Hypothesis: Selection of Imprinted Genes Is Driven by Silencing Deleterious Gene Activity in Somatic Tissues

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In mammals and plants, parental genomic imprinting restricts expression of certain loci to one parental allele. In mammals, imprinted genes affect various aspects of maternal care and nutrition of offspring from embryogenesis until adulthood. In plants, the expression of imprinted genes is mostly restricted to the endosperm, which nurtures the embryo. Although this restricted domain of expression suggests that the selection of imprinted genes is related to their role in endosperm, supporting evidence is still limited. In contrast, our literature survey supports a significant impact of ectopic expression of imprinted genes on vegetative tissues that affects plant fitness. We propose that silencing of gene function in vegetative tissue is the primary cause of selection of imprinted genes that may be followed by acquisition of major roles in seed development.

Parental genomic imprinting is an epigenetic regulation that causes preferential expression of certain loci to one parental allele (Feil and Berger 2007; Bartolomei 2009; Ferguson-Smith 2011). In mammals, sex-dependent de novo deposition of DNA methylation by specific methyltransferases Dnmt3a and Dnmt3b affects imprinted loci during male or female gametogenesis leading to asymmetric patterns of DNA methylation, which differentiate parental alleles and are further preserved in the embryo by the maintenance of DNA methyltransferase Dnmt1 (Bartolomei 2009; Ferguson-Smith 2011). In contrast, the plant homolog of Dnmt1, the DNA methyltransferase 1 (MET1), and the DNA demethylase DEMETER (DME) control parent-specific gene activation leading to imprinted expression after fertilization (Kohler and Weinhofer-Molisch 2011; Wollmann and Berger 2012). Histone methylation by the Polycomb group also assists imprinting both in plants and mammals (Feil and Berger 2007).

Plant sexual reproduction involves two parallel fertilization events (Berger et al. 2008). Two sperm cells fertilize two distinct female gametes, the egg cell and the central cell, producing the embryo and the endosperm, respectively. The endosperm nurtures embryogenesis during seed development (Li and Berger 2012). Genome-wide surveys of parental allele-specific expression in *Arabidopsis*, rice, and maize have shown that imprinting is largely confined to genes expressed in endosperm (Gehring et al. 2011; Hsieh et al. 2011; Luo et al. 2011; Waters et al. 2011; Wolff et al. 2011; Zhang et al. 2011). Although a few genes show imprinted expression in the embryo in rice and maize (Luo et al. 2011; Waters et al. 2011; Zhang et al. 2011) and likely *Arabidopsis* (Nodine and Bartel 2011), this status is transient and to date there has been no report of imprinted expression in plants after seed

germination. Hence, unlike mammals in which imprinting affects expression in adult tissues, plant-imprinted genes are expressed only during a limited period after fertilization.

How imprinting evolved remains unknown, but it is striking that both in plants and mammals imprinting impacts the endosperm and the placenta, respectively, dedicated to nutrition of the developing embryo. It was logical to hypothesize that the function of imprinted genes in the embryo-nurturing annexes played a major role in the evolution and selection of imprinting (Constancia et al. 2004; Charalambous et al. 2007; Berger and Chaudhury 2009; Kohler and Weinhofer-Molisch 2011). Some of these considerations led to the parental conflict theory, which predicts a positive selection of maternally expressed growth inhibitors and paternally expressed growth enhancers (Wilkins and Haig 2003; Haig 2004; Haig and Wilczek 2006). This theory is based on a scenario in which the mother contributes large resources to her offspring from different fathers. Embryos carrying different paternal genomes compete for resource allocation from the mother. It is beneficial for each father to deviate as many maternal resources as possible for his own embryos. It is thus advantageous for the mother to prevent such interference from the father to ensure equitable distribution of nutrients to each of her offspring.

Parental conflict theory suffers several shortcomings (de Jong and Scott 2007; Ferguson-Smith 2011; Li and Berger 2012). It applies to certain mammalian and outcrossing plant species but would not apply to self-fertilizing *Arabidopsis*, in which imprinting, nonetheless is found to be active. Parental conflict theory also predicts that maternally expressed imprinted genes should negatively regulate endosperm growth. Although this is the

