Balance between maternal and paternal alleles sets the timing of resource accumulation in the maize endosperm

Na Li and Hugh G. Dickinson*

Department of Plant Sciences, South Parks Road, Oxford OX1 3RB, UK

Key aspects of seed development in flowering plants are held to be under epigenetic control and to have evolved as a result of conflict between the interests of the male and female gametes (kinship theory). Attempts to identify the genes involved have focused on imprinted sequences, although imprinting is only one mechanism by which male or female parental alleles may be exclusively expressed immediately post-fertilization. We have studied the expression of a subset of endosperm gene classes immediately following interploidy crosses in maize and show that departure from the normal 2:1 ratio between female and male genomes exerts a dramatic effect on the timing of expression of some, but not all, genes investigated. Paternal genomic excess prolongs the expression of early genes and delays accumulation of reserves, while maternal genomic excess foreshortens the expression period of early genes and dramatically brings forward endosperm maturation. Our data point to a striking interdependence between the phases of endosperm development, and are consonant with previous work from maize showing progression from cell proliferation to endoreduplication is regulated by the balance between maternal and paternal genomes, and from Arabidopsis suggesting that this ‘phasing’ is regulated by maternally expressed imprinted genes. Our findings are discussed in context of the kinship theory.

Keywords: endosperm; imprinting; interploidy crosses; kinship theory; maize (Zea mays); plant fertilization

1. INTRODUCTION

Maternal control of early seed development is held to be an important driver in the evolution of genes regulating flowering plant reproduction (Chaudhury & Berger 2001). As male and female gametic genomes can be considered to have differing evolutionary ‘interests’, a complex situation may pertain where conflict between these parental interests has resulted in the epigenetic modification of seed-expressed genes such that early development is regulated through a balance of maternally, paternally and biparentally expressed genes (Haig & Westoby 1989). This hypothesis requires that this epigenetic ‘marking’ (imprinting) should target genes regulating the provision of resources—but to date few genetic ‘marking’ (imprinting) should target genes regulating the provision of resources—but to date few have been identified. The MEG1 gene of maize is an exception (Gutiérrez-Marcos et al. 2004), for it encodes a putative signal protein located at the basal transfer layer of the endosperm, which is required for grain filling as well as for correct development of the cell layer itself. This absence of imprinted genes involved in resource acquisition may be explained either by imprinting controlling major upstream regulators rather than physiologically functional genes or by the presence of other epigenetic systems that also modulate seed gene expression. Importantly, evolutionary fitness depends on the sum of these systems, so to identify the effects of the totality of these processes on seed fitness, we have analysed the consequences of fertilization involving different numbers of complete genomes—so-called ‘unbalanced crosses’.

Flowering plants have double fertilization where fusion of sperm with the haploid egg and the diploid central cell generates the diploid zygote and triploid endosperm, respectively. The endosperm may either develop transiently, as in Arabidopsis, or be dispersed with the seed as in the grasses (Costa et al. 2004). A key feature of most endosperms is an initial period of nuclear division in the absence of cell walls. Several days after fertilization, these coenocytes cellularize and develop the characteristic ‘tissues’ of the endosperm (for maize: a central starchy region, a bounding layer of specialized aleurone cells, the basal endosperm transfer layer (BETL) through which resources are imported into the endosperm and an embryo-surrounding region (ESR) (Vijayaraghavan & Prabhakar 1984; Thompson et al. 2001; Costa et al. 2004)). Endosperm maturation is accompanied by significant levels of nuclear endoreduplication (Dilkes et al. 2002). Cooper (1951) showed the balance between the maternal and paternal genomic contributions to the endosperms of maize was critical to seed development, and any departure from a balanced cross between diploid parents resulted in kernel abortion. Subsequently, Lin (1984) was able to show that successful endosperm development in maize depended on the donation of two maternal and one paternal genomes, or multiples of this 2:1 ratio. Unlike in maize, interploidy crosses are fertile in Arabidopsis, but unbalanced transitory endosperms still differ strikingly from those resulting from balanced crosses, depending on the direction of the cross. Indeed,
Dilkes et al. (2002) have shown that crosses between diploid and tetraploid lines within particular genotypes can result in lethality, and have identified the cause of this lethality to involve a pathway modified by the maternal effect transcription factor \textit{TRANSPARENT TESTA GLABRA2} (TTG2). However, in those interploidy crosses involving diploid, tetraploid and hexaploid lines giving rise to viable seeds, Scott et al. (1998) showed that donation of excess maternal genomes (maternal genomic excess: MGE) resulted in smaller seeds, while extra paternal genomes (paternal genomic excess: PGE) generated larger seeds. Cytological analyses of these seeds showed PGE resulted in an increased number of endosperm divisions and late cellularization, while MGE induced an abbreviated period of endosperm proliferation. These early data confirmed that maternal and paternal gametic genomes are not functionally equivalent, and must be differentially marked, or imprinted, during male and female gametogenesis.

