Regulation of stem cell maintenance by the Polycomb protein FIE has been conserved during land plant evolution

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The Polycomb group (PcG) complex is involved in the epigenetic control of gene expression profiles. In flowering plants, PcG proteins regulate vegetative and reproductive programs. Epigenetically inherited states established in the gametophyte generation are maintained after fertilization in the sporophyte generation, having a profound influence on seed development. The gametophyte size and phase dominance were dramatically reduced during angiosperm evolution, and have specialized in flowering plants to support the reproductive process. The moss Physcomitrella patens is an ideal organism in which to study epigenetic processes during the gametophyte stage, as it possesses a dominant photosynthetic gametophytic haploid phase and efficient homologous recombination, allowing targeted gene replacement. We show that P. patens PcG protein FIE (PpFIE) accumulates in haploid meristematic cells and in cells that undergo fate transition during dedifferentiation programs in the gametophyte. In the absence of PpFIE, meristems overproliferate and are unable to develop leafy gametophytes or reach the reproductive phase. This aberrant phenotype might result from failure of the PcG complex to repress proliferation and differentiation of three-faced apical stem cells, which are designated to become lateral shoots. The PpFIE phenotype can be partially rescued by FIE of Arabidopsis thaliana, a flowering plant that diverged >450 million years ago from bryophytes. PpFIE can partially complement the A. thaliana fie mutant, illustrating functional conservation of the protein during evolution in regulating the differentiation of meristematic cells in gametophyte development, both in bryophytes and angiosperms. This mechanism was harnessed at the onset of the evolution of alternating generations, facilitating the establishment of sporophytic developmental programs.

KEY WORDS: Apical cell, Arabidopsis thaliana, BiFC, CLF, PcG complex, Physcomitrella patens, Protein-protein interaction

INTRODUCTION
All land plants are characterized by an alteration of two generations: the haploid gametophyte and the diploid sporophyte. In flowering plants, the sporophyte comprises complex organs including leafy shoots and flowers. Here, this phase dominates over the diminutive and ephemeral gametophytic phase. The gametophytes of flowering plants, namely the pollen and female embryo sacs in which fertilization occurs, are epiphytic to the diploid plant body. In contrast to flowering plants, in bryophytes, the earliest diverging group in land plant evolution, the gametophytic generation is photosynthetically active and dominates the epiphytic sporophyte (reviewed by Reski, 1998a). Consequently, bryophytes propagate through haploid spores, whereas flowering plants propagate via diploid seeds. The last common ancestor of bryophytes and flowering plants was estimated to live around 500 million years ago (Zimmer et al., 2007), an evolutionary distance similar to that between human and fish.

In recent years it has become evident that mechanisms for gene silencing play a role in regulating developmental programs. In general, silencing involves both nucleic acid-based mechanisms, such as small RNA molecules (Bartel, 2004; Jones-Rhoades et al., 2006; Zhang et al., 2007) or DNA methylation (Ginder et al., 2008; Henderson and Jacobsen, 2007; Reik et al., 2001; Saurin et al., 2001), as well as histone-based modifications (Jenuwein and Allis, 2001), such as methylation of lysine 27 on histone 3 (H3K27me3) (Lachner et al., 2003). Methylation of H3K27 is mediated by the Polycomb recruiting complex 2 (PRC2) (Czermin et al., 2002; Ketel et al., 2005; Muller et al., 2002; Nekrasov et al., 2005), also designated the Polycomb group protein (PcG) complex. The PcG complex was first identified in Drosophila melanogaster (Jurgens, 1985; Lewis, 1978) and subsequently in Caenorhabditis elegans (Holdeman et al., 1998), Homo sapiens (Chen et al., 1996; Deniseno and Bomsztyk, 1997), as well as in flowering plants (Goodrich et al., 1997; Grossniklaus et al., 1998; Ohad et al., 1999; Luo et al., 1999).

