone turnover.</td>
<td>Chd1 is also required for proper termination of rDNA transcription by RNAPI in S. cerevisiae</td>
</tr>
</tbody>
</table>

**1.6.4.2 Plant CHD proteins—PKL, PKR1, PKR2 and CHR5**

Phylogenetic analysis reveals that there is only one CHD1 protein (CHR5) in the genome of Arabidopsis, no CHD2 subfamily protein exists in plants, in contrast, three members belong to CHD3 subfamily (Figure 11) (Hu et al., 2012). In plant, CHD1 protein (CHR5) has not been studied.

Among plant CHD3 members, PICKLE (PKL) is the most studied. The hallmark of pkl seedlings is a green, tuberous and opaque region at the primary root, referred to as the “pickle root” (Figure 12) (Ogas et al., 1997). Pickle primary roots can express numerous embryonic differentiation characteristics such as expression of storage protein genes and accumulation of storage lipids and undergo spontaneous somatic embryogenesis (Ogas et al., 1997; Henderson et al., 2004). This pickle root phenotype is related to fail to repress embryo identity genes, such as LEC1, LEC2,
ABI3, and FUS3 after seed germination (Figure 12) (Ogas et al., 1999; Zhang et al., 2008; Aichinger et al., 2009; Zhang et al., 2012).

PKL contributes to other developmental processes in addition to repression of embryonic traits. PKL plays a role in repression of ectopic stipules and meristems in leaf tissue (Hay et al., 2002). PKL is involved in repressing meristematic genes in carpel tissue (Eshed et al., 1999). Loss of PKL results in hypersensitivity to cytokinin with respect to callus growth and greening (Furuta et al., 2011). PKL is also required for proper root development and has been found to work in two somewhat opposing
ways: PKL is a negative regulator of auxin-mediated lateral root initiation by regulating \( \textit{ARF7/9} \) transcription (Fukaki et al., 2006) and yet also promotes root growth by increasing expression of root stem cell and meristem marker genes (Aichinger et al., 2011). Recently, PKL is found to be a repressor of photomorphogenesis by interacting with HY5 to regulate cell elongation-related genes in hypocotyls (Jing et al., 2013).

1.6.4.3 The mechanism of PKL regulating embryonic genes

In contrast to animal CHD3 proteins functioning in histone deacetylation, comparative genomic analyses reveal that PKL acts to promote trimethylation of histone H3 lysine 27 (H3K27me3) (Zhang et al., 2008; Zhang et al., 2012). As mentioned above, H3K27me3 is a repressive mark for gene expression in both plants and animals (Zheng and Chen, 2011). PRC2 is the main factor responsible for catalyzing trimethylation of H3K27 (Schwartz and Pirrotta, 2007; Schmitges et al., 2011). In \textit{Arabidopsis}, mutants of PRC2 genes substantially reduce H3K27me3 levels and exhibit profound developmental defects including the derepression of embryonic traits (Chanvivattana et al., 2004; Schubert et al., 2006; Bouyer et al., 2011). Presently, it is controversial how PKL represses embryo identity genes. Some results support that PKL directly associates and represses the embryonic genes by regulating H3K27me3 on the loci. In particular, PKL was found to present at the promoters of \( \textit{LEC1} \) and \( \textit{LEC2} \) during germination (Zhang et al., 2008; Zhang et al., 2012). Whereas, other results suggest that PKL represses embryonic traits in an indirect way. In this case, PKL, like a transcriptional activator, binds to and up-regulates PRC2 genes rather than embryonic genes (Aichinger et al., 2009).

1.7 Embryo development

Seed development is an intriguing, specific and crucial phase of angiosperm plant life cycle, which begins with a double fertilization process that occurs within the ovule and ends with a dormant seed primed to become the next plant generation. Embryo
development consists of the morphogenesis and maturation phases as shown in Figure 13. Morphogenesis refers to the differentiation of cell fates in initially equivalent cells, which results in an embryo established with the specification of the shoot root axis and the formation of discernible major organ and tissue systems (Capron et al., 2009).

Figure 13. Embryo development in seed plants (Braybrook and Harada, 2008).

Maturation, the second phase of zygotic embryogenesis, occurs exclusively in seed plants. Upon entering the maturation stage, embryo ceases cell division and continues growing by cell expansion filling up the entire seed. One of the characteristics of this phase is the synthesis and accumulation of carbohydrates, lipids, and seed storage proteins (SSP), which will provide nutrients to the growing seedling before the photosynthetic capacity is fully acquired (Miquel and Browse, 1998). The embryo also accumulates late embryogenesis abundant (LEA) proteins, dehydrins, and osmocompatible solutes, serving to protect the embryo from desiccation (Ingram and Bartels, 1996). Developmental arrest and the ability to withstand drying enable the embryo to remain in a quiescent or dormant state until the seed encounters a favorable set of conditions that promote germination (Bewley, 1997).

1.7.1 LEC1/AFL transcription factors

Genetic studies have uncovered a number of factors that act as positive regulators of seed developmental programs. Among them, LEC1/AFL (ABI3, FUS3, LEC2), as the main regulators, have been characterized at greater depth. The LEC and FUS3 were originally identified as regulators of cotyledon identity, as recessive mutations in these genes partially convert the cotyledons into vegetative leaves (Figure 14), hence, the name LEAFY COTYLEDONS (Meinke, 1992; Meinke et al., 1994). The name
FUSCA is derived from Greek meaning ‘to darken’, and is designated to mutant loci with dark seeds (Figure 14) (Keith et al., 1994). The dark color of the seed is due to the accumulation of anthocyanins in the embryo. Recessive mutations in \textit{abi3} were originally identified in screens aiming to identify mutants insensitive to ABA during germination (Koornneef et al., 1984). The \textit{LEC1/AFL} genes, as the master regulators of late embryogenesis and seed maturation, share overlapping but not identical mutant phenotypes (Parcy et al., 1997; Vicent et al., 2000; Harada, 2001). Mutants of these genes exhibit reduced dormancy and precocious germination of immature seeds. \textit{LEC1/AFL} can trigger the expression of genes of seed storage protein (SSP) and the oil body protein, as a consequence, the seeds of the mutants are desiccation intolerant and non dormant except \textit{lec2} embryo (Giraudat et al., 1992; Keith et al., 1994; Meinke et al., 1994; Stone et al., 2001). \textit{Lec2} mutants are desiccation tolerant, do not germinate precociously, and show a pattern of storage product accumulation closer to wild type than to other mutants (Keith et al., 1994; Meinke et al., 1994). Only \textit{abi3} mutants show ABA insensitivity and defects in chlorophyll degradation (Giraudat et al., 1992). The \textit{lec1}, \textit{lec2} and \textit{fus3} mutations cause partial conversion of cotyledons into leaf-like state by the development of trichomes and the partial leaf ultrastructure (Keith et al., 1994; Meinke et al., 1994). The differences of \textit{lec1} and \textit{fus3} embryos are restricted mostly on the frequency of stomata and the position of anthocyanin accumulation (Meinke, 1992; Keith et al., 1994). In general, the analyses of \textit{LEC1/AFL} mutations indicate these genes, as the main positive regulators during seed maturation, have redundant and distinctive roles in embryo formation, cotyledon identity, seed storage protein expression and desiccation tolerance.

\textbf{Figure 14.} Seed phenotype of mutants in \textit{lec1}, \textit{abi3}, \textit{fus3} and \textit{lec2} (Meinke, 1992; Keith et al., 1994; To et al., 2006).
1.7.1.1 Structure and targets of LEC1/AFL genes

LEC1/AFL genes encode two different classes of transcriptional factors. ABI3, FUS3 and LEC2 belong to the B3-domain transcription factor family, which are only found in plants. The conserved B3 domains have similar DNA binding specificities and recognize the RY/Sph I cis-regulatory motif (purine-pyrimidine, CATGCA as the core sequence), which is found in the many seed storage protein genes (Kroj et al., 2003; Monke et al., 2004; Roschztarttz et al., 2009). It explains why these regulators have partially redundant roles, as they are likely to share downstream targets. In contrast, LEC1 encodes a protein homologous to HAP3 subunit of CCAAT-binding protein complex (CBF), which is conserved among eukaryotes (Lotan et al., 1998; Lee et al., 2003). LEC1 is able to activate the expression of cruciferin C (CRC) seed storage protein when co-expressed with ABRE-binding bZIP transcription factors (Yamamoto et al., 2009). In general, LEC1/AFL proteins act through direct interactions with regulatory elements present in the promoters of maturation-related genes to control the various features of seed development.

1.7.1.2 Expression profiles of LEC1/AFL genes

In agreement with their embryonic mutant phenotypes, LEC1/AFL genes are primarily expressed in embryos as shown in Figure 15. LEC1 is expressed in seed (in both embryo and endosperm). Specially, LEC1 mRNA is present at the protoderm and is detected throughout the developing embryo by the bent-cotyledon stage (Lotan et al., 1998). LEC2 is expressed throughout the embryo in early stages but primarily to the hypocotyl and the embryo axis at later stages (Kroj et al., 2003; To et al., 2006). ABI3 is expressed broadly in embryo tissues throughout embryogenesis except the root meristem (To et al., 2006). FUS3 transcripts can be detected in apical region and suspensor of the globular early heart stage, as well as in the vasculature, root tip, aleurone of the mature embryo (Gazzarrini et al., 2004; Tsuchiya et al., 2004). LEC2 and ABI3 are also expressed in vegetative tissues, where ABI3 is involved in lateral meristem development (Rohde et al., 2000; Stone et al., 2001; Kroj et al., 2003; To et
LEC1/AFL genes also have distinctive temporal expression profiles (Figure 15). LEC1 is expressed at early stages of embryogenesis, followed by LEC2 (Stone et al., 2001; Kroj et al., 2003). FUS3 and ABI3 expression levels peak after the maximum of LEC2, with FUS3 levels decreasing before maturation and ABI3 levels remaining high throughout the late embryo development (Parcy et al., 1994; Luerssen et al., 1998).

Figure 15. Spatial and temporal expression pattern of LEC1/AFL in developing embryos. Left: Tissue-specificity of LEC1/AFL genes in embryo which are indicated in red. (Santos-Mendoza et al., 2008). Right: temporal expression pattern from the website http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi. (3 d, globular; 4 d, heart; 5 d, torpedo; 7 d, walking stick; 9 d, curled cotyledons; 10 d, green cotyledons).

1.7.2 A network of interacting LEC1/AFL factors

Genetic analysis has revealed the existence of a complex interacting network among the LEC1/AFL genes. According to a previously established model (To et al., 2006), LEC1 and LEC2 act upstream of ABI3 and FUS3, and promote their expression. LEC1 and LEC2 also regulate each other. ABI3 and FUS3 also mutually regulate their own expression (Figure 16) (To et al., 2006). However, these functional interactions may be of direct or indirect effects and the molecular mechanism still remains to be elicited. It was reported that LEC2 binds specially to the RY sequence on the promoter of AGAMOUS-Like15 (AGL15) in vitro and activates AGL15 expression in vivo (Figure 16) (Braybrook et al., 2006). AGL15 is a MADS domain transcriptional regulator accumulating in embryos (Wang et al., 2002). By using ChIP-chip approach, it was shown that AGL15 directly targets to LEC2, FUS3, ABI3 and activates their
expression (Figure 16) (Zheng et al., 2009). Similarly, it was confirmed that FUS3 directly binds to LEC1, ABI3, AGL15 and itself in vivo, and upregulates these target gene transcription levels (Figure 16) (Wang and Perry, 2013). The cross-regulation between these embryonic regulators partially explains the complex and overlapping phenotypes displayed by each mutant.

Figure 16. A model for LEC1/AFL regulatory interaction network during embryogenesis.

1.7.3 Epigenetic regulation of LEC1/AFL genes

Genetic analysis has revealed the importance of chromatin modification in the control of the expression of LEC1/AFL genes. As discussed above, PKL, the CHD3 chromatin remodeling factor, acts as a transcriptional repressor for LEC1/AFL genes during germination and vegetative phases. pkl mutant displays embryonic trait in the primary roots (Ogas et al., 1997). PKL-dependent repression of LEC1/AFL genes, to some extent, is associated with regulation of H3K27me3 levels (Zhang et al., 2008; Aichinger et al., 2009; Zhang et al., 2012). VP1/ABI3-LIKE (VAL, also known as HSI) 1-3 proteins also play negative roles in seed developmental programs (Suzuki et al., 2007). VAL genes encode B3 transcription factors, containing PHD-like and CW domains often associated with chromatin factors (Perry and Zhao, 2003; Bienz, 2006). Double mutants of val1val2 show strong embryonic phenotype including callus proliferation in shoot and root regions as well as arrested shoot apical meristem development that prevents formation of leaves and progression to vegetative development (Suzuki et al., 2007). The embryonic phenotype of val1val2 is associated
with de-repression of \textit{LEC1/AFL} genes in seedlings. The \textit{VAL} genes are independently identified as sugar signaling factors (\textit{HIGH-LEVEL EXPRESSION OF SUGAR-INDUCIBLE GENE}2 (\textit{HSI2}/\textit{VAL1}), \textit{HSI2-LIKE}1 (\textit{HSL1}/\textit{VAL2}), and \textit{HSI2-LIKE}2 (\textit{HSL2}/\textit{VAL3}) (Tsukagoshi et al., 2005; Tsukagoshi et al., 2007). Interestingly, in the \textit{hsi2 hsl1} background the expression of \textit{AFL} genes can be induced by sugar, suggesting that the \textit{AFL} genes may be involved in sugar signaling (Tsukagoshi et al., 2007). Recently, it is reported that H3K27me3 levels of \textit{LEC1}, \textit{FUS3}, \textit{ABI3} are reduced in \textit{val1val2}, accompanied with the decreased levels of H2Aub, indicating that \textit{VAL} proteins interact with Polycomb Repressive complex1 (PRC1) and recruit PRC1-mediated H2Aub to initiate repression of embryonic genes after germination (Yang et al., 2013).

\textit{LEC1/AFL} genes are epigenetically repressed after germination by both PRC1 and PRC2 via histone modifications. As mentioned before, PRC2 mutants \textit{clf swn and pie} result in neoplastic, callus-like structures during vegetative phase because of the elevated expression of \textit{LEC2}, \textit{FUS3}, \textit{ABI3} (Chanvivattana et al., 2004; Bouyer et al., 2011). \textit{Arabidopsis} PRC1, constituted of two RING1 proteins (AtRING1a and AtRING1b), Like Heterochromatin1 (LHP1), and three BMI proteins (AtBMI1a, AtBMI1b and AtBMI1c), functions in the modification of histone H2A mono-ubiquitination (H2Aub) (Sanchez-Pulido et al., 2008; Bratzel et al., 2010; Chen et al., 2010). Similar to \textit{PRC2} mutants (\textit{clf swn, fie}), the double mutants \textit{AtRING1a AtRING1b, AtBMI1a AtBMI1b} show the embryonic traits in somatic tissues, which is associated with increased \textit{LEC1/AFL} gene expression, indicating that PRC1 represses the embryonic program after germination (Bratzel et al., 2010; Chen et al., 2010). Recently, it is shown that H3K27me3 at \textit{LEC1/AFL} genes are strongly reduced in \textit{val1 val2} and \textit{atBMI1a atBMI1b atBMI1c}, while H2Aub level at these genes is significantly decreased in \textit{val1 val2} but not in \textit{emf1} and \textit{clf swn}, indicating that \textit{VAL} proteins and AtBMI1-mediated H2Aub first initiate repression of seed maturation genes and then the repression is maintained by PRC2-mediated H3K27me3 (Figure 17) (Yang et al., 2013).
On the other hand, the histone deacetylase hda6 hda19 double mutants show growth arrest and somatic embryo formation, and this embryonic phenotype can be suppressed by the lec1, abi3 and fus3 mutations suggesting that LEC1, ABI3 and FUS3 expressions are repressed by HDA6 and HDA19 (Tanaka et al., 2008). Recently, it is found that HDA19 interacts with HSL1 (VAL2) in vitro and in vivo (Zhou et al., 2013). HDA19 could directly bind to the chromatin of the seed maturation genes and the ectopic expression of these genes in hda19 seedlings is associated with increased levels of H3ac, H4ac and H3K4me3 and decreased levels of H3K27me3, similar to that of hsl1. These results suggest that HDA19 and HSL1 may act together to repress seed maturation gene expression during germination. The embryonic lethal phenotype of hsl1 hda19 double mutants also indicates that HDA19 and HSL1 may play a vital role during embryogenesis (Zhou et al., 2013).