Subsequently, many genes expressed during endosperm (but not embryo) development have been demonstrated to be imprinted, with only either the male or the female allele expressed (Köhler & Makarevich 2006; Huh et al. 2007). Importantly, many imprinted genes in both Arabidopsis and maize encode polycistron-protein complexes, which operate in chromatin-remodelling complexes that regulate development through repression of target genes (Francis & Kingston 2001). For example, members of the \textit{FERTILIZATION-INDEPENDENT SEED} (FIS) class of genes, which include \textit{MEDEA} (MEA), \textit{FIS2} and \textit{FERTILIZATION-INDEPENDENT ENDOSPERM} (FIE), are imprinted in Arabidopsis, and FIS proteins form part of the plant polycistron-repressive complex (PRC) that regulates endosperm development (Grossniklaus et al. 1998; Luo et al. 1999; Ohad et al. 1999; Chanvivattana et al. 2004). Endosperm development in \textit{fs} mutants commences normally, but the transition from the coenocytic to cellular stage, when functional domains of the endosperm are established, is disrupted, suggesting that the PRC regulates the ontogenetic sequencing of endosperm development, but not the events themselves (Ingouff et al. 2005).

Specific genes, imprinted or otherwise, have yet to be identified as responsible for aberrant development following interploidy crosses in maize, but a study of cell cycle progression (Leblanc et al. 2002) has shown MGE to shorten the early proliferation phase by the precocious induction of programmed cell death, and PGE to directly disrupt endoreduplication which characterizes maturation of the endosperm. Leblanc et al. (2002) suggest that \textit{CYCZme1} (a mitotic B1 cyclin), \textit{ZmWEE1} (a CDK kinase) and RB-like proteins may play key roles in the establishment of endoreduplication following proliferation, and thus are likely to be affected in interploidy crosses. Combining data on early development both from plants and animals, von Wangenheim & Peterson (2004) propose that endosperm development is regulated by an intracellular timer of differentiation rather than an imprinting-based system. This ‘timer’ is held to pace cell division on the basis of cytoplasmic growth, and is capable of counting meiotic cycles.

While PGE and MGE clearly affect the progression of endosperm development in species both with transitory (Arabidopsis) and persistent (maize) endosperms, it is unclear how these differences are manifest at the transcriptional level—and particularly in terms of the expression of sequences associated with the accumulation of reserves that the kinship theory predicts should be the targets of parental conflict. We have therefore measured changes in the timing and levels of transcription of a selected subset of genes following reciprocal interploidy crosses. At very early stages in endosperm development, we show that MGE brings forward the expression of genes responsible for reserve accumulation, and shortens the expression period of early-expressed factors held to be responsible for endosperm patterning, while PGE delays expression of genes regulating reserve acquisition, and prolongs expression of early-expressed sequences. Importantly, both MGE and PGE fail to affect the timing of expression of most endosperm-expressed genes, and although imprinting must certainly play a role in the changes observed, very few of the genes affected are themselves imprinted.