In A. thaliana genetic and biochemical analyses predict several PcG-like PRC2 complexes (Goodrich et al., 1997; Grossniklaus et al., 1998; Ohad et al., 1999; Luo et al., 1999), some of which have been isolated and identified (De Lucia et al., 2008; Wood et al., 2006). All PcG complexes in A. thaliana comprise the WD40 motif-containing proteins FERTILIZATION INDEPENDENT ENDOSPERM (FIE) and MULTICOPY SUPPRESSOR OF IRA 1 (MSI1) (Kohler et al., 2003b; Ohad et al., 1999). In addition, each PcG complex is predicted to contain one of the three SET domain proteins CURLY LEAF (CLF), SWINGER (SWN) or MEDEA (MEA) (Chanvivattana et al., 2004; Luo et al., 1999; Katz et al., 2004; Yadegari et al., 2000). The SET domain protein acts as the catalytic subunit and methylates H3K27me3 (Czermin et al., 2002; Ketel et al., 2005; Muller et al., 2002; Nekrasov et al., 2005). Members of the SET domain PcG proteins may interact with one of the zinc-finger PcG proteins, including EMBRYONIC FLOWER 2 (EMF2), VERNALIZATION 2 (VRN2) or FERTILIZATION INDEPENDENT SEED 2 (FIS2), via the VEFS domain (Chanvivattana et al., 2004).

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The modular nature of flowering plant PcG complex composition leads to the formation of individual PcG complexes, which facilitate the control of different developmental programs along the plant life cycle. Whereas PcG complexes containing either CLF or SWN act during the sporophytic stage, for example in flowers and fruits (Chanvivattana et al., 2004; Katz et al., 2004), PcG complexes containing either MEA or SWN act at the gametophytic stage, as evident from their mutant phenotype characterized by abnormal endosperm in the absence of fertilization and embryo abortion after fertilization.

In view of the central role of the FIE PcG complex in regulating the transition of the female gametophyte to the sporophyte in flowering plants (Goodrich, 1998; Guittion et al., 2004; Kohler et al., 2003; Ohad et al., 1996; Ohad et al., 1999), it is intriguing to analyze the evolution of this function in basal land plants. For this purpose, we chose the model bryophyte Physcomitrella patens, with its dominant gametophytic phase. Furthermore, different types of stem cells can be analyzed in this plant, as the juvenile gametophyte (the protonema) is a filamentous tissue growing solely by apical cell division, whereas the transition to the adult gametophyte (the gametophore) is characterized by a cell-fate transition to a three-faced apical cell (the bud). This transition can specifically be triggered by the plant hormone cytokinin (reviewed by Becker et al., 2006). Unique to land plants, reverse genetics approaches via gene targeting are highly efficient in P. patens (Reski, 1998b). In addition, the genome of P. patens has been entirely sequenced (Rensing et al., 2008), facilitating evo-devo studies with emphasis on the evolution of specific transcription factors (Maizel et al., 2005; Sakakibara et al., 2008). Here we show that P. patens FIE protein (PpFIE) accumulates only in gametophyte apical cells and cells that undergo fate transition. Moreover, using targeted gene deletion and replacement, in the absence of PpFIE moss gametophore meristems overproliferate, but fail to develop and reach the reproductive phase, illustrating the key role of FIE in regulating proper differentiation and proliferation of P. patens gametophytic stem cells. This aberrant phenotype can be partially rescued by the FIE gene of A. thaliana, indicating functional conservation over more than 450 million years. Accordingly, PpFIE can partially complement the A. thaliana fie mutant. Thus the essential FIE PcG function in regulating developmental programs along the plant life cycle was established early in evolution, around the water-to-land transition of plant life.

MATERIALS AND METHODS

Plant material, culture conditions and treatments

The ‘Gransden 2004’ strain of P. patens (Ashton and Cove, 1977; Rensing et al., 2008) was propagated on BCD and BCDAT media (Ashton and Cove, 1977) at 25°C under a 16-hour light and 8-hour dark cycle (Frank et al., 2005). All transgenic lines described in this study are deposited in the International Moss Stock Center with the accessions IMSC 40319-40324 and 40265-40267 (PpFIE-GUS, ΔPpFIE- and AtFIE-co mutants).