LEC2 and FUS3 expressions are also regulated by microRNA, as mutation of DICER-LIKE1 leads to premature expression of the maturation program during early embryogenesis accompanied with elevated levels of LEC2 and FUS3, indicating the microRNA processing machinery negatively regulates LEC2 and FUS3 transcription during early embryogenesis (Willmann et al., 2011).

Recently, it is found that BRM, a SNF2 chromatin remodeling factor, has a role in repressing ABI5 expression after seed germination and during vegetative development and ABI3 during seed germination. BRM is strongly associated with the region of ABI5 locus occupied by the +1 nucleosome. Loss of BRM activity leads to
destabilization of a nucleosome at *ABI5* locus, indicating that BRM represses *ABI5* transcription by promoting high occupancy of the +1 nucleosome and by directing this nucleosome from a more favorable predicted position to a position more proximal to the TSS (Han et al., 2012).

In general, the above data have shown that epigenetic modifications play important roles in the repression of *LEC1/AFL* genes especially during and after seed germination. However, little is known concerning how these transcription factors are activated during seed development. In particular, the mechanism of initiation and establishment the activate state of *LEC1/AFL* genes during embryogenesis and maturation process is not understood and remains to be elucidated.
1.8 Objective and Organization of this thesis

Chromatin remodeling and histone modification play important roles in the establishment and dynamic regulation of gene expression states. However, little is known regarding to the regulatory mechanism of chromatin modification and remodeling that control gene expression involved in plant development and responses to environmental cues. My thesis work concerns the analysis of a chromatin remodeling factor CHR5 and a histone demethylase gene JMJ15 for their function in regulating chromatin structure or in resetting chromatin modifications that control the expression of plant developmental and stress responsive genes.

The first result chapter (Chapter 2) aims to analyze the temporal and spatial expression pattern and function of CHR5 in late embryogenesis and seed maturation process. The key points of this part were (1) the expression pattern of CHR5 in plant development; (2) characterization of chr5 T-DNA mutants; (3) the effect of CHR5 mutations on the LEC1/AFL transcription during embryogenesis; (4) the antagonistic role between CHR5 and PKL in the control of LEC1/AFL gene expression; (5) the chromatin mechanism of LEC1/AFL gene regulation by CHR5 and PKL during seed maturation program.

The objective of the second part of results (Chapter 3) is to investigate the biological and molecular function of JMJ15 in plant development. To examine the biological function, JMJ15 tissue expression pattern and jmj15 mutants (gain-of-function and loss-of-function mutants) were characterized. The effects of the mutations on plant growth and development were evaluated. For the molecular function, the transcriptome of jmj15 overexpression mutants was analyzed by microarray followed by RT-PCR validation. The de-regulated genes were analyzed for GO function category classification, for comparison with microarray data from atx1/sdg2 mutants, and for enrichment for histone H3K4 modification.

Finally a general discussion section is provided that discusses the main results and outlines the perspectives of the work.
CHAPTER 2

Functional analysis of a chromatin remodeling factor CHR5 in *Arabidopsis*
CHAPTER 2—CHR5

Introduction

CHR5 belongs to the CHD1 subfamily of chromatin remodeling factors, the function of which is not yet studied in plants. *LEC1/AFL* genes, as the master transcriptional factors that control seed development, have been found to be expressed during embryo development but repressed during vegetative phase by several negative epigenetic regulators including PKL (a CHD3 chromatin remodeler). However, the mechanism of activation of *LEC1/AFL* gene expression during embryogenesis is unknown.

In this part, I first studied the expression pattern of CHR5 by using transgenic plants containing *proCHR5-GUS* construct and RT-PCR approaches. The results showed that CHR5 was highly specifically expressed during late embryogenesis. To study CHR5 function in gene expression and plant development, I obtained 6 lines of *chr5* T-DNA insertion mutants and the complementation of a mutant allele with the *proCHR5-CHR5-HA* fusion construct was obtained. The analysis showed that *CHR5* was involved in the regulation of *LEC1/AFL* gene expression during embryo development and seed maturation process. In order to analyze the relationship between CHR5 and PKL in seed maturation gene expression, the double mutant *chr5 pkl* was generated and analyzed. The results indicate that CHR5 and PKL function antagonistically in the control of *LEC1/AFL* transcription during seed developmental and vegetative phases. The chromatin modifications of *LEC1/AFL* loci in *chr5* and *pkl* mutants were further detected, also confirming the opposite role of CHR5 and PKL in *LEC1/AFL* expression. Finally, the mechanism by which *CHR5* regulates *LEC1/AFL* genes was studied. The key points of this were (1) if CHR5 directly associates with *LEC1/AFL* genes during embryogenesis; (2) how CHR5 regulates the transcription level of *LEC1/AFL* genes—nucleosome positioning, histone modification or others. ChIP experiment proved that CHR5 directly binds to the promoter region of *FUS3* and *ABI3*. At the same time, CHR5 was shown to reduce nucleosome occupancy near the transcription start site (TSS) of *FUS3*.

This part of the results is written in an article that is currently submitted for publication.
Chromodomain, Helicase and DNA-binding CHD1 and CHD3 proteins act antagonistically to regulate seed maturation program in *Arabidopsis*

Running title: Regulation of embryo genes by CHD proteins
Chromodomain, Helicase and DNA-binding CHD1 and CHD3 proteins act antagonistically to regulate seed maturation program in *Arabidopsis*

2.1 Abstract

Chromatin modification and remodeling are the basis for epigenetic regulation of gene expression. LEAFY COTYLEDON1 (LEC1), LEAFY COTYLEDON 2 (LEC2), ABSCISIC ACID-INSENSITIVE 3 (ABI3), and FUSCA3 (FUS3) are key regulators of seed maturation and are expressed during embryo development but epigenetically repressed after seed germination. The CHD3 protein PICKLE (PKL) is involved in the epigenetic silencing of the genes. However, the chromatin mechanism that establishes the active state of the genes during embryogenesis is not clear. We show that the *Arabidopsis* CHD1-related gene, *CHR5*, displayed a similar expression pattern as *ABI3* and *FUS3* during embryo development. The mutation of the gene led to decreased expression of *LEC1, ABI3* and *FUS3* in developing seeds and reduced seed storage protein accumulation. Analysis of double mutants revealed an antagonistic function between *CHR5* and *PKL* in embryo gene promoter activity and seed storage protein accumulation. *CHR5* was directly associated with the promoters of *ABI3* and *FUS3* and *chr5* mutations led to increased nucleosome occupancy near the transcriptional start site. The results suggest that *CHR5* is involved in nucleosome occupancy to regulate embryo identity genes expression, which is counterbalanced by *PKL* during embryo development.
2.2 Introduction

Chromatin modification and remodeling are the biochemical basis for epigenetic regulation of gene expression. The nucleosome is the basic repeating unit of chromatin and is composed of an octamer of histones and a segment of 147 bp DNA. Histone modification such as histone lysine acetylation and methylation play important roles for gene activity. Histone lysine acetylation is generally involved in gene activation, whereas histone lysine methylation may have either a positive or a negative effect on gene expression (Berger, 2007; Mosammaparast and Shi, 2010). In plants tri-methylation of H3 lysine 4 (H3K4me3) is enriched at the 5’ end of actively transcribed genes, whereas tri-methylation of H3 lysine 27 (H3K27me3) marks repressed developmental and stress responsive genes (Liu et al., 2010; Li et al., 2013).

Chromatin remodeling involves altering histone-DNA contacts, sliding nucleosomes, and exchanging or removing histones and entire nucleosomes. Chromatin remodelers which are ubiquitous in eukaryotic cells (Flaus et al., 2006), are compositionally and functionally diverse, but they all share the presence of a subunit that belongs to the SNF2-like family of ATPases, among which are the Chromodomain, Helicase/ATPase and DNA-binding domain (CHD) proteins (Lusser and Kadonaga, 2003). Besides Saccharomyces cerevisiae that has only one CHD protein (Chd1), other higher eukaryotes have several CHD members that are divided into CHD1, CHD2 and CHD3 subfamilies (Hall and Georgel, 2007). The two chromodomains in CHD1 proteins are essential for recognition of di- or tri-methylated lysine 4 of histone H3 (H3K4me2/3) (Flanagan et al., 2005; Sims et al., 2005; Vermeulen et al., 2010). CHD1 proteins are implicated in gene expression at different levels (Ho and Crabtree, 2010). Recent results suggests that CHD1 proteins have both chromatin assembly and remodeling functions to direct the positioning of nucleosomes required for gene transcription (Gkikopoulos et al., 2011; Torigoe et al., 2013). In addition to the double chromodomains and the helicase/ATPase, CHD3 subfamily proteins contain one or two Plant Homeodomain (PHD) fingers at the N-terminus. CHD3 members in Drosophila melanogaster and mammalian cells are the central components of the Nucleosome Remodeling and histone Deacetylase (NuRD) or Mi-2 complexes regulating transcriptional repression (Hall and Georgel, 2007; Ramirez and Hagman, 2009). However, other studies revealed that CHD3 members
can also function as a transcriptional coactivator (Saether et al., 2007; Murawska et al., 2008).

Several CHD3 members are identified in plants (Hu et al., 2012). The *Arabidopsis thaliana* (*Arabidopsis*) CHD3 protein PICKLE (PKL) was initially found to repress embryonic traits after seed germination (Ogas et al., 1997). PKL functions as a transcriptional repressor of embryo identity genes such as *LEAFY COTYLEDON1 (LEC1)*, *LEAFY COTYLEDON 2 (LEC2)*, *ABSCISIC ACID-INSENSITIVE 3 (ABI3)*, and *FUSCA3 (FUS3)* in seedlings (Ogas et al., 1999; Zhang et al., 2008; Aichinger et al., 2009; Zhang et al., 2012). In contrast to animal CHD3 proteins, PKL is found to promote trimethylation of histone H3 lysine 27 (H3K27me3) over target genes rather than histone deacetylation (Zhang et al., 2008). But other results suggest that the PKL protein may be a transcriptional activator required for the expression of genes encoding Polycomb Repressive Complex2 (PRC2) that catalyzes trimethylation of H3K27 (Aichinger et al., 2009). Recent data revealed that the rice (*Oryza sativa*) CHD3 protein, CHR729, is a bifunctional chromatin regulator that recognizes and modulates H3K4 and H3K27 methylation over repressed tissue-specific genes (Hu et al., 2012). By contrast, only one CHD1 gene is found in the genome of *Arabidopsis* or rice (Hu et al., 2012). Its function in plant gene expression and development remains unknown.

LEC1 and the B3-domain ABI3, FUS3, and LEC2 (referred to as AFL) are key transcriptional regulators of zygotic embryo development (Giraudat et al., 1992; Lotan et al., 1998; Stone et al., 2001). These factors activate the seed maturation gene expression program in a complex network (Kagaya et al., 2005; Santos-Mendoza et al., 2008; Suzuki and McCarty, 2008; Monke et al., 2012; Wang and Perry, 2013). These genes are expressed specifically during embryo development and epigenetically repressed after seed germination primarily by PRC2-mediated H3K27me3 (Makarevich et al., 2006; Aichinger et al., 2009; Berger et al., 2011). *Arabidopsis* PRC2 mutants with reduced H3K27me3 display derepression of *LEC1* and *AFL* genes and embryonic traits in seedlings (Chanvivattana et al., 2004; Schubert et al., 2006; Bouyer et al., 2011). Recent data indicate that the E3 H2A monoubiquitin ligase activity of the Polycomb Repressive Complex1 (PRC1) that recognizes and binds to
H3K27me3 is also required for the post-germination repression of the genes (Bratzel et al., 2010; Yang et al., 2013).

Besides the epigenetic repression of the embryo identity or seed maturation genes after seed germination, little is known about the chromatin mechanism that establishes the active state of these genes during embryogenesis and seed development. In this work we show that the Arabidopsis CHD1 gene, known as CHR5, is expressed during embryo development and seed maturation and is directly involved in the activation of ABI3 and FUS3 expression. In addition, we show that CHR5 and PKL have antagonistic function in ABI3 and FUS3 expression in developing seeds. CHR5 binds to the promoter of ABI3 and FUS3 and regulates nucleosome occupancy near the transcriptional start sites of the genes, whereas PKL represses the expression of ABI3 and FUS3 genes during seed maturation. The data suggest that interplay between CHD proteins regulates seed maturation gene expression program.
2.3 Results

2.3.1 CHR5 is expressed during late embryogenesis

Analysis of microarray data suggested that CHR5 is highly expressed in developing and mature seeds, shoot apex and floral organs (http://bbc.botany.utoronto.ca/efp/cgi-bin/efpWeb.cgi?primaryGene=AT2G13370&modeInput=Absolute). To confirm the data, we produced >10 independent transgenic plants expressing the GUS reporter gene under the control of a 2 kb promoter region of CHR5. Most of the transgenic lines displayed a similar GUS staining pattern that was detected in seeds, seedlings, flower buds and floral organs such as carpel, stigma, stamen and pollen (Figure S1). In young seedlings GUS staining was mostly detected in root tip, shoot apex, and vasculature (Figure S1). In developing seeds GUS expression started at about late globular-triangular stages and gradually increased till the mature stage of embryogenesis (Figure 1A). To further study CHR5 expression in developing seeds, we analyzed CHR5 transcript levels by RT-qPCR using mRNA isolated from siliques from stage 3 to stage 10 as defined at https://www.genomforschung.unibielefeld.de/GF-research/AtGenExpress-SeedsSiliques.html. Stages 1 to 4 correspond to the zygote to globular stages of embryo development. The CHR5 transcript was undetectable before stage 4 (Figure 1B). After stage 4, the CHR5 mRNA level increased gradually till the embryo maturation stage (Figure 1B). This confirmed the GUS staining data and indicated that CHR5 is activated during embryo development, which roughly corresponded to that of the late AFL genes (i.e., FUS3 and ABI3) (Wang et al., 2007). These observations suggested that CHR5 might play a role in late embryo development and seed maturation.

2.3.2 chr5 mutants characterization

To study CHR5 function in gene expression and plant development, we characterized Arabidopsis T-DNA insertion lines of the gene in Columbia-0 (Col-0) and Wassilewskija (Ws) backgrounds (Figure S2). The insertions interrupted the production of the full length transcript of the gene (Figure S2). The mutants did not display any visible morphological defect, except a weak long hypocotyl phenotype in different light conditions (Figure S3).
CHAPTER 2—CHR5

Because *CHR5* expression was activated during embryo development, we examined whether the *chr5* mutations affected the expression of the embryo regulatory genes in developing siliques (at stage 6) of by RT-qPCR. Two mutant alleles, *chr5-1* and *chr5-6*, were selected for the analysis. In the mutants, the mRNA levels of *LEC1*, *FUS3* and *ABI3* were reduced compared to wild type, while that of *LEC2* was not clearly affected (Figure 2A). In addition, the expression of seed storage protein genes (i.e., 2S2, 7S1, *OLE1* and *CRA1*) which are downstream targets of LEC1 and AFL (Kagaya et al., 2005), was also reduced (Figure 2A). By contrast, the expression of *PIL5*, a *PHYTOCHROME-INTERACTING FACTOR3-LIKE* gene that inhibits seed germination (Oh et al., 2004), was not changed in the mutants (Figure 2A). To confirm the data, we analyzed the seed storage protein accumulations by SDS-PAGE according to previous description (Finkelstein and Somerville, 1990). Fifty seeds per genotype were used for protein extraction; one fifth of the extraction was loaded for the analysis. The analysis revealed a decrease of 2S albumin and 12S globulin proteins in mature seeds of the mutants compared to wild type (Col-0) (Figure 2B). More pronounced decrease was also detected in *abi3* and *fus3* loss-of-function mutants (Figure 2B).

To confirm the effect of *chr5* mutation on seed gene expression and storage protein accumulation, we made complementation tests by transforming *chr5-6* plants with the *pCHR5-CHR5-HA* fusion construct under the control of the 2.0 kb promoter region of *CHR5*. The production of the fusion protein in the complementation plants was detected by western blotting methods using the anti-HA antibody (Figure S4). The levels of seed storage proteins in *chr5-6* were restored to wild type levels in the complementation plants (Figure 2B), indicating that the decrease of storage proteins was caused by the mutation of *CHR5*. These data suggested that *CHR5* might be involved in the gene expression program of embryo development and seed maturation in *Arabidopsis*.