2. MATERIAL AND METHODS

(a) Plant material

Diploid and tetraploid W23 inbred lines of maize (\textit{Zea mays}) were greenhouse grown under a 16 h daylight cycle with supplementary lighting, at 22–28°C (day) and 16–20°C (night). Plants were watered to capacity and pollinations were carried out as described in \textit{The maize handbook} (Freeling & Walbot 1996).

To confirm the ploidy of individual diploid and tetraploid lines, leaf material was analysed using flow cytometry (FACScan; BD Biosciences, San Jose, CA, USA) as described by Pennington (2005). Peaks were measured using CELLQUEST software (BD Biosciences).

(b) Endosperm isolation

Endosperms were excised from kernels at 5 days after pollination (DAP) by microdissection according to Pennington (2005). Endosperm forms by far the major component of the kernel at 10 and 15 DAP; for this reason, entire kernels were sampled at these later time points.

(c) Semiquantitative reverse transcription–polymerase chain reaction analysis

RNA was extracted (TRizol Reagent, Invitrogen, 15596-018) with additional DNase treatment (TURBO DNA-free, Ambion, AM1907) from each sample. For cDNA synthesis, 1 μg of each purified total RNA was used (RETOscript Kit, Ambion, AM1710). PCR reactions were carried out in 50 μl volume reactions, with 1 μl of 10 times diluted cDNA templates. The PCR amplifications were performed with the following programme: one step of 1 min at 95°C, 25, 30 and/or 35 cycles of 30 s at 95°C, 30 s at 58°C and 30 s or 1 min at 72°C (depends on different genes and fragment lengths) and a final step of 5 min at 72°C. PCR-amplified products were electrophoresed in 1.5 per cent agarose gels for approximately 40 min at 160 V and images taken using a UV transilluminator. All the reactions were repeated twice. Primers used for the amplification are listed in electronic supplementary material, table S1.

(d) Real-time quantitative polymerase chain reaction

Real-time quantitative PCR (qPCR) was carried out in triplicate with SYBR Green PCR Master Mix (ABsolute; Blue QPCR SYBR Green ROX Mix, Thermo SCIENTIFIC,
ABgene Nucleic Acid Amplification, AB–4162/A) using an Applied Biosystems Prism-7300. Levels of specific mRNA and maize Actin1 control were calculated by the standard curve method (Applied Biosystems User Bulletin 2). The relative expression (arbitrary units) of each gene of interest was obtained by dividing by the equivalent Actin1 expression. No-template controls were included as negative controls for each set of reactions. Three independent biological repeats gave similar results. Gene-specific primers are listed in electronic supplementary material, table S2.

3. RESULTS

Development of endosperm tissue domains following balanced crosses has already been reported (Thompson et al. 2001; Pennington et al. 2008), and although maize kernels abort following unbalanced interplody crosses (Cooper 1951; Lin 1984), they remain viable until 20–30 DAP during which time the key endosperm tissue domains develop, but to different extents and at different rates (Pennington et al. 2008). We thus selected time points for our gene expression study covering the period during which the endosperm tissue domains are ‘mapped out’, but prior to any indication of tissue necrosis. Tetraploid and diploid lines W23 of maize were reciprocally pollinated and RNA extracted at 5, 10 and 15 DAP, as described in Pennington et al. (2008). As controls, similar extracts were made from endosperms resulting from diploid and tetraploid balanced crosses.