case for imprinted genes *MEDEA* (*MEA*) and *FERTILIZATION INDEPENDENT SEED 2* (*FIS2*) (Gehring et al. 2004; Kohler and Weinhofer-Molisch 2011), the actin nucleator FORMIN HOMOLOG 5 in *Arabidopsis* (Fitz Gerald et al. 2009) and the gene *Maternally Expressed Gene 1* in maize (Costa et al. 2012) have effects opposite to that predicted by parental conflict theory. Among recently identified imprinted genes, very few show a function linked with growth regulation (Gehring et al. 2011; Hsieh et al. 2011; Luo et al. 2011; Waters et al. 2011; Wolff et al. 2011; Zhang et al. 2011). And contrary to the expectation of parental conflict theory, the genome-wide census of imprinted genes in *Arabidopsis*, rice, and maize showed limited conservation among related genes or even functional classes. One exceptional major example of conservation appears to be that imprinting affects genes encoding components of Polycomb repressive complex 2 (PRC2) including *MEDEA* (Li and Berger 2012). However, *MEA* has not been subjected to a strong positive selection in *Arabidopsis* (Kawabe et al. 2007; Spillane et al. 2007; Miyake et al. 2009). Similarly, no positive selection was detected for the *MEA* maize homolog *Mez1* (Haun et al. 2007). Together with the lack of obvious function of several imprinted genes identified in *Arabidopsis*, these facts question the hypothesis that the selection of imprinted genes operate by their functions in endosperm. Here, we report that silencing imprinted genes in somatic tissues is essential for a significant proportion of imprinted genes. We further propose a new hypothesis to explain the origin of the primary selection of imprinted genes.

LIMITED IMPACT OF IMPRINTED GENES ON SEED DEVELOPMENT

We compiled three lists of candidate imprinted genes obtained from genome-wide studies of transcriptomes from crosses among different wild-type accessions of *Arabidopsis* (Gehring et al. 2011; Hsieh et al. 2011; Wolff et al. 2011). The relative lack of overlap among the three lists is likely explained by the different accessions used, the different stages of seed development, and the relative amount of endosperm versus remaining surrounding tissues (seed coat) in the samples. We restricted the lists to maternally expressed candidate imprinted genes that showed a highly enriched expression in early endosperm (Le et al. 2011) and did not show expression in vegetative tissue (Schmid et al. 2005). We thus aimed to compile genes with temporal and spatial expression profiles that are similar to widely studied imprinted genes *MEA*, *FIS2*, and *FWA* (Table 1). To test for the similarity of expression pattern among selected genes, we applied a K-means algorithm (Herwig et al. 1999) to the *Arabidopsis* plant life-cycle transcriptome data set (Schmid et al. 2005). All genes presented in the ATH1 array are clustered into 15 groups based on their expression similarity. Among 26 imprinted genes, 19 imprinting genes could be clustered in two groups (both *P* values are $<<0.0001$) (Fig. 1). One group contains *MEA* and *FIS2*, with a rel-

atively longer expression during endosperm development (Fig. 1, top panel). The other group contains *FWA* and other genes encoding transcription factors from the AGAMOUS-LIKE families with a relatively shorter expression during the early syncytial (noncellular) phase of endosperm development (Fig. 1, bottom panel).

We further explored reports related to all selected imprinted genes relative to their functions. We found only very limited evidence relating to functions in the seed (Table 1). The effect of *MEA* and *FIS2* on endosperm development has been extensively characterized. *MEA* and *FIS2* act in a Polycomb repressive complex, which represses expression of several genes expressed in endosperm and controls growth, temporal development, and patterning (Luo et al. 2000; Ingouff et al. 2005; Weinhofer et al. 2011). Maternal effects on seed development have been reported for *MEE27* (Pagnussat et al. 2005) and *MPC* (Tiwari et al. 2008) but their exact role remains unknown. We did not find evidence in the current literature for major function in seeds for other maternally expressed imprinted genes. Similarly in maize (Waters et al. 2011; Zhang et al. 2011) and rice (Luo et al. 2011), although hundreds of candidate imprinted genes have been detected, there is still limited evidence to suggest an important role of imprinted genes in seeds (Li and Berger 2012).

IMPACT OF ECTOPIC EXPRESSION OF IMPRINTED GENES ON VEGETATIVE DEVELOPMENT

Although neither *FWA* nor *SDC* play obvious roles in endosperm (F Berger et al., unpubl.), both genes affect vegetative development. Ectopic expression of demethylated alleles of *FWA* delays flowering owing to the interaction between *FWA* and *FLOWERING LOCUS T* (*FT*) (Ikeda et al. 2007). Similarly, ectopic expression of *SDC* perturbs leaf development and plant growth (Henderson and Jacobsen 2008). We thus searched for detailed studies reporting the impact of ectopic expression of other imprinted genes from our selected list.