Construction of the phylogenetic tree

Initially, sequences for which BLAST hits were at least 30% identical over a length of 80 amino acids were selected in order to avoid inclusion of false-positive hits from the twilight zone of protein alignment (Rost et al., 1999). Only FIE homologs from organisms (plants and animals) for which the whole genome sequence had been determined were taken into account. An amino acid sequence alignment was generated using MAFFT G-INS-i version 5.860 (Katoh et al., 2005) and manually curated using Jalview version 2.4 (Clamp et al., 2004). Based on the conserved core of this alignment (essentially comprising several WD40 domains), a hidden Markov model was generated (HHMER 2.3.2; http://hmmer.janelia.org/), a gathering cutoff of 400 was defined based on searches among several plant and animal genomes, and this was subsequently used to detect and retrieve FIE homologs from a locally complete set of sequenced genomes. Based on this set of sequences, a second alignment was constructed. The most appropriate evolutionary model was selected using ProTest version 1.3 (Abascal et al., 2005) and 2005 turned out to be WAG (Whelan and Goldman, 2001) with gamma-distributed rate categories. Bayesian inference (BI) was carried out with the predetermed model using MrBayes version 3.1.2 (Ronquist and Huelsenbeck, 2003) with eight gamma-distributed rates categories (four chains, two runs) until convergence (average s.d.<0.01).

Trees were visualized using FigTree version 1.2.2 (http://tree.bio.ed.ac.uk/software/figtree/) and manually rooted. Support values at the nodes (Fig. 1) are BI posterior probabilities. In addition, a neighbor-joining (NJ) tree was calculated using QuickTree version 1.1 (Howe et al., 2002) with bootstrap resampling 1000 times. Neither the NJ nor the ProTest maximum likelihood tree was found to be significantly different from the BI tree.

Accession numbers are as follows: PpFIE, Pannya 61985 (Physcomitrella Patens); AtFIE, AAD23584 (Arabidopsis thaliana); ARAFY 89508 (Arabidopsis lyrata); EED, AAB38319 (Mus musculus); EED, AAH74672 (Homo sapiens); CAG3170 (Gallus gallus); AAV36839 (Drosophila melanogaster); EED, BAD22546 (Oryzias latipes); AAHA93351, LOC550463 (Danio rerio); POPTR, 688045 (Populus trichocarpa); FIE1, Os08g04270.1 (Oryza sativa); FIE2, Os08g04290.1 (O. sativa); XNETR 293769 (Xenopus laevis); FUGRU 713547 (Takifugu rubripes); OSTLU 37673 (Ostroococcus linumii); OSTZA 22117 (Ostroococcus taurii); PHATR 9860 (Phaeodactylum tricornutum); THAPS 118885 (Thalassiosira pseudonana); CHLRE 193732 (Chlamydomonas reinhardtii); CYAME_CMK173C (Cyanidioschyzon merolae); Selmio1_2_143777 (Selaginella moellendorffii); VITIV1 ATM079 (Viitis vinifera); ZEAMA_148924 P.01 (Zea mays); ZEAMA_118205 P.01 (Z. mays); (Danilevskaya et al., 2003); ZEAMA 006312 P.01 (Z. mays); RICCO 28166 (Ricinus communis); FIE1, GYMA 10g02690.1 (Glycine max); FIE2, GYMA 02g17110.1 (G. max); FIE3, GYMA 13g36310.1 (G. max); FIE4, GYMA 12g34240.1 (G. max); CARPA_7_67 (Curcica papaya); FIE1, SORB1 4986219 (Sorghum bicolor); FIE2, SORB1 4838275 (S. bicolor); NEMVE 102199 (Nematostella vectensis); VOLOC 58949 (Volvox carteri); MICP1 49065 (Micromonas pusilla); CHLSP_19370 (Chlorella sp. NC64A).

Gene isolation

The PpFIE and PpCLF complete coding regions were amplified from cDNA by PCR using primers based on the ‘Joint Genome Institute’ (JGI) P. patens version 1.1 database (http://www.jgi.doe.gov) and were subsequently cloned and sequenced. PpFIE turned out to be identical to Pannya 61985 (as available on www.cosmoss.org, version 1.2). The cDNA of PpCLF has been submitted to GenBank (accession: bankit117809 FJ917288, www.ncbi.nlm.nih.gov), as no appropriate gene model is present at the genomic locus (lucass.100.678012-693616) in genome versions 1.1 and 1.2. PpFIE is encoded by 1089 bp organized in a single exon, whereas PpCLF is encoded by 3000 bp spliced from 19 exons.