To determine whether observed differences in the development of the endosperm tissue domains were reflected in gene expression, genes were selected from the literature and available databases representing genes expressed early, late and throughout kernel development, genes expressed in key tissue domains and genes known to be imprinted (table 1). Only genes identified in maize and for which expression data have been reported were selected, for, while a more comprehensive list of sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes, sequences could have been made using sequences with homology to Arabidopsis endosperm-expressed genes. Two ‘early’ genes, EBE-1 and EBE-2, similar to the DUF239 proteins of Arabidopsis (Magnard et al. 2003), are confirmed by our data to be expressed early in development, being represented in the 15 and 10 DAP samples. EBE-2, and to a lesser extent EBE-1, expression is affected by parental imbalance; following 4n × 2n crosses, expression is suppressed in the 10 DAP sample, whereas after 2n × 4n pollinations, EBE-2 expression persists until 15 DAP (as also does expression of EBE-1, but at the limits of detection by semiquantitative RT–PCR).

‘Late’ genes, OPAQUE2 and γ-ZEIN, principally involved in reserve accumulation in the central endosperm (Vicente-Carbajosa et al. 1997; Woo et al. 2001), are expressed between 10 and 15 DAP in balanced crosses, but are delayed in their expression to 15 DAP in PGE, and expressed as early as 5 DAP in MGE. NRP1, an imprinted ‘late gene’ encoding a putative transcription factor (Guo et al. 2003), behaves similarly. Two genes, the BETL-specific MEG1 (Gutiérrez-Marcos et al. 2004) and MRP1, a transcription factor believed to regulate it (Gómez et al. 2002), exhibited similar but phased expression patterns. MRP1 expression peaked at 5 DAP, and MEG1 at 10 DAP in balanced crosses, but following 2n × 4n pollinations, MRP1 expression continued unchanged while MEG1 expression increased from 5 to 10 DAP, and thereafter remained constant. 4n × 2n pollinations resulted in high expression of MRP1 and MEG1 at 5 DAP, followed by a dramatic fall to undetectable levels by 10 DAP. However, by 15 DAP, transcripts of both genes were again detectable.

Although the RT–PCRs were repeated using biological replicates, we considered the errors inherent in the method (exemplified by the 25 and 30 cycle samples of 4n × 2n 5 DAP samples of FIE1) required that our data be further validated. Real-time qPCR was therefore used to investigate the expression of genes representative of the three general classes of expression pattern; those unaffected by parental imbalance (MEZ1), early genes for which the expression period is ‘shifted’ by parental excess (EBE-2) and late-expressed genes that are similarly affected (OPAQUE2). The results shown in electronic supplementary material, figure S2, confirm that expression patterns revealed by qPCR reflect very closely those of the semiquantitative RT–PCR data, confirming the validity of this latter dataset. ANOVA analysis of the qPCR data followed by Tukey’s pairwise testing (electronic supplementary material, figure S2) highlights the striking difference between expression of EBE-2 in 2n × 4n and 4n × 2n endosperms at 10 and 15 DAP, and for OPAQUE2, the difference between 2n × 4n and 4n × 2n at 5 DAP and the low expression in 2n × 4n endosperms at 10 DAP. Both the semiquantitative RT–PCR and the qPCR confirm that although the timing of transcription varies for many of the genes studied, the overall level of expression of each gene in MGE and PGE is very similar to that occurring in balanced crosses.

Table 1. Genes involved in maize endosperm development.