Opposite to *FWA* ectopic expression, overexpression of the JmjC-domain-containing H3K4 demethylase *JMJ15* caused early flowering (Yang et al. 2012). *JMJ15* is a member of the H3K4 demethylase JARID1 family and displays H3K4me3 demethylase activity. The mutation of *JMJ15* does not produce an obvious phenotype. In contrast, overexpression of *JMJ15* reduces H3K4me3 at the *FLC* locus and represses *FLC* transcript levels, resulting in increased *FT* expression and precocious flowering. Similarly, *AtBMI1C* overexpression causes early flowering in *Arabidopsis* via silencing of the flowering repressor *FLC* and by promoting expression of the flowering activator *FT* (Li et al. 2011). *AtBMI1C* is a component of a PRC1-like complex that shows H2A monoubiquitination activity. Early flowering also results from overexpression of *AGAMOUS LIKE 28* (*AGL28*), but the pathway involved is independent of *FT* and *FLC*. *AGL28* up-regulates the expression of *FCA* and *LUMINIDEPENDENS*

SELECTION OF IMPRINTED GENES

25

Table 1. Survey of imprinted genes and their effect on seed and vegetative development

Gene ID	Gene name	Function	Seed-specific expression?	Deleterious if ectopically expressed?	Effect on endosperm/seed?
AT1G69520		Methyltransferase			
AT5G42930		Lipid metabolism			
AT2G17690	<i>SDC</i>	Unknown	Yes	Yes	No
AT4G00220	<i>JLO</i>	Lob domain	Yes	Yes	
AT4G31060	<i>ERF015</i>	AP2 TF	Yes	Yes?	
AT1G20500	<i>GAMT1</i>	Gibberelin metabolism	Yes	Yes	
AT1G62333		Unknown			
AT1G34060		Secondary metabolism			
AT3G49540		Unknown			
AT3G16720	<i>ATL2</i>	Response to pathogens		Yes	
AT1G14580		Zn-finger protein	No, but higher in seed		
AT4G23020	<i>TRM11</i>	Microtubule associated?			
AT1G73500	<i>MAPKK9</i>	MAPKK response to pathogen	No, but increases in seed	Yes	
AT5G22020		Strictosidine synthetase			
AT5G64430		Unknown			
AT2G38250	<i>SRO3</i>	TF response to pathogen	More, but low		
AT1G27730		Response to stress Zn finger	No, but higher in seed		
AT5G26700		Response to pathogen			
AT1G02580	<i>MEA</i>	Chromatin modification	Yes	Yes?	Yes
AT2G35670	<i>FIS2</i>	Chromatin modification	Yes	Yes?	Yes
AT3G03260	<i>HDG8</i>	TF	Yes		
AT3G19350	<i>MPC</i>		Yes		?
AT4G00540	<i>MYB3R2</i>	myb TF		Yes	
AT4G25530	<i>FWA/HDG6</i>	Homeodomain TF	Yes	Yes	No
AT5G17321		Homeodomain TF?	Yes		
AT5G17322	<i>JMJ15</i>	dsRNA binding/miRNA function	Yes	Yes	Yes?
AT5G17323	<i>SUVH8</i>	Set domain	Yes		
AT5G17324	<i>SUVH7</i>	Set domain			
AT5G17325		Nodulin-like transporter	Yes		
AT1G52460		Hydrolase	Yes		
AT3G23060	<i>BMI1C</i>	Zn-finger PRC1	Yes	Yes	
AT5G03020		Kelch domain	?		
AT1G60970		SNARE-like	?	Link with cytokinin; link with pathogen disease resistance	
AT2G19400	<i>AGC</i>	ser/Thr protein kinase			
AT4G29570		Cytidine deaminase			
AT5G46300		Unknown	Yes		
AT3G10590		Homeodomain	Yes?		
AT3G21830	<i>ASK8</i>	Interact with F-box proteins			
AT1G51000		Unknown			
AT5G26650	<i>AGL36</i>	TF	Yes		
AT1G01530	<i>AGL28</i>	TF	No, but increases in seed	Yes	
AT5G06500	<i>AGL96</i>	TF	Yes?		
AT1G20730		Unknown	Yes?		

(LD) within the autonomous pathway (Yoo et al. 2006). In addition to these four imprinted genes that impact flowering time via three different pathways, misexpression of the MYB transcription factor MYB3R2 confers aberrant circadian rhythms that also impact the plant developmental temporal program (Hanano et al. 2008). In conclusion, repression of at least five imprinted genes is required to program proper flowering time in *Arabidopsis*.