2.3.3 Antagonistic function between *CHR5* and PKL in seed maturation gene expression

The *pickle* (*pkl*) mutation derepresses embryo regulatory genes in young seedlings with the production of embryonic traits in the primary root of seedlings, accumulation
of seed storage reserves, and formation of somatic embryos (Ogas et al., 1997). However, this *pickle* root phenotype only occurs with a low penetrance (Ogas et al., 1997). To study functional interaction between *CHR5* and *PKL*, we generated *chr5-6 pkl* double mutants and examined the seedling root phenotype. The penetrance of the embryonic root in *pkl* (*pkl1* allele) (about 15%), revealed by Fat red dye staining of fatty acids present in embryonic roots, was decreased to about 5% in the double mutants (Figure 3A, 3B). Similar results were obtained in the *chr5-2 pkl1* double mutant (Figure S5). Ectopic expression of *LEC1*, *ABI3*, and *FUS3* in *pkl* seedlings or seedling roots was suppressed in the double mutants (Figure 3C, 3D), suggesting antagonistic actions of the two CHD proteins on the expression of *LEC1*, *ABI3* and *FUS3*. No clear decrease of *LEC2* ectopic expression in the double mutant siliques (Figure 3E), corroborated the observation that *CHR5* was not or weakly involved in the activation of the gene (Figure 2A).

In *pkl* siliques, the expression levels of *LEC1*, *ABI3* and *FUS3* were higher than in wild type (Figure 3E), indicating that *PKL* may also repress these genes during embryo and seed development. This was in agreement of gradual activation of the *PKL* gene during seed maturation (Fig. 1B). Consistently, a higher accumulation of seed storage proteins was detected in *pkl* compared to wild type (Figure 2B). In the siliques of the *chr5-6 pkl* double mutants, the expression of *LEC1*, *ABI3* and *FUS3* was lower than that in *pkl* (Figure 3E). In addition, the increased accumulation of seed storage proteins in *pkl* was restored to wild type levels in the double mutants (Figure 2B), further supporting the idea that *CHR5* and *PKL* have an opposite function to regulate the seed maturation gene expression program.

2.3.4 *CHR5* acted on the promoter of *ABI3* and *FUS3*

We next studied whether *chr5* and *pkl* mutations affected the expression pattern of the embryo regulatory genes during embryo development. Because of the similar expression pattern of *CHR5* with *ABI3* and *FUS3*, we chose the promoter region of *ABI3* and *FUS3* (with 5’-UTR) to control GUS expression (translational fusion) in transgenic wild type, *chr5-6* and *pkl* single and double mutant plants. A 4 kb promoter region of *ABI3* and a 2.2 kb promoter region of *FUS3* were used. Several (6-11) independent transgenic lines for each construct in each genotype were characterized.
GUS staining revealed that *ABI3* and *FUS3* promoters started to be active in the embryo during the late globular or early heart stages in the wild type (Figure 4A), which corresponded to the expression profile of the genes (Wang et al., 2007) indicating that the used promoter regions contained necessary elements for the expression patterns. We also noticed that the *FUS3* promoter was active in the suspensor in the early stages of embryogenesis. The *chr5* and *pkl* single and double mutations did not clearly alter the expression pattern during embryo development (Figure 4A). Quantification of the GUS transcripts in siliques (at stage 6) of several independent transgenic plants indicated that the promoter activities of both genes were reduced in *chr5-6*, but increased in *pkl* background compared to wild type (Figure 4B). In the double mutants, the promoter activities were lower than that in *pkl* (Figure 4A, 4B). These results confirmed the above data and revealed that *CHR5* and *PKL* act antagonistically to regulate the promoter activity of *ABI3* and *FUS3* in developing embryo.

### 2.3.5 CHR5 binds directly to the promoter region of *ABI3* and *FUS3*

To examine whether CHR5 was directly associated with the embryo regulatory genes, we isolated chromatin from *chr5-6* plants complemented by *pCHR5-CHR5-HA* (Figure S4). The chromatin fragments were immuno-precipitated with anti-HA and analyzed by qPCR using primer sets corresponding to several regions of *AFL* and *LEC1* loci and to *ACTIN2* gene and Ta3 transposon as controls (Figure 5). The analysis revealed that only the regions upstream to or near the transcription start site (TSS), not the gene body regions, of *ABI3* and *FUS3* were clearly enriched in the precipitated fractions (Figure 5), indicating that CHR5 was associated with the promoter and TSS of *ABI3* and *FUS3*. No association with *LEC1* or *LEC2* was detected, suggesting that CHR5 was not directly involved in their expression. The effect of *chr5* mutations on *LEC1* may be due to an indirect effect.

### 2.3.6 Chromatin modifications of *LEC1* and *AFL* loci in *chr5* and *pkl* mutants

To study whether *chr5* mutations affected histone modification on *LEC1* and *AFL* genes during seed development, chromatin fragments isolated from wild type and *chr5-6* developing seeds (from siliques at stage 6) were immunoprecipitated by
antibodies of H3K4me3 and H3K27me3 and analyzed by qPCR using primer sets corresponding to the 5’-UTR region of FUS3, ABI3, LEC1, LEC2 and, as a control, PIL5. The analysis revealed that LEC2 and PIL5 displayed relatively higher levels of H3K4me3 compared to the other genes (Figure 6A). However, there was no clear difference observed between the mutant and wild type. By contrast, relatively higher levels of H3K27me3 were detected on FUS3, ABI3 and LEC2 and LEC1 compared to the control genes RBCS and PIL5 (Figure 6B). The chr5 mutation led to about 2 fold increases of H3K27me3 on LEC1 and AFL (including LEC2) genes, but not on the control genes (Figure 6B). Similar assays with chromatin fragments directly isolated from siliques (stage 6) of the two chr5 mutant alleles confirmed the results (Figure 6C). These data suggested that CHR5 was not involved in modulating H3K4me3 for LEC1 and AFL activation during seed development. The increased H3K27me3 on LEC1 and the late AFL genes may be associated with their repression in chr5 mutants.

We also analyzed histone methylation in chr5 and pkl seedlings. The results revealed that the amount of H3K4me3 on LEC1, LEC2, FUS3 and ABI3 was not clearly altered in chr5-6, pkl and chr5 pkl compared to wild type, except some increase on LEC2 was observed in pkl plants (Figure S6). This corroborated the data obtained in developing seeds/siliques (Figure 6). In pkl seedlings that ectopically express LEC1 and AFL genes, H3K27me3 was reduced on LEC1 and LEC2, but not on ABI3 and FUS3 (Figure S6), confirming previous observations (Aichinger et al., 2009; Zhang et al., 2012). Unlike in developing seeds, the chr5 mutation did not lead to any clear change of H3K27me3 on the seed maturation genes in seedlings. In addition, the decrease of H3K27me3 on LEC1 and LEC2 in pkl was maintained in the chr5 pkl double mutants, suggesting that the antagonistic function of CHR5 and PKL on these genes expression in seedlings may not rely on the regulation of H3K27me3 level.

2.3.7 CHR5 may modulate nucleosome occupancy on FUS3 promoter

Recent results have shown that CHD1 protein is involved in nucleosome positioning and turnover and thus regulates transcription rate (Zentner et al., 2013). To study whether CHR5 was involved in chromatin structure of target genes, we next examined nucleosome positioning and occupancy at the FUS3 TSS region in chromatin isolated
from siliques (stage 6) using high-resolution micrococal nuclease (MNase) mapping (Chodavarapu et al., 2010; Han et al., 2012). We identified one nucleosome upstream of the likely nucleosome-free region (NFR) between -182 and -17 relative to TSS and two nucleosomes downstream of the NFR of \textit{FUS3}. NFR that is located just upstream of the TSS is commonly found in eukaryotic promoters. A typical nucleosome protects about 140-150 bp of genomic DNA from MNase digestion (Yen et al., 2012), as was the case for the three nucleosomes near the TSS of \textit{FUS3}. The upstream one was roughly located between -465 and -265, the two downstream ones protected from -40 to +97 and from 122 to 259 relative to the TSS (Figure 7). In \textit{chr5} mutants, we observed reproducibly a moderate increase in nucleosome occupancy at the three positions compared to wild type (Figure 7). This was consistent with the lower expression of \textit{FUS3} in the mutants. No alteration in positioning of the three nucleosomes was observed. Thus, CHR5 was likely to be required to reduce nucleosome occupancy near the NFR of \textit{FUS3}, which might contribute to increased activation of the gene in developing seeds.
2.4 Discussion

2.4.1 CHD1 (CHR5) and CHD3 (PKL) function in embryo/seed gene expression

In this work, we have shown that the Arabidopsis CHD1 gene CHR5 is involved in embryo regulatory gene expression and seed storage protein accumulation. The observations that chr5 mutations reduced the levels, but not patterns of LEC1 and AFL expression in developing embryo suggest that CHR5 may be mostly involved in modulating gene expression levels instead of defining expression pattern of the key regulatory genes. The CHR5 expression pattern is similar to that of ABI3 and FUS3 during embryo development (Figure 1) (Wang et al., 2007). However, expression of ABI3 and FUS3 has been detected in earlier stages (Le et al., 2010; Raissig et al., 2013). In addition FUS3 expression was first detected in the suspensor when the embryo was at octant stage and was not stained (Figure 4A.). Therefore, CHR5 expression in the seed partially overlaps with that of ABI3 and FUS3, suggesting that CHR5 may be involved in establishing a favorable chromatin environment to increase the expression levels of the seed maturation genes instead of initiating the transcriptional activation process. This is consistent with normal embryo development in the mutants. The high accumulation of CHR5 transcripts in mature embryo/seed and the effects of the mutation of the gene on seed storage protein accumulation suggest that, in addition to LEC1, AFL and the tested seed storage genes, CHR5 may regulate many other seed maturation genes. Nevertheless, unlike lec1, abi3 or fus3 loss-of-function mutants that display a wrinkled seed phenotype with accumulation of anthocyanin in lec1 and fus3 cotyledons or chlorophyll in lec1 and abi3, the chr5 mutant seeds germinated normally and did not display any visible abnormality. Possibly, the reduction (about 50%) of ABI3, FUS3, LEC1 expression and storage protein accumulation in chr5 mutants was not sufficient to lead to a seed phenotype.

In addition to developing seeds, CHR5 is also expressed in many rapidly growing organs/tissues, suggesting that the gene may be involved in other plant developmental processes. However, loss-of-function mutations of the gene did not produce any severe developmental defects. This is consistent with the observations that D. melanogaster chd1 mutant zygotes are viable and display only a mild notched-wing phenotype (McDaniel et al., 2008). In yeast, the phenotype associated with Chd1
deletion was also minor, whereas deletion of Chd1 together with two additional chromatin remodeling factor genes ISWI and ISW2 results in synthetic phenotypes (Tsukiyama et al., 1999). This indicates the existence of functional redundancy between CHD1 and other chromatin remodeling factors, which may explain partly the mild developmental phenotype observed in chr5 mutants.

Previous studies have shown that the Arabidopsis CHD3 protein PKL represses embryo regulatory genes after seed germination. The present data revealed that PKL also represses these genes during embryo development and seed maturation (Figure 2-4). Although PKL transcripts started to be detected after stage 4, its repressive function may act mostly during the maturation stages. Since the expression of PKL was sharply increased after stage 7 (Figure 1B), the repressive role of PKL may be effective during late embryogenesis as well. This is consistent with previous results showing that PKL-dependent repression of embryonic gene expression extends to late-embryogenesis genes during germination under stress or ABA (Perruc et al., 2007). The increase of pABI3-GUS and pFUS3-GUS expression in pkl developing seeds suggests that PKL may act on the promoter of the genes. However, it was shown that PKL is not directly involved in the repression of ABI3 (Aichinger et al., 2009), while recent data indicated that PKL is present at LEC1, LEC2 and FUS3 loci during germination to repress these master regulators of embryonic identity (Zhang et al., 2012). Increased ABI3 and FUS3 promoter activities in pkl may be mediated by LEC1 that was induced in pkl developing seeds (Figure 3E), and was previously shown to activate expression of ABI3 and FUS3 (Kagaya et al., 2005). As PKL is associated to the FUS3 locus (Zhang et al., 2012), the derepression of FUS3 promoter activity in pkl mutants suggests that the repressive function of PKL may act on the promoter of the gene, but it is not excluded that PKL may repress FUS3 promoter through an indirect effect.

The opposite function of CHR5 and PKL on LEC1 and AFL expression suggests that chromatin state and/or chromatin remodeling controlled by the CHD proteins plays an important role for the gene expression program of embryo and seed development. PKL is suggested to repress genes by promoting H3K27me3. The mild increases of H3K27me3 on LEC1 and AFL genes in chr5 mutant siliques/seeds might be related to antagonist actions of CHR5 and PKL during embryo development.
However, the suppression of ectopic expression of LEC1 and AFL in chr5 pkl seedlings was not accompanied by an increase of H3K27me3 (Figure S6). It is possible that increased H3K27me3 on LEC1 and AFL genes in chr5 developing seeds might be a consequence of the repression of the genes, as H3K27me3 can be deposited to mark down-regulated genes and to memorize the repressive state (Bonasio et al., 2010). Although CHD1 is reported to binds to H3K4me3 (Flanagan et al., 2005; Sims et al., 2005; Vermeulen et al., 2010), our analysis indicates that CHR5 is not involved in modulating H3K4me3 for LEC1 and AFL activation during seed development (Figure 6). Therefore, CHR5-mediated gene activation may act at different levels of chromatin modification or remodeling.

### 2.4.2 Mechanism of CHR5-mediated gene activation

CHD1 was initially thought to be integral to transcriptional activity. The relatively higher enrichment of the Arabidopsis CHD1 protein, CHR5, near the transcriptional start sites (TSS) of FUS3 and ABI3 is consistent with the recent data showing that S. cerevisiae Chd1 is enriched within the nucleosome free regions in the genome (Zentner et al., 2013). The enrichment of CHD1 proteins at TSS may be mediated through the interaction of their tandem chromodomain with H3K4me3, a hallmark of actively transcribed chromatin which is enriched at the TSS (Flanagan et al., 2005; Sims et al., 2005). However, we have shown that CHR5 targets only to the promoters of ABI3 and FUS3, but not that of LEC1, LEC2 or PIL5 (Figure 5). The underlying mechanism of the locus-specific targeting of CHR5 is not known. It is unlikely that the locus-specific targeting of CHR5 is only through interaction with H3K4me3 at TSS, as the two relatively highly H3K4me3-marked genes (i.e., LEC2 and PIL5) were not targeted by CHR5 (Figure 5; Figure 6).

It is shown that the binding of human CHD1 at TSS mediates subsequent recruitment of post-transcriptional initiation and pre-messenger-RNA splicing factors (Sims et al., 2005; Sims et al., 2007). More recent data indicated that CHD1 is involved in H2B monoubiquitination (Lee et al., 2012), which may facilitate transcriptional elongation and prevent cryptic transcriptional initiation from the gene bodies (Hennig et al., 2012). The deletion of S. cerevisiae Chd1 results in a clear decrease of the overall H2Bub level but not that of H3K4me3 (Lee et al., 2012). Consistently, chr5 mutations did not affect H3K4me3 on the targeted loci (Figure 6).
However, our analysis of chr5 mutants did not reveal a clear change of the overall level of H2Bub (Figure S7), suggesting that this function of maintaining H2Bub may not be conserved in CHR5.

Nucleosomes are organized into uniformly spaced arrays at the 5’ end of the genes, which starts with the +1 nucleosome at around the TSS (Jiang and Pugh, 2009). A “-1” nucleosome located on the upstream in the promoter is positioned to potentially control access to gene regulatory sequences. It is suggested that CHD1 enrichment within the NFR is to position nucleosomes within the promoter or around the TSS to facilitate gene transcription and also to position nucleosomes within the coding regions of genes, which are aligned with respect to TSS to prevent cryptic transcription within gene bodies by suppressing histone turnover (Gkikopoulos et al., 2011; Hennig et al., 2012; Smolle et al., 2012; Zentner et al., 2013). Our data showing that chr5 mutations also led to a relatively higher occupancy of the nucleosomes located near the NFR of FUS3 are in agreement with the finding that in S. cerevisiae with the deletion of Chd1 nucleosomes near the NFR display a relatively higher occupancy genome-wide (Gkikopoulos et al., 2011). Possibly, the reduction of nucleosome occupancy in the promoter and near the TSS by the binding of CHD1 within NFR may facilitate the functioning of regulatory sequence such as transcription factor binding and transcription initiation complex recruitment to stimulate gene transcription. It remains to know whether CHR5 regulated nucleosome occupancy near the TSS of FUS3 affects the binding of transcription factors including LEC1 and AFL proteins to the gene.
2.5 Methods

Plant Growth

The *Arabidopsis thaliana* genetic resources used in this study were mostly in the Columbia ecotype. Mutant lines *chr5-1* (Sail_504_D01), *chr5-2* (Salk_020296), *chr5-3* (Flag_130A16), *chr5-4* (GABI_773A12), *chr5-5* (Sail_1259_B05) and *chr5-6* (Salk_046838) were obtained from the Nottingham *Arabidopsis* Stock Center and ABRC collections. The *pkl* mutant used in this study was the *pkl-1* allele as described (Ogas et al., 1997). The *abi3* mutant (Salk_023411) and *fus3* mutant (GABI_612E06) were used. The T-DNA insertion was confirmed by PCR using the primers described in supplemental Table online. Double mutants *chr5-6 pkl* and *chr5-2 pkl* and were obtained by genetic crossed between *chr5-6* and *chr5-2* with *pkl*. Seeds were surface-sterilized and plated on 0.5 x Murashige and Skoog medium. After stratification at 4°C for 2 d, plants were grown in a growth room under a long day photoperiod (16h light/8h dark) at 22°C.