Construction of transformation vectors

PpFIE coding sequence (1089 bp) was amplified using the following primer set: PpFIE-Fw-1, 5'-AAAGCTTTCTGAGATGGAGATCTGTCCTGCCCAGCAAC-3'; and PpFIE-Rev-1, 5'-AAACCTTTGACATGACAGAC-ACAGCTTCCAGGCGCAAAT-3’. In addition, the 5’ (805 bp) and 3’ (598 bp) of the untranslated region (UTR) of PpFIE were amplified using the following primers: PpFIE5'-UTR-Fw, 5'-GAAGCTTTGACATGACAGACCAAAAAATTGTGAGATGTGTTG-3'; PpFIE5'-UTR-Rev, 5'-GAAGCTTTGACATGACAGACCAAAAAATTGTGAGATGTGTTG-3'. All amplified fragments were subcloned into the pTZ 57 vector (Fermentas, Lithuania) and sequenced to ensure their integrity. The PCR-amplified PpFIE genomic sequence was used for constructing the disrupted vector by the insertion of the selection cassette at the BalI site. The same genomic fragment was cloned into the uidd reporter gene at the Nhel site to obtain a protein fusion between PpFIE and GUS, and then cloned into the pMBL5 vector,
followed by a nopaline synthase polyadenylation signal (NOS-ter), a nptII cassette, as described in (Nishiyama et al., 2000), and the PpFIE3'-UTR (see Fig. S1 in the supplementary material). AtFIE full-length cDNA was amplified using the primers AtFIE-F 5'-CCCGGGATCCGAAAGATAACCTAGGG-3' and AtFIE-R 5'-CAAGGTCGAGGAGTAGTGGACACAT-3'. The AtFIE cDNA was cloned into pMBL5 vector flanked by PpFIE5'-UTR at the 5' end and by the NOS terminator, the nptII cassette and PpFIE3'-UTR, respectively, at the 3' end. Prior to transformation the vectors were linearized.

**Protoplast isolation and PEG-mediated transformation of *P. patens***

PEG transformation was performed as described in PHYSCObase (http://moss.nibb.ac.jp). Six days after regeneration, transformants were selected on BCDAT medium containing 20 mg/l of G418.

**RT-PCR**

Total RNA extraction from protonemata or leaves followed by RT-PCR were performed as described (Katz et al., 2004), using the following gene-specific primers: for *PpFIE*, PpFIE-Fw-1 and PpFIE-Rev-1; for *AtFIE*, AtFIE-F and AtFIE-350-R 5'-GATGCTCGTTTCTTCGATGT-3'.

**Real-time PCR analysis of gene expression**

Real-time quantitative PCR analysis was performed by ΔΔCt method of relative quantification with a StepOne Thermal Cycler (Applied Biosystems, Foster City, CA, USA), using SYBR Green to monitor dsDNA synthesis. The following primers were used to detect PpFIE and the housekeeping genes: PpFIE-left-261-278, 5'-AGATGGCAACCCCTGGCT-3'; PpFIE-Right-302-320, 5'-CAATCAATGATGCGGAGGA-3'; 60s-Left, 5'-GGAGACACTATCTTTTCTCGT-3'; 60s-Right, 5'-TGAAATCATGGGATTGTCCTCC-3'. The amount of cDNA for each gene was quantified using a log-linear regression curve of the threshold cycle and the amount of standard template prepared from a cDNA clone.

**Identification of *A. thaliana* fie mutant allele via RFLP analysis**

*A. thaliana* fie alleles carry a single point mutation resulting in a protein length between 2277 and 2435 amino acids. Paralog retention occurred occasionally and relatively late during evolution (after the insect-vertebrate split and the monocot-eudicot split, as can be seen from the *D. melanogaster*, *O. sativa*, *Z. mays*, *S. bicolor* and *G. max* paralogs, Fig. 1). The high conservation of the FIE protein superfamily is presented in Fig. 1. Potential FIE homologs are also present in the genomes of organisms, including *C. elegans* and *Saccharomyces cerevisiae*; however, their low conservation grade does not allow for unambiguous assignment to the FIE superfamily. It is evident from the phylogenetic tree that FIE is essentially a single-copy ortholog that was already present in the last common ancestor of all eukaryotes and might subsequently have been lost in some (unicellular) lineages. The FIE phylogeny approximately reflects the taxonomic relationships of the species involved. Paralog retention occurred occasionally and relatively late during evolution (after the insect-vertebrate split and the monocot-eudicot split, as can be seen from the *D. melanogaster*, *O. sativa*, *Z. mays*, *S. bicolor* and *G. max* paralogs, Fig. 1). The high conservation of the FIE proteins (e.g. 66% identity, 81% similarity over the whole protein length between *A. thaliana* and *P. patens* and 41% identity,

**Electron microscopy**

Cryoscanning electron microscopy samples were frozen in liquid nitrogen on a copper sample holder, sputtered with 20 nm gold particles and visualized using a JEOL 6300 cryoscanning electron microscope. Environmental scanning electron microscopy was performed using the Quanta 200 FEG with a field-emission gun and a gaseous secondary electron detector for surface imaging in wet mode.