Similarly to results with *SDC*, we found reports providing evidence that overexpression of two other maternally expressed imprinted genes affects plant morphological development. *GAMT1* is involved in methylation of gibberelins and its overexpression hampers plant development (Varbanova et al. 2007). Plants produce rosettes of slow-growing little downward-curved dark green leaves and abnormal flowers with reduced reproductive

organs, leading to a degree of sterility. Similarly, the *JAGGED LATERAL ORGANS (JLO)* gene, which encodes a member of the LATERAL ORGAN BOUNDARY DOMAIN proteins, affects the activity of another plant hormone, auxin. Inducible *JLO* misexpression activates expression of the KNOX genes *SHOOT MERISTEMLESS* and *KNAT1* in leaves and down-regulates the expression of PIN auxin export facilitators (Borghiet al. 2007). Consequently, bulk auxin transport through the inflorescence stem is drastically reduced, resulting in strongly lobed leaves and termination of the shoot apical meristem with a pin-like phenotype. Vegetative plant development is thus influenced by imprinted genes if they are ectopically expressed. PRC2 is a major regulator of several aspects of plant development. *Arabidopsis* PRC2 imprinted genes *MEA* and *FIS2* belong to two families containing two other genes. *MEA* homologs *SWINGER*

Figure 1. Imprinting genes are enriched in two K-means cluster groups. The y axis shows normalized intensity (log scale). At2g35670 encodes *FIS2*, At1g02580 encodes *MEA*, and At4g25530 encodes *FWA*.

(*SWN*) and *CURLY LEAF (CLF)* and *FIS2* homologs *VERNALIZATION2 (VERN2)* and *EMBRYONIC FLOW-ER 2 (EMF2)* are expressed in vegetative tissues and act in a partially redundant manner (Hennig and Derkacheva 2009; Holec and Berger 2012). It is likely that additional dosage of PRC2 caused by ectopic expression of *MEA* or *FIS2* in vegetative tissue would perturb PRC2 function, although this remains to be tested.

In conclusion, we observed that ectopic expression of several imprinted genes caused various types of deleterious effects on plant development. Our analysis reveals that a third class of imprinted genes is associated with plant defense and response to stress. Among the *ETHYLENE RESPONSE FACTOR (ERF)* gene family, *AtERF015* is linked to *AtERF2*, which when overexpressed in transgenic *Arabidopsis* plants activated transcription from genes encoding basic chitinase, suggesting hyperactivation of plant defense (Brown et al. 2003). Similarly, *ARABIDOPSIS TOXICOS EN LEVADURA 2 (ATL2)* is involved in response to elicitors such as chitin (Serrano and Guzman 2004). *ATL2* is a member of a multigene family coding highly related RING-H2 zinc-finger proteins that may function as E3 ubiquitin ligases. Constitutive expression of *ATL2* causes activation of two early chitin-induced genes and known pathogenesis-related genes that are markers of the salicylic acid

(SA) and jasmonate (JA) defense response. In the field, priming of SA-related defense responses significantly increases disease resistance and plant fitness (Traw et al. 2007) but reduces fitness in the absence of pathogens, as determined in laboratory growth conditions (Abreu and Munne-Bosch 2009). Also related to plant defense mechanisms, the mitogen-activated protein kinase (MPK) cascades play important roles in regulating plant growth, development, and responses to various environmental stimuli (Pitzschke et al. 2009; Zhang and Zhou 2010). Ectopic expression of the imprinted gene *MKK9* in transgenic plants induces the synthesis of ethylene and camalexin through the activation of the endogenous MPK3 and MPK6 kinases and enhances the sensitivity of transgenic seedlings to biotic stress (Xu et al. 2008).

DISCUSSION AND HYPOTHESES

Our survey identifies a class of maternally expressed imprinted genes displaying expression patterns similar to classically studied genes *MEA* and *FWA*. When expressed ectopically in vegetative tissues, more than 25% of these 43 imprinted genes were shown to affect plant life in a manner that is likely deleterious for plant fitness. These genes belong to three functional classes, a class with

broad impact on plant development linked to a role in hormones or in chromatin regulation, a second class of regulators of flowering, and a third class related to response to pathogens. Reports regarding the effect of ectopic expression are missing for the remaining 75% of genes surveyed. Most genes studied so far belong to families comprising several homologs expressed in vegetative tissues. It is thus intriguing that ectopic expression of an additional member of a family has an impact and we can hypothesize that this results from either an imbalance of dosage or that imprinted genes encode proteins that cause dominant negative effects when competing for formation of complexes that involve other members of the family. We conclude that silencing imprinted genes in vegetative tissues is beneficial for plant development and fitness. In contrast, a function in seed development was shown only for a few imprinted genes in *Arabidopsis*. These observations suggest that it is more essential to keep imprinted loci silent in vegetative tissues to ensure proper plant development than to ensure their function during endosperm development.