Constructs and Transformation

For the histochemical GUS assay, the 2 kb promoter of *CHR5* was amplified from WT DNA using proCHR5-F and proCHR5-R and then cloned into the pPR97 vector. For the complementation experiment, the full length cDNA without a stop codon was amplified from total cDNA of Col-0 using primers comCHR5-F and comCHR5-R. *CHR5* promoter and cDNA were inserted into the binary vector pFA1300, which was modified based on pCAMBIA1300 (CAMBIA) and contained 2 x HA tag. The *pCHR5-GUS* and *pCHR5-CHR5-HA* constructs were introduced into Col-0 and *chr5* mutants via Agrobacterium-mediated transformation by the floral dip method. The *pABI3:GUS* and *pFUS3:GUS* were made using a PCR-based Gateway system. The promoter and 5' UTR of 4 kb for *ABI3* and 2.2 kb for *FUS3* were inserted as translational fusion with the *uidA* gene into the vector pGWB553.

Gene Expression Analysis

Definition of stages for seed and silique development were according to previous description (Kleindt et al., 2010). Total RNA of siliques was extracted as described (Meng and Feldman, 2010) with minor modification. The crude RNA was further
purified via the clean-up protocol of the RNeasy Plant RNA isolation kit (Qiagen) according to the manufacturer’s protocol instead of Trizol reagent. Two micrograms of total RNA were treated with DNase I (Promega) and transcribed into cDNA by ImPromII reverse transcriptase (Promega). Real-time PCR was performed with the LightCycler® 480 SYBR Green I Master (Roche) following the manufacturer’s instructions. Primers are listed in Supplemental Table 1. Three biological replicates were performed for each sample and the expression level was normalized with that of ACTIN2.

**ChIP Assay**

The ChIP experiment was performed as previously described (Benhamed et al., 2006). Chromatin was isolated from siliques and dissected seeds after cross-linking proteins and DNA with 1% formaldehyde for 1 hr under vacuum and termination of the reaction with glycine. Chromatin was fragmented to 200–1000 bp by sonication, and ChIP was performed using the following antibodies: anti-H3H4me3 (Millipore, 07–473), anti-H3K27me3 (Millipore, 07–449), anti-H3 (Abcam, ab1791), anti-H3ac (Millipore, 06–599), and anti-HA antibody (Sigma, H6908).

**Histochemical GUS and Lipid Staining**

GUS staining was performed as previously described (Bertrand et al., 2003). Briefly, plant siliques were fixed with 90% acetone on ice for 30 min and were washed with staining buffer (0.2% Triton X-100, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 100 mM NaH2PO4 and 100 mM Na2HPO4 pH 7.2). The dissected seeds from the fixed siliques were immersed in GUS staining solution with 1 mM X-Gluc and placed under vacuum for 1 h. After incubation at 37°C overnight, the staining solution was removed and samples were cleared by sequential changes of 75 and 95% (v/v) ethanol. Lipid staining with Fat red 7B was carried out as described previously (Ogas et al., 1997). Whole seedlings were incubated for 1 h in filtered Fat red solution (0.5% Fat red 7B in 60% isopropanol), washed three times with water and analyzed under a dissecting microscope.

**Seed Protein Analysis**
Seed protein was extracted from 50 seeds/genotype by grinding mature seeds in an ice-cold motor with 20 \( \mu \text{L/mg} \) seed of extraction buffer (100mM Tris-HCl, PH 8.0, 0.5% SDS, 10% glycerol and 2% \( \beta \)-mercaptoethanol). Extracts were boiled for 3 min and centrifuged. The gel was loaded on a seed number basis and the proteins were resolved by 12% SDS-PAGE. Proteins were visualized by Coomassie blue staining.

**MNase Assay**

Siliques were harvested in liquid nitrogen after cross-linking in 1% formaldehyde. Nuclei and chromatin were isolated as described (Chodavarapu et al., 2010) with the following changes. The isolated chromatin was digested with 0.1 units/\( \mu \text{L} \) of Micrococcal Nuclease (Takara) for 10 min in digestion buffer at 37\( ^\circ \)C. Mononucleosomes were excised from 1.5% agarose gels and purified using a gel purification kit (MACHEREY-NAGEL). The purified DNA was quantified using a NanoDrop-1000 spectrophotometer. Two nanograms of purified DNA were used for qPCR to monitor nucleosome occupancy. The fraction of input was calculated as \( 2^{-\Delta C_{\text{t}}} \) \( (2^{\text{Ct(\text{mono})}-\text{Ct(gDNA)})}) \) using undigested genomic DNA followed by normalization over that of gypsy-like retrotransposon -73 loci for each sample according to previous description (Gevry et al., 2009). The tiled primer sets used for realtime PCR are listed in Supplemental Table online.

**Accession Numbers**

Sequence data for the genes in this articles can be found in the *Arabidopsis* Genome Initiative under the following accession numbers: *CHR5* (AT2G13370), *PKL* (AT2G25170), *ABI3* (AT3G24650), *FUS3* (AT3G26790), *LEC1* (AT1G21970), *LEC2* (AT1G28300), *2S2* (AT4G27150), *7S1* (AT4G36700), *CRA1* (AT5G44120), *OLE1* (AT4G25170), *PIL5* (AT2G20180), *RBCS1A* (AT1G67090), *ACTIN2* (AT3G18780), and gypsy-like retrotransposon (AT4G07700). Mutants investigated in this study are listed in Methods.

Acknowledgments: We thank F. Barneche for help in H2Bub detection, B. Dubreucq and M. Miquel for helpful discussion, G. Barthole for providing *fus3* and *abi3* mutants. This work was supported by the Agence National de Recherche (ANR 2010-BLAN-1238 CERES).
2.6 References


2.7 Figures

**Figure 1.** Expression pattern of CHR5 in developing embryo. **A.** Developing seeds of *Arabidopsis* plants transformed by pCHR5-GUS were stained for GUS activity detection. Photographs of representative seeds at different stages of embryo development (a - j) are shown. White arrow heads indicate unstained embryo at the early stages. Scale bars= 0.1 mm. **B.** qRT-PCR detection of *CHR5* and *PKL* transcripts during the different stages of silique development as defined previously (https://www.genomforschung.uni-bielefeld.de/GF-research/AtGenExpress-SeedsSiliques.html). Relative expression levels (with *ACTIN2* mRNA set as 1) are shown.
Figure 2. *CHR5* mutations reduced the mRNA levels of embryo and seed maturation genes and seed storage protein accumulation. **A.** Transcript levels of LEC1, AFL and the indicated seed storage genes in siliques harvested at stage 6. Bars = means values +/-SD from three biological repeats. **B.** SDS-PAGE analysis of mature seed proteins from the wild type (Col-0), mutants (*chr5-6, fus3, abi3, pkl* and *chr5-6 pkl*) and *chr5-6* complementation (pCHR5-CHR5-HA) plants. Peptides corresponding to 2S albumin and 12S globulin are indicated.
Figure 3. CHR5 and PKL have antagonistic function in the expression of embryo regulatory genes. A. Seedling phenotype of wild type (Col-0), chr5-6, pkl and chr5 pkl double mutants stained by Fat red dye. Bar= 5mm. B. Embryonic root penetrance of the 4 genotypes calculated from 82 – 129 plants. Asterisks indicate the significance of difference by Student’s t-test. C-E. Relative expression of LEC1 and AFL genes in 5 day-old seedlings (C), 5 day-old seedling roots (D) and Siliques (E), with the levels in wild type set as 1. Bars = means values +/-SD from three biological repeats.
Figure 4. Promoter activity of ABI3 and FUS3 in wild type (Col-0), chr5-6, pkl and chr5-6 pkl double mutants. A. GUS staining of developing seeds of plants transformed by pABI3-GUS (left panels) and pFUS3-GUS right panels. B. Quantification of GUS transcripts (relative to ACTIN2 mRNA) from 6-10 independent transgenic lines per genotype for each construct. Insets: means values +/-SD are shown. Significance of differences by Student’s t-test is indicated by asterisks.
Figure 5. CHR5 is enriched near the transcriptional start site of ABI3 and FUS3. ChIP-qPCR analyses for the binding of CHR5 to LEC1 and AFL genes. Chromatin isolated from siliques of chr5-6 complementation plants by pCHR5-CHR5-HA (CHR5-HA) was immunoprecipitated with anti-HA antibody, and the amount of precipitated DNA was measured by quantitative PCR using 3-4 primer sets (A-D) as indicated on the 4 genes (top). Transcriptional start sites of the four genes are indicated by arrows. Levels in non-complemented mutant (chr5-6) were set to 1 after normalization to the levels of input DNA. ACTIN2 and Ta3 DNA were tested as controls.
Figure 6. Histone methylation on LEC1, AFL and PIL5 genes in wild type and chr5 mutants. A. H3K4me3 on the 5 genes in seeds harvested from developing siliques (at stage 6) of wild type and chr5-6. B. H3K27me3 on the 5 genes and RBCS (as a control) in seeds harvested from developing siliques (at stage 6) of wild type and chr5-6. C. H3K27me3 on the 5 genes in developing siliques (at stage 6) of wild type, chr5-1 and chr5-6. Levels are relative to H3K4me3 or H3K27me3 levels on the ACTIN2 locus.
Figure 7. CHR5 mutations lead to increased nucleosome occupancy near the transcriptional start site of FUS3. Chromatin isolated from wild type (Col-0), chr5-1 and chr5-6 was digested by micrococcal nuclease, then analyzed tiled primer qPCR to monitor nucleosome positioning and occupancy at the 5’-end of the FUS3 locus. The fractions of input were calculated as $2^{-\Delta Ct} (2^{-\Delta Ct(mono)-\Delta Ct(gDNA)})$ using undigested genomic DNA followed by normalization over that of gypsy-like retrotransposon -73 loci for each sample. NFR, nucleosome free region.
2.8 Supplemental data

**Figure S1.** The CHR5 2 kb promoter activity in transgenic plants. GUS staining of germinating seeds (1-5 days, A-D), young seedlings (G), flowers and floral organs (H-K) of transgenic plants with the pCHR5-GUS construct. GUS activity in a 5 day-old apex (E), in a 4 day-old primary root (F) and in funiculus (L, M) are shown. Bars=0.1 mm.
Figure S2. Characterization of chr5 T-DNA insertion mutants. Upper part: six T-DNA insertions in the locus are indicated by arrows. The positions of the primer sets used for genotyping and RT-PCR analysis are indicated. Lower parts: RT-PCR analysis of CHR5 transcripts in wild type (Col-0 or Ws) and the 6 mutant alleles by using the indicated primer sets.
Figure S3. CHR5 mutations display a slight long hypocotyl phenotype. A. Hypocotyl length of chr5 mutants grown in the dark, low white light (12 µmol m⁻² s⁻¹) and high white light (35 µmol m⁻² s⁻¹) with 8h light/16h dark cycles for 5 days. Bar = 1 cm. B. Quantification of hypocotyl lengths of the seedlings shown in A. Data represent the mean ± SD of 50 seedlings. The asterisks indicate that the difference is significant at P < 0.01 between mutants and Col-0 according to Student’s t test.
Figure S4. Characterization of a complementation line of the chr5-6 allele. Western blot analysis of nuclear proteins extracted from chr5-6 and chr5-6 transformed with pCHR5-CHR5-HA construct using anti HA antibody.
Figure S5. Comparison of Fat red dye stained seedling phenotypes of wild type, chr5-2, pkl and chr5-2 pkl double mutants. Percentages of embryonic roots (stained red) were calculated from 85-94 seedlings.
Figure S6. Histone modifications on LEC1 and AFL loci in seedlings of wild type, chr5-6, pkl, and chr5-6 pkl double mutants. Chromatin fragments isolated from 5 day-old seedlings were immunoprecipitated with antibodies of histone H3, H3K4me3, H3K27me3 and acetylated H3 (H3ac), and quantified by qPCR using primer sets corresponding to the 4 genes and, as a control, to the Ta3 locus. Y-axis: relative levels to histone modifications on ACTIN2.
Figure S7. CHR5 mutations do not affect the overall levels of histone H2B monoubiquitination (H2Bub). Histones isolated from wild type and chr5-1 and chr5-6 were analyzed by western blotting with anti H2B antibody.
Supplemental Table 1. Sequences of primers used in this study.

### Primers used for genotyping

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### Primers used for RT-qPCR and ChIP-qPCR

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### Primers used for cloning

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### Primers used for FUS3 nucleosome mapping

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CHAPTER 3

Functional characterization of a histone demethylase JMJ15 in *Arabidopsis*
Introduction

JMJ15 belongs to the KDM5/JARID1 group of JmjC-domain-containing proteins, which was previously shown to be a H3K4 demethylase (Liu et al., 2010; Yang et al., 2012a). However, little is known concerning to its function in stress-responsive gene regulation and plant growth. In this work, I analyzed the tissue expression pattern of JMJ15 during different plant development stages using proJMJ15-GUS construct. To study the function of JMJ15 in gene expression and plant development, I obtained 3 alleles of T-DNA insertion mutants: jmj15-1 and jmj15-2 were gain-of-function lines, and jmj15-3 was loss-of-function line. The jmj15-3 mutant did not show obvious phenotypes, whereas gain-of-function mutations reduced the length of hypocotyls and inflorescence stems with higher accumulation of lignin. Furthermore, the gain-of-function mutants showed enhanced salt tolerance whereas the loss-of-function mutant was more sensitive to salt compared to the wild type. To study the effect of JMJ15 over-expression on gene expression, we analyzed the transcriptome of the jmj15-1 and jmj15-2 mutant alleles using Affymetrix ATH1 microarrays. The transcriptomic analysis revealed that there were much more down-regulated genes compared to up-regulated ones in the over-expression plants. Most of the down-regulated genes are related to stress, among which most encode transcription factors, suggesting that JMJ15 may be a higher hierarchical regulator involved in stress-responsive gene expression. On the other hand, the H3K4 methylation level of down-regulated genes was analyzed using publicly epigenomic datasets. The result showed that most down-regulated genes were highly enriched for H3K4me3 and H3K4me2. In general, our results indicate that JMJ15, as a H3K4 demethylase, plays important roles in plant responses to stress. This part of the results is written in an article that will be submitted for publication.
Over-expression of Histone H3K4 Demethylase Gene \textit{JMJ15} Enhances Stress Tolerance in \textit{Arabidopsis}

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$^2$UMR 8618, CNRS, Orsay, France

Running title: Function of H3K4me3 demethylation in stress tolerance

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\textbf{Keywords:} Histone methylation; Jumonji demethylase; JMJ15; Abiotic stress tolerance gene; epigenetic regulation; H3K4me3; chromatin modification
3.1 Abstract

Histone H3 lysine 4 trimethylation (H3K4me3) has been shown to be involved in stress-responsive gene expression and gene priming in plants. However, the role of H3K4me3 resetting in stress tolerance is not clear. In this work we studied the expression and function of Arabidopsis H3K4 demethylase gene JMJ15. We show that the expression of JMJ15 was restricted to a few tissues during vegetative growth but relatively highly expressed in young floral organs. Over-expression of the gene in gain-of-function mutations reduced the length of seedling hypocotyls and inflorescence stems with higher accumulation of lignin in the stem, while the loss-of-function mutants did not show any visible phenotype. The gain-of-function mutants showed enhanced salt tolerance, whereas the loss-of-function mutants were more sensitive to salt compared to the wild type. Transcriptomic analysis revealed a much higher number of genes down-regulated in JMJ15 over-expression plants, which are highly enriched for H3K4me3 and H3K4me2. Among the down-regulated genes, many encode transcription regulators of stress responsive genes. The data suggest that increased JMJ15 levels may regulate the gene expression program that enhances stress tolerance.
3.2 Introduction

Histone lysine methylation is an important epigenetic modification for gene expression in eukaryotic cells (Martin and Zhang, 2005; Kouzarides, 2007). Histone lysines can be mono-, di-, and tri- methylated. Genome-wide analysis has indicated that about two-thirds of *Arabidopsis* genes are marked by mono-, di- or trimethylation on histone H3 at residue lysine 4 (H3K4me1/2/3) (Zhang et al., 2009). H3K4me3 is predominantly found at the promoter and 5’ regions of genes and is strongly associated with transcriptional activation in plants. H3K4me3 was found to be increased on responsive genes upon stress treatment, but the increase was found to be lagged behind gene activation in a few experiments (Kim et al., 2008; Hu et al., 2011), suggesting that H3K4me3 may have a function to mark the active gene state. In addition, H3K4me3 in gene bodies has been suggested to play a role in transcriptional memory of stress-responsive genes in *Arabidopsis* (Alvarez-Venegas et al., 2007; Jaskiewicz et al., 2011). Recent results indicated that the enriched H3K4me3 in gene bodies decreased after stress recovery but remained higher than basal state, suggesting that a regulated resetting mechanism is involved for partial removal of H3K4me3 and that remaining H3K4me3 may contribute for the transcriptional memory in *Arabidopsis* (Ding et al., 2012; Kim et al., 2012).