**Bimolecular fluorescence complementation analysis**

Protein-protein interactions in plants were examined by bimolecular fluorescence complementation (BiFC) assay. *PpFIE*, *PpCLF*, *AtFIE*, *AtMEA*, *AtCLF* and *AtSWN* full-length cDNAs were cloned into pSY 735 and pSY 736 vectors at the SpeI site, which contain the N-terminal (YN) and the C-terminal (YC) fragments of the YFP protein, respectively (Bracha-Drori et al., 2004). Equal concentrations of *Agrobacterium tumefaciens* strain GV3101/pMP90 containing plasmids of interest (see Table 1) were transiently coexpressed in *N. benthamiana* leaves via the leaf injection procedure (Bracha-Drori et al., 2004). Image annotation was performed with Zeiss AxioVision, Zeiss CLSM-5 and Adobe Photoshop 7.0 (Mountain View, CA, USA). The expression of each construct was verified by its ability to interact with AtFIE (see Fig. S4G-I in the supplementary material). Negative controls with vectors bearing only YN or YC alone were carried out in every experiment to verify the specificity of the interactions.

**RESULTS**

The FIE sequence is highly conserved among the eukaryotic crown kingdoms

Putative homologs of *A. thaliana* FIE were collected using hidden Markov model (HMM) searches for organisms from which the whole genome sequence had been determined. The phylogeny of the FIE protein superfamily is presented in Fig. 1. Potential FIE homologs are also present in the genomes of organisms, including *C. elegans* and *Saccharomyces cerevisiae*; however, their low conservation grade does not allow for unambiguous assignment to the FIE superfamily. It is evident from the phylogenetic tree that FIE is essentially a single-copy ortholog that was already present in the last common ancestor of all eukaryotes and might subsequently have been lost in some (unicellular) lineages. The FIE phylogeny approximately reflects the taxonomic relationships of the species involved. Paralog retention occurred occasionally and relatively late during evolution (after the insect-vertebrate split and the monocot-eudicot split, as can be seen from the *D. melanogaster*, *O. sativa*, *Z. mays*, *S. bicolor* and *G. max* paralogs, Fig. 1). The high conservation of the FIE proteins (e.g. 66% identity, 81% similarity over the whole protein length between *A. thaliana* and *P. patens* and 41% identity,

**Table 1. Vectors used in this study**

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60% similarity between *A. thaliana* and *H. sapiens*) across the millennia underlines its conserved structure and indicates its crucial function for higher eukaryotes (Fig. 1).

**PpFIE-GUS accumulates in all meristematic cells and gametophytic cells undergoing fate transition**

To determine PpFIE temporal and spatial accumulation during *P. patens* development, we generated five transgenic plants in which the *uidA* (GUS) reporter gene was inserted via homologous recombination, replacing the *PpFIE* stop codon. The resulting plants express a PpFIE-GUS fusion protein under control of its native promoter within the endogenous genomic environment.

The PpFIE-GUS staining pattern was identical among all five moss transgenic lines generated. None of these lines exhibited any obvious abnormalities as compared with wild-type plant morphology, nor were any changes detected in the course and timing of their life cycle. Therefore, we conclude that PpFIE function for developmental control in PpFIE-GUS plants was not impaired.

During the life cycle of wild-type *P. patens*, the fertilized zygote develops into a sporophyte consisting of a reduced seta and the spore capsule. Several days after spore dispersal, the wild-type haploid spores germinate forming the juvenile gametophyte, a branched filamentous tissue growing by apical cell division. This protonema tissue comprises two subsequently occurring cell types, the chloronemata and the caulonemata. The division of the apical cell produces protonemal filaments, whereas subapical cells may divide to produce either side branch initials or three-faced apical cells, the buds. These buds subsequently develop into the adult gametophyte, the leafy shoots (gametophores) that bear the sex organs (Cove et al., 2006; Cove and Knight, 1993; Decker et al., 2006; Reski, 1998a; Schaefer and Zryd, 2001).