We propose that silencing is the primary event that is selected and leads to imprinted expression. What mediates the initial silencing? The frequent association of transposons to imprinted genes in plants may provide a mechanism to explain the origin of methylation of *cis* elements that would initiate silencing of new imprinted loci (Walter and Paulsen 2003; Okamura et al. 2004; Wilkins 2005; Fujimoto et al. 2008; Hsieh et al. 2011; Kaneko-Ishino and Ishino 2011; McCole et al. 2011; Wolff et al. 2011). In plants, although the mechanism that silences transposons—RNA-directed DNA methylation (RdDM) (Saze and Kakutani 2007; Martienssen et al. 2008; Mirouze et al. 2009)—is not associated with imprinting (Wollmann and Berger 2012), recent reports have suggested that RdDM is active in pollen on imprinted loci (Calarco et al. 2012), suggesting a role of de novo DNA methylation in imprinting, which still needs to be shown.

How would silencing by DNA methylation result in imprinted expression during seed development? Several key members of the DNA methylation pathway are repressed in the female gametes but are active in the male gametes, and this repression is required for activation of imprinted genes in the central cell (Jullien et al. 2008, 2012). In addition the DNA demethylase DEMETER (DME) expressed in the central cell plays an important additional role for the activation of maternal alleles of imprinted genes (Gehring et al. 2004). The conjunction of both mechanisms results in demethylation of the central cell, which still remains to be confirmed directly, whereas DNA methylation on CG and CHG is maintained in male gametes (Calarco et al. 2012). For our hypothesis, we consider loci that are expressed from both alleles in endosperm in an ancestral state. According to the supposed imbalance of general status of DNA methylation between male and female gametes, any event causing silencing by DNA methylation of such a locus results in maternal expression. In more complex cases, demethylation of *cis* elements may impact paternal expression, as shown for the paternally expressed imprinted

gene *PHERES1* (Makarevich et al. 2008). We propose that results of the initial silencing event from neoproduction of siRNAs (small interfering RNA) would attract DNA methylation de novo. This can result from transposition but also from many other events such as gene duplications, events leading to initiation of antisense transcripts, deletion, or insertions. We assume that the methylated locus includes sufficient numbers of CG and CHG residues that allow the DNA methylation pattern to be inherited through cell division in a semiconservative manner by the maintenance of DNA methyltransferases MET1 and CMT3. If the effect of the methylated *cis* element is beneficial or neutral for the plant vegetative development, the new event is retained and selected positively. The gene then becomes expressed only in the endosperm from the parental allele that retains the epigenetic methylation marks removed differentially during gametogenesis. In rare cases, the gene acquires a positive function for endosperm and seed development, and its mutation causes a maternal gametophytic effect such as that shown for *MEA* and *FIS2*. In other cases, the function of imprinted genes in endosperm might not be of importance, which would explain the lack of conservation of imprinting genes across species.

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REFERENCES

- Abreu ME, Munne-Bosch S. 2009. Salicylic acid deficiency in NahG transgenic lines and *sid2* mutants increases seed yield in the annual plant *Arabidopsis thaliana*. *J Exp Bot* **60**: 1261–1271.
- Bartolomei MS. 2009. Genomic imprinting: Employing and avoiding epigenetic processes. *Genes Dev* **23**: 2124–2133.
- Berger F, Chaudhury A. 2009. Parental memories shape seeds. *Trends Plant Sci* **14**: 550–556.
- Berger F, Hamamura Y, Ingouff M, Higashiyama T. 2008. Double fertilization – caught in the act. *Trends Plant Sci* **13**: 437–443.
- Borghi L, Bureau M, Simon R. 2007. *Arabidopsis* JAGGED LATERAL ORGANS is expressed in boundaries and coordinates KNOX and PIN activity. *Plant Cell* **19**: 1795–1808.
- Brown RL, Kazan K, McGrath KC, Maclean DJ, Manners JM. 2003. A role for the GCC-box in jasmonate-mediated activation of the *PDF1.2* gene of *Arabidopsis*. *Plant Physiol* **132**: 1020–1032.
- Calarco JP, Borges F, Donoghue MT, Van Ex F, Jullien PE, Lopes T, Gardner R, Berger F, Feijo JA, Becker JD, et al. 2012. Reprogramming of DNA Methylation in Pollen Guides Epigenetic Inheritance via Small RNA. *Cell* **151**: 194–205.
- Charalambous M, da Rocha ST, Ferguson-Smith AC. 2007. Genomic imprinting, growth control and the allocation of nutritional resources: Consequences for postnatal life. *Curr Opin Endocrinol Diabetes Obes* **14**: 3–12.
- Constancia M, Kelsey G, Reik W. 2004. Resourceful imprinting. *Nature* **432**: 53–57.
- Costa LM, Yuan J, Rouster J, Paul W, Dickinson H, Gutierrez-Marcos JF. 2012. Maternal control of nutrient allocation in plant seeds by genomic imprinting. *Curr Biol* **22**: 160–165.
- de Jong TJ, Scott RJ. 2007. Parental conflict does not necessarily lead to the evolution of imprinting. *Trends Plant Sci* **12**: 439–443.