Histone methylation marks are established by evolutionarily conserved SET-domain proteins (named after 3 *Drosophila* genes: Su(var)3-9, Enhancer of zeste and Trithorax). H3K4 methylation is mediated by the Trithorax group proteins (TRX). *Arabidopsis* Trithorax ATX1 and ATX2 respectively trimethylates and dimethylates H3K4 (Saleh et al., 2008). ATX1 is found to be necessary for stress-induced gene expression (Alvarez-Venegas and Avramova, 2005; Alvarez-Venegas et al., 2007; Ding et al., 2011). Other SET-domain genes (SDG) such as SDG4 and SDG2 also methylate H3K4 and are involved in the control of many aspects of plant development (Cartagena et al., 2008; Berr et al., 2010; Guo et al., 2010).

Histone methylation is reversed by histone demethylases. Lysine Specific Demethylase 1 (LSD1) is the first identified histone demethylase to remove mono-
and di-methyl groups from H3K4 (Shi et al., 2004). In Arabidopsis there are 4 LSD1-like genes including FLOWERING LOCUS D (FLD), LSD1-LIKE 1 (LDL1) and LSD1-LIKE 2 (LDL2) that are shown to be involved in flowering time control (Jiang et al., 2007). The second class of histone demethylases containing the jumonji C (JmjC) domain catalyze histone lysine demethylation through a ferrous ion (Fe(II)) and α-ketoglutaric acid (α-KG)-dependent oxidative reaction (Tsukada et al., 2006). Multiple JmjC domain-containing histone demethylases are identified in animal cells, which are divided into distinct groups including JARID/KDM5, JMJD1/JHDM2/KDM3, JMJD2/KDM4, JMJD3/UTX/KDM6, JHDM1/FBX/KDM2 and the “JmjC domain-only” group. Members of each group target to specific histone lysine residues at different methylation states (Klose et al., 2006). About 20 JmjC domain-containing protein genes are found in Arabidopsis (Lu et al., 2008; Sun and Zhou, 2008; Chen et al., 2011). Most animal and plant JmjC proteins are conserved, while some animal proteins, such as JMJD3/UTX/KDM6 group that has the H3K27 demethylase activity, is not found in plants. Recent data have shown that plant JMJD2/KDM4 homologues can demethylate H3K27 (Lu et al., 2011; Li et al., 2013).

The JARID/KDM5 group catalyzes H3K4me2/3 demethylation in mammalian cells. Arabidopsis genome has one JARID/KDM5-like gene (JMJ17), whose function is presently unknown. There is a specific group in plants which includes Arabidopsis JMJ14, JMJ15, JMJ16, JMJ18 and JMJ19. The JmjC domains of this group are more closely related to that of the JARID, but structurally similar to that of JMJD2/KDM4 (Chen et al., 2013). JMJ14, JMJ15 and JMJ18 have been reported to have the H3K4me2/3 demethylase activity and to regulate diverse aspects of chromatin function and plant development (Deleris et al., 2010; Lu et al., 2010; Searle et al., 2010; Le Masson et al., 2012; Yang et al., 2012a; Yang et al., 2012b; Cui et al., 2013). However, the function of these H3K4 demethylases in plant stress tolerance has not been evaluated. In this work we provide evidence that increased expression of JMJ15 preferentially down-regulates H3K4me2/3-marked stress-related genes and enhance salt stress tolerance.
3.3 Materials and methods

Plant growth

The *Arabidopsis thaliana* ecotype Columbia (Col-0) was used throughout this study. T-DNA mutant lines *jmj15-1* (GABI_257F10), *jmj15-2* (GABI_876B01) and *jmj15-3* (GABI_663C11) were obtained from the Nottingham *Arabidopsis* Stock Center (NASC) and confirmed by PCR. Seeds were surface-sterilized and plants were grown on 0.5 x Murashige and Skoog (MS) medium after stratification at 4°C for 2 days. Plants were analyzed on plates under long-day (LD, 16h light/8h dark) or short-day (SD, 8h light/16h dark) photoperiods at 20°C. Ten days after germination, plants were transferred to soil and kept in growth rooms under LD condition.

To test JmjC gene expression in response to salt, experiments were carried out with 8 day-old plants, treated with 0.5 x MS supplemented with or without 100 mM NaCl for 5h. For germination tests, seeds of WT and *jmj15* mutants were sown on medium containing indicated concentration NaCl. Images of the Petri dishes were taken 10 days after germination.

Constructs and Transformation

For the histochemical GUS assay, the 2 kb promoter of *JMJ15* was amplified from wild type genomic DNA using the following primers: 5’-GGATCCAGAGCTTGGCCATTTCTTGA-3’ (forward) and 5’-GGTACCAGCTGAAAGGCTCCATTG-3’ (reverse). BamHI and KpnI (underlined) were used for digestions. The *JMJ15* promoter fragment was inserted as translational fusion with the *uidA* gene into the pPR97 vector. To generate the 35S-*JMJ15-HA* construct, the full length cDNA without a stop codon was amplified from total cDNA of Col-0 using primers: TCTAGACCTTTGGGTTTTGTGGAGTG (forward) and TCTAGACCTTCAATCAACTCAACCCAAAA (reverse). Using XbaI site, *JMJ15* cDNA was inserted into the binary vector pFA121, which was modified based on pBI121 and contained 2 x FLAG-HA tag. The pJMJ15-GUS and
35S-JMJ15-HA constructs were transformed into Agrobacterium tumefaciens strain GV3101 and then transformed the plants using floral dip method.

Microarray analysis

Total RNA was extracted from 12 day-old seedling using Trizol (Invitrogen) and cleaned using the RNeasy isolation kit (Qiagen). Hybridization with Affymetrix GeneChip Arabidopsis ATH1 Genome Array was performed at CapitalBio Corporation. Wild type and both jmj15 overexpression alleles were performed in two biological repeats. Gene expression changes between the samples were analyzed by the AffylmGUI package from R software. GO annotation was carried out with the GO terms of the TAIR database (http://arabidopsis.org/tools/bulk/go/index.jsp). The percent of significantly changed genes in each TAIR annotated category was calculated as follows: percent = the number of significantly changed genes divided by N x 100, where N represents the total number of genes annotated in each ontology. Significantly changed genes were subsequently analyzed for their H3K4 methylation levels at epigenomics database (http://epigenomics.mcdb.ucla.edu/H3K4m1m2m3/). The microarray data are deposited to the NCBI databases (accession number pending).

Real-Time PCR

For gene expression analysis, two micrograms of total RNA were reversed transcribed into cDNA by ImPromII reverse transcriptase (Promega). Real-time PCR was performed with the LightCycler® 480 SYBR Green I Master (Roche) on a LightCycler 480 (Roche). At least two biological replicates and two technical repeats for every biological replicate were tested. The primers used in this study are listed in supplementary Table 1.
**Histochemical GUS and Lignin Staining**

GUS staining was performed as previously described (Bertrand et al., 2003). Briefly, plant samples were fixed with 90% acetone on ice for 20 min and were washed with staining buffer (0.2% Triton X-100, 5 mM potassium ferrocyanide, 5 mM potassium ferricyanide, 100 mM NaH₂PO₄ and 100 mM Na₂HPO₄ pH 7.2). Then the samples were immersed in GUS staining solution with 1 mM X-Gluc and placed under vacuum for 20 minutes. After incubation at 37°C overnight, the staining solution was removed and samples were cleared by sequential changes of 70% (v/v) ethanol and stored at 4°C.

The histological comparative analysis of inflorescence stems between Col-0 and *jmj15* mutants was done at the stage of newly formed green siliques, about 2 weeks after bolting, when the inflorescence stems of wild type reach 20 cm in height. Cross-sections of the inflorescence stems at the basal end were stained for 3 min in phloroglucinol-HCl reagent (Prolabo, VMR International, France) and then observed in ethanol 100 % : HCl 37 % (9/1, v/v) using a light microscope (Nikon, MULTIZOOM AZ 100).
3.4 Results

3.4.1 Expression levels of H3K4 demethylase genes

To investigate whether H3K4 demethylase genes are involved in plant stress responses, we analyzed the mRNA levels of \textit{JMJ14}, \textit{JMJ15}, \textit{JMJ16}, \textit{JMJ17}, \textit{JMJ18} and \textit{JMJ19} genes in 8 day-old seedlings grown in $\frac{1}{2}$ MS media under continuous light, then transferred to 100 mM NaCl or to $\frac{1}{2}$ MS solution for 5 hours. In untreated ($\frac{1}{2}$ MS) seedlings, the expression levels of the 6 genes varied considerably. The relative expression levels of \textit{JMJ17}, \textit{JMJ18} and \textit{JMJ19} were much higher ($>10^2$) than that of \textit{JMJ14}, \textit{JMJ15} and \textit{JMJ16} (Supplementary Figure 1). NaCl treatment did not dramatically affect the expression of these genes, although some decrease of \textit{JMJ14} and \textit{JMJ18} and some increase of \textit{JMJ15} transcript levels were detected.

3.4.2 \textit{JMJ15} displayed a highly tissue-specific expression pattern

The relatively low expression level of \textit{JMJ15} was in agreement with previous data showing that the 1.5 kb promoter region of \textit{JMJ15} is weak in vegetative tissues (Hong et al., 2009). To study the temporal and spatial expression pattern of \textit{JMJ15}, we used a larger promoter region of \textit{JMJ15} (-2051 bp to +14 bp relative to ATG) to make a \textit{GUS} reporter translational fusion construct and transformed \textit{Arabidopsis} plants. Three independent GUS reporter lines were characterized. All showed the same pattern of GUS expression. In seedlings, GUS activity was detected only at the base of rosette leaves and root vascular tissues, but not in the root tip (Figure 1). Interestingly, a higher accumulation of GUS activity was detected in pericycle cells that initiated to lateral root meristem. The GUS activity remained to be detected at the base of the growing lateral roots (Figure 1). In the inflorescence, GUS activity was strong in the young anthers and detected in carpels, but the activities become weaker in the mature flower (Figure 1). This temporal and tissue-specific expression pattern suggested that \textit{JMJ15} may have a function in plant development.
3.4.3 JMJ15 gain-of-function mutations showed a reduced plant height phenotype

The *JMJ15* gene contains 10 exons and encodes a polypeptide of 806 amino acids with distinct domains, including the JmjN domain, JmjC domain, a C5HC2 zinc finger and the FY-rich N-terminus (FYRN)/FY-rich C-terminus (FYRC) domains, which are conserved in JMJ14, JMJ16, and JMJ18 (Supplementary Figure 2) (Lu et al., 2008). To study the function of JMJ15 in gene expression and plant development, we characterized 3 T-DNA insertion mutants: *jmj15-1* (GK-257F10), *jmj15-2* (GK-876B01) and *jmj15-3* (GK-663C11). In *jmj15-1* and *jmj15-2*, the T-DNA was inserted in the 5' end, and in *jmj15-3* the T-DNA was inserted in the seventh exon of the gene (Figure 2A). RT-PCR analysis with 4 pairs of primers that covered the whole coding region of the gene, revealed that the transcript level of *JMJ15* was dramatically increased in *jmj15-1* and *jmj15-2*, but the transcript was interrupted in *jmj15-3* compared to wild-type (Figure 2B). The insertion in *jmj15-1* and *jmj15-2* did not alter the 5’ end of the coding region, as the primer set F1 (that cover the 5’end of the coding region) and R1 successfully amplify the transcripts from the mutants. The data suggested that *jmj15-1* and *jmj15-2* were gain-of-function mutants that overexpressed the gene and that *jmj15-3* was a loss-of-function mutant.

The *jmj15-3* loss-of-function mutation did not display any visible phenotype in normal growth conditions, confirming previous results (Yang et al., 2012a). However, in short day (8h light/16h dark) grown seedlings, *jmj15-1* and *jmj15-2* mutants produced slightly shorter hypocotyls compared to wild type (Figure 3A). At the mature stage, the plant height of *jmj15-1* and *jmj15-2* were also reduced compared to wild type (Figure 3B). The stronger phenotypes in *jmj15-1* were correlated with the higher expression of the gene in the allele compared to in *jmj15-2*. To study whether the plant height phenotype of *jmj15-1* and *jmj15-2* was due to increased expression of the gene, we made 35S-*JMJ15-HA* construct and obtained *JMJ15* over-expression transgenic plants. The transgenic plants also displayed the reduced plant height phenotype at mature stage (Figure 3B).
The plant height phenotype of the jmj15 gain-of-function mutants prompted us to further investigate the stem cell structure by using histochemical method. Sections of the basal part of the inflorescence stem of 5 week-old plants (grown in long day) were stained with phloroglucinol and examined by light microscopy. Phloroglucinol reacts with coniferaldehyde groups in lignin, and the color intensity reflects the total lignin content. The analysis revealed that jmj15-1 and jmj15-2 exhibited a significantly deeper red staining in the stem vascular system and interfascicular fibers compared to that in wild type and jmj15-3 (Figure 4). This observation suggested that over-expression of JMJ15 resulted in an increase of the total lignin content in the stems concurrently with stem growth reduction.

3.4.4 Over-expression of JMJ15 preferentially repressed genes marked by H3K4 methylation

To determine the effect of JMJ15 over-expression on gene expression, the transcriptomes of jmj15-1, jmj15-2 and wild type seedlings (12 day-old) were analyzed by using the Affymetrix Arabidopsis ATH1 Genome Array. Two biological replicates for each sample were analyzed. Pair-wise plots of the microarray data revealed a good correlation of the hybridization signals between the biological replicates of each sample and between the 2 mutant alleles (Figure 5A). The average hybridization signals of the replicates of both mutants were normalized and compared with the wild type signals. Up- and down-regulated genes in both jmj15-1 and jmj15-2 were filtrated with the threshold >2 fold changes compared to wild type. The analysis revealed 23 up-regulated and 194 down-regulated genes in the jmj15 mutant lines (Supplementary Dataset 1). The analysis revealed a much high expression level of JMJ15 itself (>7-8 folds) in the mutants compared to wild type (Supplementary Dataset 1), confirming the over-expression of the gene in the mutants. The higher number of down-regulated genes compared to up-regulated ones suggested that elevated JMJ15 expression mainly repressed genes and that JMJ15 acted as a transcriptional repressor, consistent with its H3K4 demethylase activity (Liu et al., 2010; Yang et al., 2012a). To validate the microarray data, we checked 4
down-regulated genes by RT-qPCR. The relative transcript level changes in the mutants compared to wild type detected by RT-qPCR were in agreement with that from the microarray analysis (Figure 5B).