<table>
<thead>
<tr>
<th>gene</th>
<th>function</th>
<th>timing of expression in endosperm</th>
<th>reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>CR4</td>
<td>encodes a receptor-like kinase that is implicated in aleurone cell fate</td>
<td>expressed throughout the plant</td>
<td>Becraft et al. (1996)</td>
</tr>
<tr>
<td>DEK1</td>
<td>maintain and restrict aleurone cell fate imposed by CR4</td>
<td>expressed throughout the plant</td>
<td>Lid et al. (2002)</td>
</tr>
<tr>
<td>EBE-1</td>
<td>potentially involved in development of endosperm domains</td>
<td>commences in the central cell, maternally expressed in endosperm; peaks at 7 DAP expression 10× less than EBE-2</td>
<td>Magnard et al. (2003)</td>
</tr>
<tr>
<td>EBE-2</td>
<td>as EBE-1, but no parent-of-origin effect</td>
<td>as EBE-1, but no parent-of-origin effect</td>
<td>Magnard et al. (2003)</td>
</tr>
<tr>
<td>FIE1</td>
<td>maize homologue of the Arabidopsis polycomb-group gene FIE</td>
<td>endosperm-specific, maternally expressed 2–10 DAP</td>
<td>Hermon et al. (2007)</td>
</tr>
<tr>
<td>FIE2</td>
<td>as FIE1 likely to be the functional orthologue of Arabidopsis FIE</td>
<td>bi-allelic expression in the embryo, and later in the endosperm. FIE2 mRNA levels are significantly lower than those of FIE1</td>
<td>Hermon et al. (2007)</td>
</tr>
<tr>
<td>MEG1</td>
<td>may function in regulating nutrient trafficking into endosperm</td>
<td>maternally expressed in the BETL of the endosperm. BETL marker</td>
<td>Gutiérrez-Marcos et al. (2004)</td>
</tr>
<tr>
<td>MEZ1</td>
<td>putative histone methyltransferase related to the Drosophila PcG gene</td>
<td>maternally expressed in endosperm tissue, but bi-allelic elsewhere</td>
<td>Haun et al. (2007)</td>
</tr>
<tr>
<td>MRPI</td>
<td>a transfer-cell–specific MYB-related transcriptional activator</td>
<td>expressed at 3 DAP; maximum at 11 DAP; decreasing after 16 DAP</td>
<td>Gómez et al. (2002)</td>
</tr>
<tr>
<td>NRPI</td>
<td>putative transcription factor</td>
<td>maternally expressed only in the endosperm after fertilization expressed in the endosperm</td>
<td>Guo et al. (2003)</td>
</tr>
<tr>
<td>OPAQUE2</td>
<td>activates alpha-zein class of storage proteins</td>
<td>expressed in the endosperm subaleurone layer from 10 DAP endosperm specific; 10–15 DAP</td>
<td>Vicente-Carbajosa et al. (1997)</td>
</tr>
<tr>
<td>PBF</td>
<td>member of the Dof class of plant Cys2–Cys2 zinc-finger DNA-binding proteins</td>
<td>expressed in embryos at 10 DAP, peaking at 16 DAP and then decreasing gradually. Aleurone/embryo marker</td>
<td>Vicente-Carbajosa et al. (1997)</td>
</tr>
<tr>
<td>SAL1</td>
<td>vacuolar protein sorting gene implicated in membrane vesicle trafficking</td>
<td>expressed throughout the plant</td>
<td>Shen et al. (2003)</td>
</tr>
<tr>
<td>VPI</td>
<td>transcriptional activator required for seed maturation</td>
<td>expressed throughout the endosperm by 10 and 15 DAP</td>
<td>McCarty et al. (1991)</td>
</tr>
<tr>
<td>γ-ZEIN</td>
<td>endosperm-specific storage protein</td>
<td>expressed throughout the endosperm by 10 and 15 DAP</td>
<td>Woo et al. (2001)</td>
</tr>
</tbody>
</table>

4. DISCUSSION

Both Arabidopsis and maize show dramatic parental excess phenotypes. The large seeds that result from pollination by a 4n or 6n male parent in Arabidopsis show an extended phase of endosperm proliferation such that after 5 DAP endosperms contain twice the number of endosperm nuclei as are formed after a 2n × 2n balanced cross (Scott et al. 1998). Cellularization is also significantly delayed in these seeds. Pollination of polytene females by diploid pollen results in small seeds, containing half the numbers of endosperm nuclei at 5 DAP, and in which cellularization is brought forward. Although potentially confounded by abortion of interplody kernels late in development (20+ DAP), data from early maize endosperms show very different phenotypes depending on the direction of the interplody cross (Cooper 1951; Charlton et al. 1995; Pennington et al. 2008). 4n × 2n pollinations result in comparatively normal development of the endosperm and embryo over the first 15 DAP, with correct formation of the aleurone, BETL and ESR domains. However, the kernels are smaller than that of wild-type, contain fewer endosperm cells (Pennington 2005) and accumulate starch between 8 and 10 DAP, far earlier than wild-type (normally 10–14 DAP) (Pennington et al. 2008). Patterning of the endosperm is strongly affected in 2n × 4n crosses with disruption of the aleurone and BETL domains. The endosperm itself, although larger and containing more cells (Pennington 2005), becomes misshapen by 18–20 DAP (Pennington et al. 2008).