- Feil R, Berger F. 2007. Convergent evolution of genomic imprinting in plants and mammals. *Trends Genet* **23**: 192–199.
- Ferguson-Smith AC. 2011. Genomic imprinting: The emergence of an epigenetic paradigm. *Nat Rev Genet* **12**: 565–575.
- Fitz Gerald JN, Hui PS, Berger F. 2009. Polycomb group-dependent imprinting of the actin regulator AtFH5 regulates morphogenesis in *Arabidopsis thaliana*. *Development* **136**: 3399–3404.
- Fujimoto R, Kinoshita Y, Kawabe A, Kinoshita T, Takashima K, Nordborg M, Nasrallah ME, Shimizu KK, Kudoh H, Kakutani T. 2008. Evolution and control of imprinted *FWA* genes in the genus *Arabidopsis*. *PLoS Genet* **4**: e1000048.
- Gehring M, Choi Y, Fischer RL. 2004. Imprinting and seed development. *Plant Cell* **16** Suppl: S203–S213.
- Gehring M, Missirian V, Henikoff S. 2011. Genomic Analysis of Parent-of-Origin Allelic Expression in *Arabidopsis thaliana* Seeds. *PLoS One* **6**: e23687.
- Haig D. 2004. Genomic imprinting and kinship: How good is the evidence? *Annu Rev Genet* **38**: 553–585.
- Haig D, Wilczek A. 2006. Sexual conflict and the alternation of haploid and diploid generations. *Philos Trans R Soc Lond B Biol Sci* **361**: 335–343.
- Hanano S, Stracke R, Jakoby M, Merkle T, Domagalska MA, Weisshaar B, Davis SJ. 2008. A systematic survey in *Arabidopsis thaliana* of transcription factors that modulate circadian parameters. *BMC Genomics* **9**: 182.
- Haun WJ, Laouelle-Duprat S, O'Connell MJ, Spillane C, Grossniklaus U, Phillips AR, Kaeppeler SM, Springer NM. 2007. Genomic imprinting, methylation and molecular evolution of maize Enhancer of zeste (Mez) homologs. *Plant J* **49**: 325–337.
- Henderson IR, Jacobsen SE. 2008. Tandem repeats upstream of the *Arabidopsis* endogene *SDC* recruit non-CG DNA methylation and initiate siRNA spreading. *Genes Dev* **22**: 1597–1606.
- Hennig L, Derkacheva M. 2009. Diversity of Polycomb group complexes in plants: Same rules, different players? *Trends Genet* **25**: 414–423.
- Herwig R, Poustka AJ, Muller C, Bull C, Lehrach H, O'Brien J. 1999. Large-scale clustering of cDNA-fingerprinting data. *Genome Res* **9**: 1093–1105.
- Holec S, Berger F. 2012. Polycomb group complexes mediate developmental transitions in plants. *Plant Physiol* **158**: 35–43.
- Hsieh TF, Shin J, Uzawa R, Silva P, Cohen S, Bauer MJ, Hashimoto M, Kirkbride RC, Harada JJ, Zilberman D, et al. 2011. Regulation of imprinted gene expression in *Arabidopsis* endosperm. *Proc Natl Acad Sci* **108**: 1755–1762.
- Ikeda Y, Kobayashi Y, Yamaguchi A, Abe M, Araki T. 2007. Molecular basis of late-flowering phenotype caused by dominant epi-alleles of the *FWA* locus in *Arabidopsis*. *Plant Cell Physiol* **48**: 205–220.
- Ingouff M, Haseloff J, Berger F. 2005. Polycomb group genes control developmental timing of endosperm. *Plant J* **42**: 663–674.
- Jullien PE, Mosquana A, Ingouff M, Sakata T, Ohad N, Berger F. 2008. Retinoblastoma and its binding partner MSI1 control imprinting in *Arabidopsis*. *PLoS Biol* **6**: e194.
- Jullien PE, Susaki D, Yelagandula R, Higashiyama T, Berger F. 2012. DNA Methylation Dynamics during Sexual Reproduction in *Arabidopsis thaliana*. *Curr Biol* **22**: 1825–1830.
- Kaneko-Ishino T, Ishino F. 2011. Retrotransposon silencing by DNA methylation contributed to the evolution of placentation and genomic imprinting in mammals. *Dev Growth Differ* **52**: 533–543.
- Kawabe A, Fujimoto R, Charlesworth D. 2007. High diversity due to balancing selection in the promoter region of the *Me-dea* gene in *Arabidopsis lyrata*. *Curr Biol* **17**: 1885–1889.
- Kohler C, Weinhofer-Molisch I. 2011. Mechanisms and evolution of genomic imprinting in plants. *Heredity* **105**: 57–63.
- Le BH, Cheng C, Bui AQ, Wagmeister JA, Henry KF, Pelletier J, Kwong L, Belmonte M, Kirkbride R, Horvath S, et al. 2011. Global analysis of gene activity during *Arabidopsis* seed development and identification of seed-specific transcription factors. *Proc Natl Acad Sci* **107**: 8063–8070.