To evaluate whether there was any enrichment of the deregulated genes for H3K4me2/3, we compared the deregulated genes with the genome-wide H3K4me2/3/1 data obtained from wild type seedlings (Zhang et al., 2009). The analysis revealed that about 85% of the down-regulated genes were marked by the H3K4 methylation (mostly by H3K4me2, H3K4me3, or both) in the gene bodies, compared to about 50% of up-regulated genes (Figure 6, Supplementary Dataset 1). About 60% of the down-regulated genes were marked by H3K4me3, H3K4me2 or H3K4me2/3 in the promoter region (in the -500 bp region relative to TSS), compared to about 30% of up-regulated genes. Compared to up-regulated genes, the down-regulated ones were clearly enriched for the H3K4me2/3 double methylation marks. This analysis suggested that JMJ15-mediated gene repression might be achieved by demethylating H3K4 and indicated that JMJ15 preferentially repressed genes that have the H3K4me2/3 double methylation marks.

3.4.5 Over-expression of JMJ15 preferentially repressed stress regulatory genes

Gene ontology (GO) analysis of the deregulated genes using the GO Slim Classification (http://www.arabidopsis.org/help/helppages/go.slim.help.jsp) revealed that a large proportion of the deregulated genes (23.73%) in the jmj15 mutants had a function in the nucleus (Supplementary Figure 3A). Interestingly, 37 out of the 194 down-regulated genes were transcriptional regulators (Supplementary Dataset 1). Remarkably, more than 32% of the down-regulated genes belonged to the stress-responsive categories (Supplementary Figure 3B), suggesting that JMJ15 may have a function in stress-responsive gene expression. We noticed that among the greater than 5 fold down-regulated genes, more than 50% were transcription factors or stress-responsive signalling protein genes (Supplementary Dataset 1). These included the stress-responsive zinc finger protein STZ/Zat10 (At1g27730) (Sakamoto et al., 2000), the stress-responsive WRKY proteins WRKY40 (At1g80840) and WRKY33
(At2g38470) (Jiang and Deyholos, 2009), the cold-responsive factor CBF2 (At4g25470) (Vogel et al., 2005), the ethylene-responsive-element binding proteins ATERF6 (At4g17490) and ATERF11 (At1g28370) (Li et al., 2011; Dubois et al., 2013), the stress-responsive F-box protein ATFBS1 (At1g61340) and the cytochrome P450 CYP707A3 (At5g45340) genes (Umezawa et al., 2006; Maldonado-Calderon et al., 2012) (Supplementary Dataset 1). The decreased expression of WRKY33 and CYP707A3 genes was validated by RT-qPCR (Figure 5B).

3.4.6 JMJ15 gain-of-function mutations enhanced salt stress tolerance

To study whether JMJ15 mutations affected plant tolerance to stress, we germinated seeds of wild type, jmj15-1, jmj15-2 and jmj15-3 mutants on ½ MS media containing 130 mM or 150 mM NaCl. The seedling growth phenotype shown in Figure 6 indicated that the gain-of-function mutations (jmj15-1 and jmj15-2) enhanced plant tolerance to salt stress, whereas the loss-of-function mutation (jmj15-3) reduced the stress resistance.
3.5 Discussion

3.5.1 Function of JMJ15 in stress tolerance

In this work we have shown that \textit{JMJ15} displayed a high tissue-specific expression pattern. Constitutive or over-expression of the gene, as a result of T-DNA insertions in the 5’ region, preferentially repressed genes marked by H3K4me2/3, suggesting that JMJ15-mediated gene repression may be mainly mediated through H3K4me2/3 demethylation. The observation that about a third of the down-regulated genes are related to stress implies that H3K4me2/3 levels are important for the expression of this category of genes. This is consistent with numerous observations that H3K4me3 is associated with the induction of biotic and abiotic stress-responsive genes (van Dijk et al., 2010; Hu et al., 2011; Jaskiewicz et al., 2011; Zong et al., 2013; To and Kim, 2014), and ATX1 that trimethylates H3K4 in the genic region is required for stress-responsive gene expression (Ding et al., 2009; Ding et al., 2011). Microarray analysis of \textit{atx1} mutant seedlings revealed that 424 genes were up-regulated and 328 genes were down-regulated more than 2 folds compared to the wild type (Alvarez-Venegas et al., 2006). Similarly, 271 genes were found to be up-regulated and 321 genes down-regulated in mutant seedlings of another H3K4 methyltransferase gene \textit{SDG2} (Guo et al., 2010). However there was no clear correlation between transcription changes in \textit{sdg2} and \textit{atx1} (Guo et al., 2010), suggesting that the two enzymes may regulate different targets. Comparison of the deregulated genes in \textit{jmj15} and \textit{atx1} or \textit{sdg2} did not reveal a clear overlap, although there were a relatively higher number of overlapped genes between \textit{jmj15} and \textit{atx1} than between \textit{jmj15} and \textit{sdg2} (Supplementary Figure 4). These proteins may targets to different loci. In addition, the data showing that the mostly down-regulated genes were those encoding transcription factors and signaling proteins involved in stress responses raise the hypothesis that \textit{JMJ15} might be a higher hierarchical regulator primarily to regulate stress-responsive gene transcription programs in \textit{Arabidopsis}. Since JMJ15 is closely related to JMJ14, JMJ16 and JMJ18 (Lu et al., 2008; Sun and
Zhou, 2008), the ectopically expressed JMJ15 may also regulate the targets of the other related demethylases.

The observations that the *jmj15* gain-of-function mutants showed enhanced salt tolerance at seedling stage and that the loss-of-function mutant was more sensitive to salt stress than the wild type, suggest that JMJ15 is required for stress tolerance. The data showing that the gain-of-function mutants displayed reduced growth and increased stem lignification, which are suggested to be associated with stress responses (Moura et al., 2010; Golldack et al., 2013), support the hypothesis that increased JMJ15 levels may regulate the gene expression program that integrates plant growth to stress tolerance. Among the mostly repressed genes in *jmj15* gain-of-function mutants was *STZ/Zat10* that encodes a C2H2-zinc finger protein associated with the ERF amphiphilic repression (EAR) domain (Supplementary Dataset 1). *STZ/Zat10* has been shown to be a transcriptional suppressor of stress-responsive genes (Sakamoto et al., 2004). Knockout and RNAi of the gene could enhance plant tolerance to abiotic stress (Mittler et al., 2006). As the STZ locus displays a high level of H3K4me3 (Supplementary Figure 5), it is possible that the repression of *STZ/Zat10* by JMJ15 through H3K4me2/3 demethylation is associated with the enhanced salt tolerance phenotype of the gain-of-function mutants. *STZ/Zat10* may be a major player in JMJ15-mediated regulatory network of stress tolerance.

### 3.5.2 Developmental function of JMJ15

Consistent with previous results (Yang et al., 2012a), the loss-of-function mutation identified in this study (*jmj15-3*) did not produce any visible phenotype. *JMJ15* was first identified as *Maternal Effect Embryo Arrest 27 (MEE27)* in a genetic screen for mutants defective in female gametophyte development (Pagnussat et al., 2005). However, no embryonic defect was observed in *jmj15* loss-of-function mutants (Yang et al., 2012a). Either the mutation was compensated by highly expressed homologues (e.g., JMJ18, Hong et al., 2009) or JMJ15-dependent H3K4 demethylation is not sufficient to lead to any morphological change. In addition, another study has identified *JMJ15* as a maternally imprinted gene (Hsieh et al., 2011), however, our
data showing the high promoter activity of JMJ15 in anthers do not support that observation.

It is reported that JMJ14 demethylates H3K4me2/3 at the Flowering Locus T (FT) locus and represses expression of the gene and that jmj14 loss-of-function mutants display an early flowering phenotype (Jeong et al., 2009; Lu et al., 2010). Conversely, JMJ18 directly binds to and represses the flowering repressor gene, Flowering Locus C (FLC), through H3K4me2/3 demethylation. Consequently, loss-of-function mutations of JMJ18 result in a weak late-flowering phenotype, while JMJ18 overexpressors exhibit an early flowering phenotype (Yang et al., 2012b). These observations support the notion that members of this H3K4 demethylase group target to different loci and have distinct functions in plant development control. However, Yang et al have shown that, like JMJ18, JMJ15 over-expression plants showed repressed FLC expression and produced an early flower phenotype (Yang et al., 2012a). But unlike jmj18 mutants (Yang et al., 2012a), the jmj15-3 loss-of-function mutation did not alter the flowering phenotype. Possibly, JMJ15 at elevated levels may demethylate and repress genes that normally targeted by JMJ18 in wild type plants. However, the jmj15-1 and jmj15-2 gain-of-mutation mutants did not show any clear flowering phenotype. This discrepancy may be due to difference in expression levels of JMJ15 in the overexpression plants and the mutant alleles.

Acknowledgements

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3.6 References


Arabidopsis chromatin modifier ATX1, the myotubularin-like AtMTM and the response to drought. Plant Signal Behav 4, 1049-1058.


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3.7 Figures

Figure 1. The 2.0 kb promoter activity of *JMJ15* in transgenic plants. In seedlings, the GUS activity was detected in the base of rosette leaves (A), root vascular tissues (B), and bases of growing lateral roots (C-G), but not in root tip (H). In flower buds, the GUS activity was detected in anthers and in carpels (I, J), which become weak in opened flowers, but remained in stamen filaments (K, L). Bar = 0.1mm.
Figure 2. Cauterization of *JMJ15* T-DNA insertion mutants. The insertion positions of the 3 alleles are indicated by open arrows. The exons are represented by black boxes. The positions of forward (F) and reverse (R) primers are indicated by arrows. The expression levels (relative to ACTIN2 mRNA) in *jmj15-1* and *jmj15-2* compared to wild type were tested by qRT-PCR using the 4 indicated primer sets. The transcript in *jmj15-3* compared to wild type was analyzed by RT-PCR using the indicated primers.
Figure 3. *jmj15* gain-of-function mutations reduced plant height. A. Phenotype of hypocotyls of short day-grown seedlings of *jmj15*-1 and *jmj15*-2 compared to wild type (left). Lengths of hypocotyls were measured from 30 wild type, *jmj15*-1 and *jmj15*-2 plants (right). B. Plant height at mature stage of *jmj15*-1 and *jmj15*-2 compared to wild type (left) and of 35S-JMJ15-HA overexpression plants compared to negative transgenic plants (middle). Plant height was measured from 10 wild type, *jmj15*-1 and *jmj15*-2 plants (right). Bar = means +/-SD. Asterisks indicate the significance of difference from wild type by student t-tests (P < 0.01).
Figure 4. Lignin accumulation in *jmj15-1*, *jmj15-2*, and *jmj15-3* mutants compared to wild type. Inflorescence sections at the base were stained by Phloroglucinol stain. Bar = 0.1 mm
Figure 5. Transcriptomic analysis of \textit{jmj15-1} and \textit{jmj15-2} (12 day-old) seedlings compared to wild type. A. Pair-wise plots of the microarray hybridization signals between the biological replicates of each sample and the between wild type and two mutant alleles. B. Four down-regulated genes in the two mutants (microarray signals relative to wild type are indicated below the respective genes) were validated by qRT-PCR. Bar = means +/-SD from 3 replicates.
Figure 6. Down-regulated genes are highly enriched for H3K4me2/3. Up-regulated (23) and down-regulated (194) genes in jmj15-1 or jmj15-2 mutants (changes >2 folds) were compared with genome-wide H3K4 methylation data. Percentages of H3K4me3, H3K4me2, H3K4me1 and their combinations on the promoter (A) and the gene body (B) regions are presented.
Figure 7. Comparison of sensitivity to NaCl of jmj15 mutants with wild type during seed germination. Wild type, jmj15-1, jmj15-2, and jmj15-3 seeds were germinated for 12 days on ½ MS supplemented with indicated concentrations of NaCl.
3.8 Supplementary Material

![Graph showing expression levels of 6 potential H3K4 demethylase genes in Arabidopsis seedlings treated with or without 100 mM NaCl for 5 hours. The transcript levels detected by RT-qPCR are presented as relative to that of the reference gene At4g34270.](image)

**Figure S1.** Expression levels of 6 potential H3K4 demethylase genes in *Arabidopsis* seedlings treated with or without 100 mM NaCl for 5 hours. The transcript levels detected by RT-qPCR are presented as relative to that of the reference gene *At4g34270.*
**Figure S2.** Comparison of protein structures of the 6 JmjC genes specific to plants.
**Figure S3.** Gene ontology analysis of down-regulated genes in *jmj15* gain-of-function mutants.
Figure S4. Overlaps of de-regulated genes between *jmj15* gain-of-function mutants and *atx1* or *sdg2* mutants.
**Figure S5.** H3K4 methylation on the STZ/Zat10 locus.

**Supplementary Dataset 1.** Down- and up-regulated genes in *jmj15-1* and *jmj15-2* mutants compared to wild type. Genes encoding transcription factors or signaling regulators are indicated. Genes that are marked H3K4me3/2/1 are also indicated.
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**Legend:**
- **Ratio:** The ratio of the expression level.
- **Data from:** The source of the data for each protein.
**Table S1.** Sequences of the primers used in this study.

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CHAPTER 4

GENERAL DISCUSSION & PERSPECTIVES
4.1 Function of CHR5 in plant gene expression

Several CHD3 proteins have been reported in plants. *Arabidopsis* CHD3 protein, PKL, represses *LEC1/AFL* gene expression via promoting H3K27me3 on these loci (Aichinger et al., 2009; Zhang et al., 2012). Rice CHD3 protein, CHR729, recognizes and modulates H3K4 and H3K27 methylation over repressed tissue-specific genes (Hu et al., 2012). Unlike the CHD3 family, only one CHD1 gene (CHR5) is found in the genome of *Arabidopsis*. CHR5 is mostly expressed in growing or developmental tissues/organs, suggesting that this chromatin remodeler may play an important role in facilitating gene expression reprogramming during plant development. Our data on the function of CHR5 to modulate seed maturation gene expression during embryogenesis support this hypothesis. The role of CHR5 in other developmental aspects could be exploited to further understand the function and mode of action of CHR5.

The CHD1 proteins in animal and yeast cells have shown to play various roles in regulating chromatin dynamics during transcription at different levels. For instance, the chromodomain of human CHD1 was found to specially bind to H3K4me3, a mark for gene activation, and to be associated with the pre-initiation transcription complex (PIC) through interacting with Mediator (Lin et al., 2011). In fly and yeast, CHD1 is localized to transcriptionally active genes and physically interacts with elongation factors and RNA Polymerase II (Simic et al., 2003; Srinivasan et al., 2005). In *S. cerevisiae*, Chd1 was shown to positively regulate gene expression through promoting nucleosome reassembly coupled with H2B monoubiquitination (Lee et al., 2012). In yeast, Chd1 was also reported to maintain chromatin structure at active genes via modulating nucleosome spacing integrated with the prevention of cryptic transcription and histone exchange within gene bodies (Hennig et al., 2012; Shim et al., 2012; Smolle et al., 2012). We have shown that the mutation of *Arabidopsis* CHR5 led to a decrease of the transcription level of *LEC1/AFL* genes accompanied with an increase of H3K27me3 on these loci. Furthermore, CHR5 was shown to directly associate with the promoter region of *FUS3* and *ABI3*, and *chr5* mutations resulted in increased nucleosome occupancy near TSS on *FUS3* loci. The data indicated that CHR5 regulates embryo identity gene expression via modulating nucleosome positioning. Only recently was reported the effect of nucleosome positioning on gene transcription...
during plant development and responsive to stress. BRM, another SNF2 chromatin remodeling factor, was reported to repress \textit{ABI5} and \textit{ABI3} expression by directing the nucleosome occupancy during postgermination development (Han et al., 2012). H2A.Z-containing nucleosomes mediate the thermosensory responsive in \textit{Arabidopsis}, linking the perception of temperature through DNA-nucleosome fluctuations (Kumar and Wigge, 2010). Furthermore, H2A.Z is enrichment across gene bodies which is negatively correlated with gene transcription levels and positively correlated with gene responsiveness—the degree to which a gene is differentially expressed in responsive to environmental and developmental stimuli (Coleman-Derr and Zilberman, 2012).

Owing to the rapid progress of high-throughput array and sequencing techniques, it is possible to detect the global nucleosome positioning and identify the position of individual nucleosome at a specific time. Given these reasons, it will be very important to investigate the genome-wide target genes of CHR5 and its effect on nucleosome positioning and global gene activities. Comparison of these data will help us to better understanding chromatin remodeling mediated by CHR5 in gene transcription during the plant development. In addition, the function of CHR5 in gene expression related to stress responses could be evaluated to study the role of CHR-dependent nucleosome positioning in inducible gene expression, which would be of significance for plant adaptation to environmental constraints. Finally, it will of great importance to study the interplay between CHR5 and other chromatin modifiers (such as enzymes involved in histone modifications) and remodelers (such as, BRM, other CHD members and proteins involved in H2A.Z deposition) in genome-wide nucleosome dynamics related to plant growth and development.
4.2 The function of JMJ15 in plant development

In plant development, \textit{JMJ15} was particularly expressed in shoot meristem and during lateral root initiation, raising the hypothesis that JMJ15 may regulate meristem function, and lateral root formation. A more detailed examination of these aspects during the plant development will be needed. On the other hand, as the stress-responsive genes account for the largest proportion of regulated genes in \textit{jmj15} overexpression mutants, the function of JMJ15 in response to salt and other stress stimuli would be chosen in a future analysis.