A preliminary RT–PCR study of endosperm gene expression, 4, 8 and 10 DAP, revealed changes in the timing of gene expression, rather than in transcript levels (Pennington et al. 2008), suggesting that the dramatic phenotypic differences between reciprocal interploidy crosses may be reflected in the phasing of gene expression programmes. Our data confirm this but, importantly, also reveal that only a subset of genes are involved; for example, genes such as CR4, DEK1 and VPI, which are crucial for endosperm formation and are activated at different phases of its development, remain unaffected by an excess of either maternal or paternal alleles. Also unaffected are the majority of imprinted genes encoding polycomb-group proteins.
Unbalanced maize endosperm development  N. Li & H. G. Dickinson 7

Figure 1. The effect of male and female genomic excess on endosperm gene expression. Semiquantitative RT–PCR on 5, 10 and 15 DAP maize endosperm. (a–e) CR4, EBE-2, FIE1, MRP1 and OPAQUE2 genes, respectively. (f) Actin1: internal control. For CR4, FIE1 and MRP1 genes, 25 and 30 cycles were used in each time point, 30–35 cycles were used for EBE-2 and OPAQUE2. Two replicates were carried out for all genes. The full semiquantitative RT–PCR dataset is shown in electronic supplementary material, figure S1.

some of which are expressed only in the early stages of endosperm development. The fact that both bi-allelicly expressed and imprinted sequences are expressed at equivalent levels (as determined by our methods) in PGE, MGE and balanced crosses confirms the presence of a highly effective dosage compensation system capable of regulating transcript levels.

We show that two early genes (EBE-1, EBE-2) are affected by genomic excess, maternal genomes curtailing and paternal genomes prolonging the period of their expression. Both genes are reported to function in early endosperm domain specialization, with ZmEBE-1 expressed from the maternal allele in the young endosperm (Magnard et al. 2003). By contrast, later-expressed genes involved in accumulation of resources are affected by genomic excess in a reciprocal fashion. Thus, expression of OPAQUE2, which regulates the expression of zein storage proteins (Vicente-Carbajosa et al. 1997), and the γ-ZEIN sequences themselves (Woo et al. 2001) are restricted to a period late in development in the presence of excess paternal genomes, while maternal excess extends the period of expression, bringing it forward significantly. The data generally confirm the structural observations from both Arabidopsis and maize and support the kinship theory (Haig & Westoby 1991; Haig 2000) which holds that the interest of the maternal genome will be in restricting endosperm development, evidenced by the curtailing of expression of early genes with roles in establishing the tissue plan of the endosperm, and the early and extended expression of the maturity phase, characterized by the accumulation of reserves. The kinship theory also predicts that the interest of the paternal genome would be opposite, promoting the establishment phase—creating the possibility of developing a larger embryo, and postponing the maturity phase (after which expansion growth is no longer possible).