- Li J, Berger F. 2012. Endosperm: Food for humankind and fodder for scientific discoveries. *New Phytol* **195**: 290–305.
- Li W, Wang Z, Li J, Yang H, Cui S, Wang X, Ma L. 2011. Overexpression of *AtBMI1C*, a Polycomb group protein gene, accelerates flowering in *Arabidopsis*. *PLoS One* **6**: e21364.
- Luo M, Bilodeau P, Dennis ES, Peacock WJ, Chaudhury A. 2000. Expression and parent-of-origin effects for *FIS2*, *MEA*, and *FIE* in the endosperm and embryo of developing *Arabidopsis* seeds. *Proc Natl Acad Sci* **97**: 10637–10642.
- Luo M, Taylor JM, Spriggs A, Zhang H, Wu X, Russell S, Singh M, Koltunow A. 2011. A genome-wide survey of imprinted genes in rice seeds reveals imprinting primarily occurs in the endosperm. *PLoS Genet* **7**: e1002125.
- Makarevich G, Villar CB, Erilova A, Kohler C. 2008. Mechanism of PHERES1 imprinting in *Arabidopsis*. *J Cell Sci* **121**: 906–912.
- Martienssen RA, Kloc A, Slotkin RK, Tanurdzic M. 2008. Epigenetic inheritance and reprogramming in plants and fission yeast. *Cold Spring Harb Symp Quant Biol* **73**: 265–271.
- McCole RB, Loughran NB, Chahal M, Fernandes LP, Roberts RG, Fraternali F, O'Connell MJ, Oakey RJ. 2011. A case-by-case evolutionary analysis of four imprinted retrogenes. *Evolution* **65**: 1413–1427.
- Mirouze M, Reinders J, Bucher E, Nishimura T, Schneeberger K, Ossowski S, Cao J, Weigel D, Paszkowski J, Mathieu O. 2009. Selective epigenetic control of retrotransposition in *Arabidopsis*. *Nature* **461**: 427–430.
- Miyake T, Takebayashi N, Wolf DE. 2009. Possible diversifying selection in the imprinted gene, *MEDEA*, in *Arabidopsis*. *Mol Biol Evol* **26**: 843–857.
- Nordine MD, Bartel DP. 2011. Maternal and paternal genomes contribute equally to the transcriptome of early plant embryos. *Nature* **482**: 94–97.
- Okamura K, Yamada Y, Sakaki Y, Ito T. 2004. An evolutionary scenario for genomic imprinting of Impact lying between nonimprinted neighbors. *DNA Res* **11**: 381–390.
- Pagnussat GC, Yu HJ, Ngo QA, Rajani S, Mayalagu S, Johnson CS, Capron A, Xie LF, Ye D, Sundaresan V. 2005. Genetic and molecular identification of genes required for female gametophyte development and function in *Arabidopsis*. *Development* **132**: 603–614.
- Pitzschke A, Schikora A, Hirt H. 2009. MAPK cascade signalling networks in plant defence. *Curr Opin Plant Biol* **12**: 421–426.
- Saze H, Kakutani T. 2007. Heritable epigenetic mutation of a transposon-flanked *Arabidopsis* gene due to lack of the chromatin-remodeling factor DDM1. *EMBO J* **26**: 3641–3652.
- Schmid M, Davison TS, Henz SR, Pape UJ, Demar M, Vingron M, Scholkopf B, Weigel D, Lohmann JU. 2005. A gene expression map of *Arabidopsis thaliana* development. *Nat Genet* **37**: 501–506.
- Serrano M, Guzman P. 2004. Isolation and gene expression analysis of *Arabidopsis thaliana* mutants with constitutive expression of *ATL2*, an early elicitor-response RING-H2 zinc-finger gene. *Genetics* **167**: 919–929.
- Spillane C, Schmid KJ, Laouelle-Duprat S, Pien S, Escobar-Restrepo JM, Baroux C, Gagliardini V, Page DR, Wolfe KH, Grossniklaus U. 2007. Positive darwinian selection at the imprinted *MEDEA* locus in plants. *Nature* **448**: 349–352.
- Tiwari S, Schulz R, Ikeda Y, Dytham L, Bravo J, Mathers L, Spielman M, Guzman P, Oakey RJ, Kinoshita T, et al. 2008. *MATERNALLY EXPRESSED PAB C-TERMINAL*, a novel imprinted gene in *Arabidopsis*, encodes the conserved C-terminal domain of polyadenylate binding proteins. *Plant Cell* **20**: 2387–2398.
- Traw MB, Kniskern JM, Bergelson J. 2007. SAR increases fitness of *Arabidopsis thaliana* in the presence of natural bacterial pathogens. *Evolution* **61**: 2444–2449.
- Varbanova M, Yamaguchi S, Yang Y, McKelvey K, Hanada A, Borochov R, Yu F, Jikumaru Y, Ross J, Cortes D, et al. 2007. Methylation of gibberellins by *Arabidopsis* GAMT1 and GAMT2. *Plant Cell* **19**: 32–45.