JMJ15 represses the expression of \textit{ARR15}, \textit{ARR5}, \textit{WRKY33}, \textit{CYP707A3} and other genes, which may account for some of the phenotypic changes seen in the \textit{jmj15} overexpression mutants. It would be important to study whether JMJ15 could directly associate with these genes and regulate their expression via demethylating H3K4 on these loci. We produced transgenic overexpression plants of FLAG-HA-tagged JMJ15 by using the 35S promoter. These transgenic lines will be used for ChIP with anti-HA antibody to examine if JMJ15 directly binds to these genes \textit{in vivo}. On the other hand, ChIP experiment will also be carried out to test if there is any change of histone modification on these loci in \textit{jmj15} mutants. In fact, it’s also worth identifying the genome-wide targets and histone methylation of JMJ15 by ChIP-seq and ChIP-chip. Then comparison of genomic targets and histone modification in combination with gene expression profiling will unravel the role of JMJ15 in the regulation of gene expression in \textit{Arabidopsis}. Because the expression of \textit{JMJ15} is restricted in a limited numbers of tissues, it will be usefully to perform the above experiments using specific tissues/organs instead of the whole plant.
REFERENCES


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plant to repress expression of embryonic traits and may play a role in gibberellin-dependent responses. Plant Physiol 134, 995-1005.


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SWI3 subunits of putative SWI/SNF chromatin-remodeling complexes play distinct roles during Arabidopsis development. Plant Cell 17, 2454-2472.


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References


APPENDIX
The Role of Histone Methylation and H2A.Z Occupancy during Rapid Activation of Ethylene Responsive Genes

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Institut de Biologie des Plantes, Université Paris-Sud, Orsay, France

Abstract

Ethylene signaling pathway leads to rapid gene activation by two hierarchies of transcription factors with EIN3/EIL proteins as primary ones and ERF proteins as secondary ones. The role of chromatin modifications during the rapid gene activation is not known. In this work we studied trimethylated histone H3 lysine 4 (H3K4me3) and lysine 27 (H3K27me3), two opposite histone methylation marks for gene activity, during the induction course of three ethylene-responsive genes (ERF1, AtERF14 and ChiB). We found that the three genes displayed different histone modification profiles before induction. After induction, H3K4me3 was increased in the 5′ region and the gene body of ERF1, while H3K27me3 was decreased in the promoter of AtERF14. But the modification changes were later than the gene activation. Analysis of other rapidly inducible ERF genes confirmed the observation. In addition, histone H2A.Z occupancy on the three genes and the association of the H3K27me3-binding protein LHP1 with AtERF14 and ChiB were not affected by the inductive signal. However, the mutation of genes encoding H2A.Z and LHP1 attenuated and enhanced respectively the induction of target genes and altered H3K4me3. These results indicate that the induction of ethylene-responsive genes does not require immediate modulation of H3K4me3 and H3K27me3 and dissociation of LHP1 and H2A.Z from the targets, and suggest that the chromatin structure of the genes before induction is committed for transcriptional activation and that H3K4me3 is not required for ethylene-responsive gene activation, but may serve as a mark for gene activity.

Introduction

In addition to transcription factors chromatin structure plays an important role in the regulation of gene expression. The basic unit of chromatin is nucleosome that is formed by histone octamer containing two copies of H3, H4, H2A and H2B wrapped around by 147 base pairs of DNA. Chromatin structure change includes histone modifications and DNA methylation, histone variant deposition and chromatin remodeling. Histone modifications, especially H3K4 trimethylation and H3K27 trimethylation, have been largely reported to be tightly associated with gene transcription activity [1,2]. H3K4me3 is associated with highly expressed and/or housekeeping genes whereas H3K27me3 marks under-expressed and/or repressed tissue-specific genes [1,2]. Both modification marks could be recognized by different chromatin factors through specific protein domains. For example, the Plant Homeodomain (PHD) of ING2 (Inhibitor of Growth 2) can bind to H3K4me3 and the chromodomains of Polycomb proteins in animal cells and LIKE HETEROCHROMATIN PROTEIN1 (LHP1) in Arabidopsis can bind to H3K27me3 [3,4]. The recognitions may serve as a mechanism by which histone modifications regulate gene expression. Histone variant H2A.Z is another important regulator of gene expression which is deposited into nucleosome by SWR complex. Recent analysis in various species has revealed that activation of H2A.Z-regulated genes was accompanied by eviction of H2A.Z or replacement of H2A.Z with H2A by INO80 complex [5,6,7]. Other studies have suggested that H2A.Z may act as an epigenetic mark to promote gene reactivation [8,9].

In plants, H3K4me3 and the H3K27me3/LHP1 module have been shown to mediate developmental genes expression such as FLC (FLOWERING LOCUS C), AG (AGAMOUS), FUS3 (FUSCA 3) and FT (FLOWERING LOCUS T) [10,11,12,13]. However, how these modifications affect rapidly induced gene activation was not clear. Ethylene is a plant hormone participating in different processes including germination, flower and leaf senescence, fruit ripening, leaf abscission, root nodulation, programmed cell death, and response to stress and pathogen attack. Genetic and molecular analyses have revealed a response pathway from perception to a series of MAP kinase and finally transduced to two hierarchies of transcription regulation [14]. The primary transcription regulation is that transcription factors EIN3 (ETHYLENE-INSENSITIVE3)/EIL1 (ETHYLENE-INSENSITIVE3-LIKE 1) directly bind to EREBP (ethylene-responsive element binding protein) genes such as ERF1 (ETHYLENE RESPONSE FACTOR 1) to activate their expression. Subsequently EREBP proteins activate downstream effector genes (e.g. ChiB, basic chitinase and PDF1.2, Plant Defense 1.2). However, it was not known whether the rapid activation of ethylene-responsive genes involves change of chromatin structure. Here, we chose ERF1 and AtERF14 (Arabidopsis thaliana Ethylene-responsive element binding factor 14) as well as 5 other ERF genes as primary and ChiB as secondary regulation...
targets to analyze whether chromatin structures of these target genes changed during rapid induction by ethylene. We used 1-aminocyclopropane-1-carboxylic acid (ACC) which is converted to ethylene by 1-aminocyclopropane-1-carboxylic acid oxidase (ACO) in plants to treat 12 day-old seedlings. Increase of H3K4me3 and decrease of H3K27me3 were observed during the treatment, but the changes of both marks were much later than the gene activation. H2A.Z occupancy and LHP1 binding did not respond to the treatment indicating that the gene induction by ethylene signaling did not require immediate change of the cognate chromatin structure. However, mutation of genes encoding H2A.Z and LHP1 affected the induction of ethylene-responsive genes, suggesting that the committed chromatin structure of these genes before induction is important for the transcriptional activation.

Results
Histone methylation profile and H2A.Z deposition over ethylene-responsive genes before induction
To assess the chromatin structure of ethylene-responsive genes before induction we tested H3K4me3, H3K27me3 and H2A.Z deposition in the promoter, the 5’ region and the gene body of ERF1, AtERF14 and ChiB (Fig. 1A). RBCS-1A (RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1A), AG and HSP70 (HEAT SHOCK PROTEIN 70) were used as positive controls.

Figure 1. Chromatin status of ERF1, AtERF14 and ChiB before ACC induction. (A) Diagrams of the gene structure of ERF1, AtERF14, ChiB, AG, and RBCS1A. The solid boxes indicate the coding regions, and the open boxes indicate untranslated regions (UTRs). The solid bars indicate the regions in which primers were designed for ChIP tests. (B) H3K4me3 on the three genes before induction. The relative enrichments were calculated by compared to input. RBCS was used as a positive control. The regions (P1, P2 and P3) shown in A represent promoter, 5’ region and gene body respectively. (C) H3K27me3 on the three genes before induction. AG was used as a positive control. (D) H2A.Z abundance on the three genes before induction. HSP70 was used as a positive control and At4g07700 was used as a negative control. Bars represent mean values +/-SD from three repeats.

doi:10.1371/journal.pone.0028224.g001
respectively for H3K4me3, H3K27me3 and H2A.Z deposition [1,5,13]. The 
Atg6/7/700 locus was used as a negative control for H2A.Z deposition [5]. Moderate levels of H3K4me3 were detected in the 5’ region and the gene body, but not the promoter, of ERF1 and ChiB compared to that of RBCS-1A (Fig. 1B). In contrast, H3K4me3 was not detected over ATERF14 (Fig. 1B). H3K27me3 was enriched in the 5’ region and the gene body of both ATERF14 and ChiB but not in ERF1 (Fig. 1C). Analysis of five additional ERF genes (ORA59, TDR1, ATERF1, ATERF2 and ATERF11) revealed that TDR1 displayed a high level of H3K27me3 but a low level of H3K4me3, while the other four genes showed a high level of H3K4me3 but a low level of H3K27me3 (Fig. S2). Similar to what found in ERF1 and ChiB, H3K4me3 levels on the promoter of these genes were relatively low (Fig. S2). This analysis revealed that the ethylene-inducible genes displayed different histone modification profiles before induction.

To test whether H2A.Z was present in the chromatin of these genes, chromatin fragments isolated from H2A.Z-GFP transgenic plants were precipitated with GFP antibody. We found that H2A.Z was incorporated into chromatin over the three genes with highest levels in the gene bodies and lowest levels in the promoters (Fig. 1D). The presence of H2A.Z was detected also over the five additional ERF genes (Fig. S2).

Histone methylation dynamics during induction of ethylene responsive genes

In order to study histone modification dynamics during gene activation, we chose five time points to monitor ACC induction time course of ethylene-responsive genes by quantitative RT-PCR. The induction of ERF1 by ACC was early, which was 4 folds after 1 hour and elevated to 40 folds after 8 hours (Fig. 2A). For ATERF14, the expression began to increase after 2 hours and reached to 12 folds after 8 hours (Fig. 2A). The induction of ChiB was moderate, only 2 to 3 folds after 8 hours (Fig. 2A). ORA59, ATERF1, ATERF2 and ATERF11 were induced as early as ERF1, while the induction of TDR1 was delayed (Fig. S2).

H3K4me3 and H3K27me3 are two opposite histone modification marks associated with gene transcription activity. However, it is still not clear whether the two modifications are involved in gene activation process. Therefore, we tested the levels of these modifications over ethylene-responsive genes during the ACC induction process. For ERF1, H3K4me3 in the 5’ region and the gene body began to increase only after 4 hours, which was later than the initial increase of gene expression (Fig. 2B). Similarly, the increase of H3K4me3 over ORA59, ATERF1, ATERF2 and ATERF11 was also later than gene activation (Fig. S2). This suggested that the induction of ERF1 did not require a concurrent increase of H3K4me3. The late increase might indicate that H3K4me3 serves as a mark of elevated transcription activity of the genes. H3K4me3 remained undetectable over ATERF14 and TDR1 and did not change over ChiB during the induction (Fig. 2B) (Fig. S2). These results indicated that H3K4me3 was not necessary for the induction of ATERF14 and TDR1. However, it was not clear whether the basal levels of H3K4me3 over ERF1 and ChiB before induction was required for the induction of the genes.

Due to the low level of H3K27me3 over ERF1 before induction we did not expect that there would be any change during the induction. So we tested H3K27me3 over ATERF14 and ChiB. H3K27me3 was not much changed in the gene body of both genes during induction, but was decreased in the promoter of the genes, especially ATERF14 (Fig. 2C). However the decrease of H3K27me3 was delayed compared to the gene induction, suggesting that rapid gene activation did not require or lead to immediate demethylation of H3K27me3 and that the presence of H3K27me3 did not prevent the induction process. Analysis of H3K27me3 over ORA59, TDR1, ATERF1, ATERF2 and ATERF11 confirmed the results (Fig. S2).

Negative function of LHP1 on the induction of ATERF14 and ChiB

H3K27me3 is recognized and bound by LHP1 that is suggested to be an H3K27me3 effector. To explore the role of LHP1 in rapid gene activation, we analyzed the induction of ethylene responsive genes in the lhp1 mutant. For ATERF14 and ChiB that displayed high levels of H3K27me3 the induction by ACC was clearly enhanced in the mutant (Fig. 3A), indicating that LHP1 had a repressive function on induction of the two genes. However, we also detected an elevated expression of ERF1 in lhp1 (Fig. 3A). Considering that there was a low level of H3K27me3 over ERF1 we speculated that this might be an indirect effect of increased expression of ATERF14, as it has been reported that overexpression of ATERF14 could lead to increased expression of ERF1 [15]. In addition, we tested H3K4me3 levels over the target genes in lhp1 in comparison with the wild type. We found that in lhp1 H3K4me3 was increased in the 5’ region and the gene body, but not the promoter, of ERF1 and ChiB. The increased H3K4me3 levels may also be a consequence of increased transcription activity of the genes as mentioned before. However, H3K4me3 remained undetectable over ATERF14 despite the increased expression of this gene in lhp1 (Fig. 3B). The early induction of 4 of the 5 additional ERF genes was found to be enhanced in the lhp1 mutant. Except TDR1 that had no H3K4me3, the other three genes displayed increased H3K4me3 (Fig. S3).

To study whether LHP1 was bound to ChiB and ATERF14, ChIP analysis of the lhp1 mutant complemented by LHP1::LHP1-MYC was performed by using anti-MYC antibodies[16]. The analysis revealed that LHP1 was associated with ChiB and ATERF14 as well as with AG, but not with ERF1 (Fig. 4). Importantly, ACC treatment did not lead to dissociation of LHP1 from these genes (Fig. 4). Therefore, although the lhp1 mutation had an effect on the induction of ethylene-induced genes, the presence of the H3K27me3/LHP1 module on the genes was insensitive to the inductive signal.

Requirement of H2A.Z for the induction of ERF1 and ChiB

In Arabidopsis, H2A.Z has been shown to be involved in multiple responses such as temperature and phosphate starvation [5,7]. It either activates or represses target genes expression by eviction from nucleosomes occupying around the transcription start site. The presence of H2A.Z was detected over the three ethylene-inducible genes before ACC induction (Fig. 1D). During ACC treatment, no immediate decrease of H2A.Z abundance over ethylene-responsive genes was detected, albeit a slight decrease was observed after induction (Fig. 5; Fig. S2), suggesting that a clear H2A.Z eviction was not required for the initial induction of the genes.

In order to study whether H2A.Z was required for the induction, we tested the expression of these genes in hta9/hta11 double mutants that have a reduced level of H2A.Z [17]. In the mutant the induction of ERF1 was reduced, while that of ATERF14 was not clearly affected (Fig. 6A). The effect of the mutations on the induction of ChiB was detected after 8 hours, but was more severe after 24 hours (Fig. 6A). These results indicated that H2A.Z was involved in the induction of ERF1 and ChiB. Then we tested H3K4me3 over ERF1 and ChiB during ACC induction in the hta9/hta11 mutants. Increase of H3K4me3 over ERF1 observed in wild type was delayed in the mutants, but the basal levels of H3K4me3 over both ERF1 and ChiB were not affected (Fig. 6B).
Figure 2. Expression and histone modification changes of three ethylene responsive genes during ACC induction. (A) Induction time course of the three genes by ACC. Twelve day-old seedlings were treated with 50 μM ACC and harvested at the indicated time points. Relative fold changes were determined by normalization with ACTIN2 transcript levels. (B) H3K4me3 detected on the three genes during ACC induction. The relative enrichments were calculated by first comparing to input and then to the reference gene RBCS-1A. The three regions were analyzed for ChIP. (C) H3K27me3 detected on the three genes during ACC induction. The relative enrichments were calculated by first comparing to input and then to
We speculated that H2A.Z had no effect on H3K4me3 and the delayed increase of H3K4me3 over ERF1 might be a result of decreased transcription activity of the gene in the mutants.