The expression patterns of three genes require further consideration. The imprinted transcription factor NRPI, which is normally expressed 15–25 DAP (Guo et al. 2003), responds similarly to OPAQUE2 and γ-ZEIN, suggesting that it is a component of the gene network regulating maturation of the kernel. The expression of MRP1, a transcription factor regulating genes in the BETL (Gómez et al. 2002), and MEG1, a putative signaling protein synthesized in the BETL and regulated by MRP1 (Gutiérrez-Marcos et al. 2004), normally peaks at about 5 and 10 DAP, respectively—consistent with MRP1 activating MEG1. Paternal excess results in continued accumulation of transcript throughout development, while maternal excess causes expression of both genes to cease at 10 DAP, only to recommence at a lower level by 15 DAP. Both genes are involved in patterning the developing endosperm, and thus would be expected to be promoted by the paternal and suppressed by the maternal genome. However, the reappearance of both transcripts after 15 DAP in MGE suggests that they may play roles in both BETL establishment and subsequently its function as a transfer layer during the accumulation of resources that characterizes endosperm maturation. We find no evidence that imprinting per se determines whether expression of a gene is affected by genomic imbalance.
While the changes in expression timing of our early and late genes map closely onto the changes in progression from the 'proliferation' to the 'endoreduplicative' phases of endosperm development described by Leblanc et al. (2002), it is not clear how alteration to the expression of cell cycle progression genes such as CYCZme1, ZmWEE1 or RB-like sequences could modulate expression of genes such as OPAQUE2, and leave the majority of other genes unaffected. Perhaps, more likely is that parental genomic balance affects the activity of major regulatory genes, which control integrated gene networks involving many facets of development. FIS genes are promising candidates for these 'regulatory genes', but fis mutant phenotypes are unavailable for maize, and at least one member of the PRC chromatin-remodelling complex, FIE, has become duplicated and sub- or neo-functionalized in maize (Danilevskaya et al. 2003; Gutiérrez-Marcos et al. 2006). Nevertheless, mutations at fie loci in Arabidopsis result in heterochronic disruption of endosperm development, particularly the progression from coenocytic to cellular development (Ingouff et al. 2005), and it is interesting that in PGE maize endosperms, where the representation of active, maternally expressed FIS loci would be attenuated, the expression of early genes (EBE-1, EBE-2) is significantly prolonged. Zein accumulation in these endosperms is also delayed, pointing to an interdependence between early development (which in Arabidopsis primarily involves cell proliferation) and the later accumulation of reserves. MGE appears to reverse this pattern, indicating that an excess of active FIS alleles results in the PRC inducing maturation events (including reserve accumulation) very early, at the expense of the proliferation phase. Thus, as proposed by Ingouff et al. (2005) for Arabidopsis, in maize it may also be that the PRC regulates the transition from proliferation to maturation, and increasing dosages of maternally expressed FIS sequences result in the increasing dominance of the later maturation phase. However, it is unlikely that the PRC is the sole regulator of endosperm development, repressing the early proliferative phases and promoting maturation and reserve accumulation, for the kinship theory suggests that paternal alleles should promote the proliferation phase of development, which sets the final size of the endosperm. Further, the mosaic of epigenetic information carried by the male and female gametic genomes is likely to be complex and comprise not only imprinted marks, but systems of dosage compensation.
and marking patterns that differentiate male from female chromosomes that enable a measured activation of the paternal genome post-fertilization (Vieille-Calzada et al. 2000; Scholten et al. 2002; Mosher et al. 2009). An understanding of the epigenetic regulation of endosperm development, and indeed the validity of the kinship theory, must thus await unequivocal data on the overall maternal, paternal and bi-allelic input into early seed development and its consequences in terms of the expression of genes that directly results in the complex phenotypes involved.

The kinship theory holds that the evolutionary interests of the male genome will be for the formation of a larger and very fit endosperm, and for the female genome a successful endosperm—but of fitness equivalent to its immediate sibs. Within its limits, our data support this assertion, and reveal that this is achieved not principally by altering the expression levels of large numbers of genes, but rather by modulating the timing of expression of a relatively small number of key sequences. This study was supported by the Biotechnology and Biological Sciences Research Council (BBSRC; BB/E007252/1 to H.G.D.). The authors thank Lili Costa and Pepe Gutierrez-Marcos for help and advice throughout the project, Harriet McWatters for assistance with the qPCR, and Qing Zhang, Helen Prescott and Caroline O’Brien for invaluable technical assistance.

REFERENCES