- Walter J, Paulsen M. 2003. The potential role of gene duplications in the evolution of imprinting mechanisms. *Hum Mol Genet* **12** Spec No 2: R215–R220.
- Waters AJ, Makarevitch I, Eichten SR, Swanson-Wagner RA, Yeh CT, Xu W, Schnable PS, Vaughn MW, Gehring M, Springer NM. 2011. Parent-of-origin effects on gene expression and DNA methylation in the maize endosperm. *Plant Cell* **23**: 4221–4233.
- Weinhofer I, Hehenberger E, Roszak P, Hennig L, Kohler C. 2011. H3K27me3 profiling of the endosperm implies exclusion of Polycomb group protein targeting by DNA methylation. *PLoS Genet* **6**: e1001152.
- Wilkins JF. 2005. Genomic imprinting and methylation: Epigenetic canalization and conflict. *Trends Genet* **21**: 356–365.
- Wilkins JF, Haig D. 2003. What good is genomic imprinting: The function of parent-specific gene expression. *Nat Rev Genet* **4**: 359–368.
- Wolff P, Weinhofer I, Seguin J, Roszak P, Beisel C, Donoghue MT, Spillane C, Nordborg M, Rehmsmeier M, Kohler C. 2011. High-resolution analysis of parent-of-origin allelic expression in the *Arabidopsis* endosperm. *PLoS Genet* **7**: e1002126.
- Wollmann H, Berger F. 2012. Epigenetic reprogramming during plant reproduction and seed development. *Curr Opin Plant Biol* **15**: 63–69.
- Xu J, Li Y, Wang Y, Liu H, Lei L, Yang H, Liu G, Ren D. 2008. Activation of MAPK kinase 9 induces ethylene and camalexin biosynthesis and enhances sensitivity to salt stress in *Arabidopsis*. *J Biol Chem* **283**: 26996–27006.
- Yang H, Mo H, Fan D, Cao Y, Cui S, Ma L. 2012. Overexpression of a histone H3K4 demethylase, JMJ15, accelerates flowering time in *Arabidopsis*. *Plant Cell Rep* **31**: 1297–1308.
- Yoo SK, Lee JS, Ahn JH. 2006. Overexpression of AGAMOUS-LIKE 28 (AGL28) promotes flowering by upregulating expression of floral promoters within the autonomous pathway. *Biochem Biophys Res Commun* **348**: 929–936.
- Zhang J, Zhou JM. 2010. Plant immunity triggered by microbial molecular signatures. *Mol Plant* **3**: 783–793.
- Zhang M, Zhao H, Xie S, Chen J, Xu Y, Wang K, Zhao H, Guan H, Hu X, Jiao Y, et al. 2011. Extensive, clustered parental imprinting of protein-coding and noncoding RNAs in developing maize endosperm. *Proc Natl Acad Sci* **108**: 20042–20047.

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