Discussion

H3K4me3 serves as a mark of gene transcription activity

Genome-wide analysis in plants indicates that H3K4me3 is associated with actively transcribed genes. But how it affects gene expression remains unclear [1,18]. Some researchers have proposed that this modification may be recognized and bound by specific proteins which act as effectors to control transcription [3,19,20]. But other studies have suggested that H3K4me3 could serve as a memory or a mark of active genes [21]. In this study we tried to find out the role of H3K4me3 during activation of ethylene-inducible genes. Our results indicated that elevated H3K4me3 was not necessary for the ethylene-induced gene activation but may serve as a mark of transcription activity of the genes. First, H3K4me3 was not detected over AtERF14 and TDR1 before induction and was not increased after ACC treatment.
Second, although some increase of H3K4me3 was detected in the 59 region and/or the gene body of ERF1, ORA59, AtERF1, AtERF2 and AtERF11 after induction, the increase of H3K4me3 lagged behind that of gene activation (Fig. 2B; Fig. S2). Finally, the level of H3K4me3 was associated with that of gene expression in lhp1 and hta9/hta11 mutant and wild type plants. For instance, H3K4me3 was increased when the induction of ERF1 and ChiB was enhanced in lhp1 over these genes (Fig. 3). Conversely, the increase of H3K4me3 was delayed when the induction of the genes was attenuated by the mutation of H2A.Z genes (Fig. 6). Although there was no concomitant increase of H3K4me3 with activation of gene expression, it is not excluded the possibility that the basal level of H3K4me3 over ERF1 and ChiB might contribute to the chromatin commitment of these genes for the induction.

Repressive function of the H3K27me3/LHP1 module on inducible genes

The observations that H3K27me3 did not change over AIERF14, ChiB and TDR1 during ACC induction are consistent with recent results showing that although H3K27me3 on the floral time repressor FLC is inversely correlated with transcriptional activity, the abundance of this mark is not diminished in the first 12h following activation of transcription [22]. Analysis of cold-inducible genes has detected H3K27me3 to decline only one to several days after application of the inductive signals [23]. These observations suggest that transcription activation may not involve immediate demethylation of H3K27me3, or the presence of H3K27me3 is not sufficient to impair transcriptional activation during induction. This is supported by a recent result showing that vernalization-mediated induction of VERNALISATION INSENSITIVE 3 (VIN3) does not lead to any decrease of H3K27me3 on the locus 40 days after exposure to cold temperature [24,25].

The observations that the binding of LHP1 to AIERF14 and ChiB was not affected by ACC induction and that the mutation of LHP1 led to increased induction of the genes suggest that the H3K27me3/LHP1 module is required for the repression of the genes and the repressive effect could be lifted by additional events during the induction. The constitutive association of LHP1 with these targets is reminiscent of the data showing that LHP1 remains to be associated with VIN3 chromatin many days after induction by vernalization [25], indicating that the LHP1 binding in that conditions does not lead to gene silencing. These observations collectively suggest that additional elements associated with the H3K27me3/LHP1 module, which can be inactivated by inductive signals, might be involved in H3K27me3/LHP1-mediated gene silencing.

Involvement of H2A.Z in the induction of gene expression

Our data showing that deposition of histone variant H2A.Z over the eight ethylene-responsive genes was not evicted after ACC induction are in agreement with the findings that H2A.Z is present in both silent and active FLC chromatin (Fig. 5; Fig. S2) [8]. Probably, the presence of H2A.Z may mark these genes for induction, supporting the notion that H2A.Z serves to mark active gene and poised silent genes for reactivation [8,9]. Recent results have shown that H2A.Z is required for both gene activation and repression in responding to warmer temperature [5]. In contrast to the observations on the ethylene-responsive genes, H2A.Z-containing nucleosomes are found to be lost from both up-
regulated and down-regulated genes after an increase of temperature. Therefore, the role of H2A.Z in chromatin structure and in gene activity is complex, which may be dependent on the chromatin context of the gene. In addition, our results showed that mutation of H2A.Z genes had an obvious negative effect on the induction of ERF1 and ChiB but not AtERF14. Considering the undetectable level of H3K4me3 over AtERF14 and moderate levels over ERF1 and ChiB we speculate that H2A.Z may have a coordinated effect with H3K4me3 on the activation of these genes during ACC induction.

Chromatin structure is considered as an important regulator of transcription in addition to transcription factors especially for the developmental genes. In this work we tried to figure out whether chromatin modifications take place during activation of rapidly inducible genes. Our work revealed that histone modifications including H3K4me3 and H3K27me3 and presence of chromatin proteins such as LHP1 and H2A.Z did not display any immediate change upon ACC treatment. However, mutation of LHP1 and H2A.Z genes had an effect on the induction suggesting that basal chromatin structure before induction is important for the induction.

Materials and Methods

Plant material and Exogenous ACC treatment

The mutants used in this study are lhp1 [26], hta9/hta11 [17], lhp1 complemented by LHP1::MYC [16] and H2A.Z-GFP transgenic plants [5]. Arabidopsis seeds were surface-sterilized and growth at 22°C with a 16 h light/8 h dark (long day) cycle. Twelve days after germination 50 μM ACC solution was added. The samples were harvested at indicated time points.

RNA extraction and reverse transcription

Total RNA was extracted from twelve day-old seedling using Trizol (Invitrogen). Four μg total RNA were treated first with 1 unit of DNase I (Promega) and then reverse transcribed in a total volume of 20 μL with 0.5 μg oligo(dT)15, 0.75 mM dNTPs, 2.5 mM MgCl2, 1 μl ImProm-II reverse transcriptase (Promega). The resulting products were tested by Real-Time PCR with gene specific primers (Table S1).

Chromatin Immunoprecipitation

Chromatin Immunoprecipitation (ChIP) experiment was performed most as described in [27]. One gram of 12 day-old seedlings before and after ACC treatment were harvested and crosslinked in 1% formaldehyde under vacuum. Nuclei were then extracted with extraction buffers. Chromatin was fragmented to 200–2000 bp by sonication and ChIP was performed using antibodies: c-Myc (Sigma, M4439), H3K4me3 (Cell Signaling, 9751S) H3K27me3 (Millipore, 07–449) and GFP antibody (Abcam, ab290). The precipitated and input DNAs were then analyzed by real-time PCR with gene specific primer sets (Fig. S1, Table S1). At least three biological repeats were performed for the ChIP experiments.

Real-Time PCR

Real-time PCR was performed in a total volume of 20 μL with 1.0 μl of the reverse transcription or ChIP products, 0.25 μM
primers, and 10 µl SYBR Green Master mix (Roche) on a LightCycler 480 real-time PCR machine (Roche) according to the manufacturer’s instructions. All primers were annealed at 60°C and run 45 cycles. The ChIP enrichment for GFP, H3K27me3 and H3K4me3 was quantified by comparing the threshold cycle (Ct) of the ChIP samples with that of the input and then normalized with the levels of control genes: 2(Ct of input-Ct of sample ChIP) /2(Ct of input-Ct of control ChIP). The expression level of target genes was normalized with that of ACTIN2: 2(Ct of actin- Ct of target).

Supporting Information

Figure S1 Genes used as controls in this study were not affected by ACC treatment. The expression of ACTIN2, AGAMOUS (AG) and RBCS-1A was not affected by ACC treatment. For ACTIN2, three biological replication of ACC induction were performed. Data represent average means and the expression before ACC induction was set as 1. The expressions of AG and RBCS-1A were normalized with that of ACTIN2.

(TIF)

Figure S2 Expression, histone methylation and H2A.Z deposition of five additional ethylene responsive factor (ERF) genes during ACC induction. RNA levels (A), H3K4me3 (B, C), H3K27me3 (D) and H2A.Z (E) of ORA59 (At1g066160), TDR1 (At3g23230), AtERF1 (At4g17500), ATER-F2 (At4g47220) and ATERF11 (At1g28370) were measured at the different time points during ACC treatment as indicated. Bars represent mean values +/− SD from three repeats. For ChIP experiments, primers corresponding to the promoter (B) and gene bodies (C-E) were used. Significance of H3K4me3 difference between WT and hta9/hta11 at different time points was determined by two-tailed Student’s t-test, * p<0.05, **p<0.005. (TIF)

Figure S3 Expression and H3K4me3 of additional ethylene responsive factor (ERF) genes between WT and lhp1 during ACC induction. RNA levels (upper) and H3K4me3 (lower) were measured during ACC treatment. Bars represent mean values +/− SD from three repeats. For ChIP experiments, primers corresponding to the gene bodies were used.
Significance of H3K4me3 levels between WT and lhp1 before and after ACC treatment was determined by two-tailed Student’s t-test. *p<0.05, **p<0.005.

(TIF)

Table S1  Sequences of primers used in this study.

(DOC)

References

Le remodelage de la chromatine et la modification des histones jouent des rôles très importants dans l’établissement et la reprogrammation de l’état de l’expression génique. Il reste largement inconnu concernant les mécanismes de la régulation de ces processus chromatiniens dans le contrôle de l’expression génique impliquée dans le développement de la plante et sa adaptation à l’environnement. Mon sujet de thèse se focalise sur l’analyse fonctionnelle d’un facteur de remodelage de la chromatine de type Chromodomain/Hélicase/DNA-binding 1 (CHD1) d’Arabidopsis, appelé CHR5 et une histone démethylase qui est spécifiquement impliquée dans la déméthylation de l’histone H3 lysine 4 (H3K4), appelée JM15. Dans la première partie de cette étude, nous avons montré que le gène CHR5 est activé au cours de l’embryogénèse et que son expression se maintient élevé dans les tissus/organes en développement. L’analyse de mutants révèle que la perte de fonction de ce gène fait réprimer l’expression de gènes régulateurs de la maturation de l’embryon tels que LEC1, ABI3 et FUS3 pendant le développement des graines, et fait baisser l’accumulation des protéines de réserve. L’analyse de double mutants a permis de démontrer une fonction antagoniste entre CHR5 et PKL, une protéine du groupe « CHD3 », dans l’activité du promoteur de gènes régulateurs du développement de l’embryon et l’accumulation de réserve de graine. Nous avons montré que la protéine CHR5 s’associe directement avec les promoteurs d’ABI3 et FUS3 et que la mutation du gène CHRS5 conduit à l’augmentation de présence de nucléosomes dans la région du départ de transcription. Ces résultats suggèrent que CHR5 est impliquée dans le positionnement de nucléosomes pour stimuler l’expression de gènes de la maturation de l’embryon, ce qui est contrebalance par l’action de PKL au cours du développement de l’embryon. La deuxième partie de cette étude a permis de montrer que l’expression du gène de l’histone démethylase JM15 manifeste une forte spécificité tissulaire. L’analyse de mutants du gène a permis de l’identification de 2 allèles de gain de fonction (avec surexpression du gène), et un allèle de perte de fonction. La surexpression du gène réduit la croissance d’hypocotyle et de tige de la plante avec accumulation de lignine dans la tige, mais le perte de fonction du gène ne produise pas de phénotype apparent. Par ailleurs, la surexpression du gène renforce la tolérance de la plante au stress salin, alors la perte de fonction du gène rend la plante plus sensible. L’analyse du transcriptome a révélé beaucoup plus de gènes réprimés qu’activés par la surexpression du gène JM15. Ces gènes réprimés sont préférentiellement marqué la H3K4me2 ou H3K4me3, parmi lesquels beaucoup codent de facteurs de transcription. Ces données suggèrent que l’induction de JM15 pourrait réguler le programme de l’expression génique qui coordonne la restriction de la croissance de la plante et la tolérance au stress. Ces travaux de thèse a permis ‘identifier quelques nouveaux éléments dans la compréhension de la fonction de régulateurs chromatiniens dans l’expression génique de la plante.

**RESUME**

Le remodelage de la chromatine et la modification des histones jouent des rôles très importants dans l’établissement et la reprogrammation de l’état de l’expression génique. Il reste largement inconnu concernant les mécanismes de la régulation de ces processus chromatiniens dans le contrôle de l’expression génique impliquée dans le développement de la plante et sa adaptation à l’environnement. Mon sujet de thèse se focalise sur l’analyse fonctionnelle d’un facteur de remodelage de la chromatine de type Chromodomain/Hélicase/DNA-binding 1 (CHD1) d’Arabidopsis, appelé CHR5 et une histone démethylase qui est spécifiquement impliquée dans la déméthylation de l’histone H3 lysine 4 (H3K4), appelée JM15. Dans la première partie de cette étude, nous avons montré que le gène CHR5 est activé au cours de l’embryogénèse et que son expression se maintient élevé dans les tissus/organes en développement. L’analyse de mutants révèle que la perte de fonction de ce gène fait réprimer l’expression de gènes régulateurs de la maturation de l’embryon tels que LEC1, ABI3 et FUS3 pendant le développement des graines, et fait baisser l’accumulation des protéines de réserve. L’analyse de double mutants a permis de démontrer une fonction antagoniste entre CHR5 et PKL, une protéine du groupe « CHD3 », dans l’activité du promoteur de gènes régulateurs du développement de l’embryon et l’accumulation de réserve de graine. Nous avons montré que la protéine CHR5 s’associe directement avec les promoteurs d’ABI3 et FUS3 et que la mutation du gène CHRS5 conduit à l’augmentation de présence de nucléosomes dans la région du départ de transcription. Ces résultats suggèrent que CHR5 est impliquée dans le positionnement de nucléosomes pour stimuler l’expression de gènes de la maturation de l’embryon, ce qui est contrebalance par l’action de PKL au cours du développement de l’embryon. La deuxième partie de cette étude a permis de montrer que l’expression du gène de l’histone démethylase JM15 manifeste une forte spécificité tissulaire. L’analyse de mutants du gène a permis de l’identification de 2 allèles de gain de fonction (avec surexpression du gène), et un allèle de perte de fonction. La surexpression du gène réduit la croissance d’hypocotyle et de tige de la plante avec accumulation de lignine dans la tige, mais le perte de fonction du gène ne produise pas de phénotype apparent. Par ailleurs, la surexpression du gène renforce la tolérance de la plante au stress salin, alors la perte de fonction du gène rend la plante plus sensible. L’analyse du transcriptome a révélé beaucoup plus de gènes réprimés qu’activés par la surexpression du gène JM15. Ces gènes réprimés sont préférentiellement marqué la H3K4me2 ou H3K4me3, parmi lesquels beaucoup codent de facteurs de transcription. Ces données suggèrent que l’induction de JM15 pourrait réguler le programme de l’expression génique qui coordonne la restriction de la croissance de la plante et la tolérance au stress. Ces travaux de thèse a permis ‘identifier quelques nouveaux éléments dans la compréhension de la fonction de régulateurs chromatiniens dans l’expression génique de la plante.

**SUMMARY**

Chromatin remodeling and histone modification play important roles in the establishment and dynamic regulation of gene expression states. However, little is known regarding to the regulatory mechanism of chromatin modification and remodeling that control gene expression involved in plant development and responses to environmental cues. My thesis work concerns functional analysis of an Arabidopsis Chromodomain/Helicase/DNA-binding 1 (CHD1) type chromatin remodeling gene known as CHR5 and a histone demethylase gene that specifically removes methyl groups from methylated histone H3 lysine 4 (H3K4me), called JM15 in regulating chromatin structure or in resetting chromatin modifications that control the expression of plant developmental and stress responsive genes. In the first part of the study we found that CHRS5 expression is activated during embryogenesis and remained to be expressed in developing organs/tissues. Analysis of mutants revealed that loss-of-function of the genes led to decreased expression of key embryo maturation genes LEC1, ABI3 and FUS3 in developing seeds and reduced seed storage protein accumulation. Analysis of double mutants revealed an antagonistic function between CHRS5 and PKL, a CHD3 gene, in embryo gene promoter activity and seed storage protein accumulation. CHRS5 was directly associated with the promoters of ABI3 and FUS3 and chr5 mutations led to increased nucleosome occupancy near the transcriptional start site. The results suggest that CHRS5 is involved in nucleosome occupancy to regulate embryo identity genes expression, which is counterbalanced by PKL during embryo development. The second part of this study showed that expression of JM15 was restricted to a few tissues during vegetative growth. The jmj15 gain-of-function mutations reduced the length of seedling hypocotyls and inflorescence stems with higher accumulation of lignin in the stem, while the loss-of-function mutants did not show any visible phenotype. The gain-of-function mutants enhanced salt tolerance, whereas the loss-of-function mutants were more sensitive to salt. Transcriptomic analysis revealed a much higher number of genes down-regulated in JM15 over-expression plants, which are highly enriched for H3K4me3 and H3K4me2. Among the down-regulated genes, many encode transcription regulators of stress responsive genes. The data suggest that increased JM15 levels may regulate the gene expression program that may coordinate plant growth restrains and enhances stress tolerance. Taken together, my thesis work brought a few new elements to the current understanding of chromatin regulators function in plant gene expression.