No FIE was detected by GUS staining in the spores after dispersal, but the protein appeared during imbibition before spore germination (Fig. 2A,B). Upon germination (Fig. 2B,C) and throughout the protonema phase, a weak GUS staining was detected in the apical cells of caulonemata and chloronemata (Fig. 2D,E).

A strong GUS staining was visible at the time of transition from the juvenile to the adult gametophyte, marked by the transition to three-faced apical cells, the buds (Fig. 2F). Subsequently, strong GUS staining was consistently detected in the apical and lateral shoot apices of the leafy gametophores (Fig. 2G-J). In the course of the GUS staining process, the apical cell of the gametophore stained first, followed by the adjacent cells (Fig. 2I,H). During gametophore development, PpFIE-GUS staining decayed gradually from the apical cell towards differentiated leaves (Fig. 2H). Throughout lateral shoot formation, the PpFIE protein could be monitored as early as in a single cell designated to form a lateral shoot (Fig. 2J, arrowheads).

Upon transition from the gametophyte to the reproductive phase, GUS signals were associated with the male and female reproductive organs antheridia and archegonia, respectively. Before fertilization, GUS activity was detected in the developing archegonia (Fig. 2K,L), where staining was particularly strong in the unfertilized egg cell (Fig. 2L, see arrow), whereas the signal gradually decayed after fertilization (Fig. 2M-O). Likewise, GUS signals were also evident in the young antheridia carrying the spermatozoids (Fig. 2P), whereas no signal was detected upon sperm maturation (Fig. 2Q). After fertilization no GUS signal was detectable, neither in the developing embryo, nor in the mature sporophyte until the stage of spore formation (Fig. 2R). Here, GUS staining was only found during spore formation in the tetrads after meiosis (Fig. 2S) and was undetectable in mature spores (Fig. 2T).
ΔPpFIE mutants overproliferate three-faced apical cells

To study PpFIE function during *P. patens* development, we generated four independent disruptant mutant lines, designated ΔPpFIE, by gene targeting via homologous recombination (see Fig. S1A in the supplementary material). Proper integration of the disrupting construct into the PpFIE locus was verified by amplifying and sequencing the junction sites between the insert and the PpFIE locus (see Fig. S1A in the supplementary material). Single event of integration was determined by Southern blot analysis (see Fig. S6 in the supplementary material) and complete loss of PpFIE transcripts due to the disruption was confirmed by RT-PCR analysis (see Fig. S2A in the supplementary material). Subsequently, the phenotype of the ΔPpFIE mutants was monitored along with their development. ΔPpFIE protonemata and bud initials appeared indistinguishable from those of wild type (Fig. 3A,F). However, during the transition from juvenile to adult gametophytes, marked by the transition from apical cells to three-faced apical bud initials, ΔPpFIE mutants displayed dramatic morphological alterations (Fig. 3B,G). Whereas wild-type protonema gave rise to buds that further developed into leafy gametophores (Fig. 3B-E), ΔPpFIE developed a mass of cone-shaped buds (Fig. 3H, insertion) that grow further, thus harboring multiple apices (Fig. 3G-J). These mutant buds developed into cone-like leafless gametophores (Fig. 3J), whereas cones remote from the main apex initiated the differentiation of leaf primordia (Fig. 3J, insertion). Each main bud continued to repeatedly produce additional successive orders of primordia, until numerous apices accumulated on the main bud surface (Fig. 3LJ).

This aberrant phenotype indicates that ΔPpFIE mutant plants fail to restrict bud proliferation, resulting in ectopic initiation and differentiation of multiple bud apices. Furthermore, these buds failed to mature or to form normal gametophores and thus are prevented from reaching the reproductive phase. However, as some of the mutated structures resembled the morphology of a sporophyte (Fig. 3H, insertion), we tested whether such structures acquire sporophytic identity. To this end we have tested the expression of the genes MKN2 and MKN5, which were shown to be expressed specifically in sporophytic tissue (Sakakibara et al., 2008). Our results show that MKN2 and MKN5 are expressed in ΔPpFIE protonemata bearing abnormal buds but not in wild-type protonemata bearing gametophores (Fig. 3N).

PpFIE is associated with the maintenance of pluripotency and cell reprogramming

*P. patens* cells have remarkable regenerative plasticity following tissue damage (Cove and Knight, 1993), indicating that cells retain their capability to exit their determined state after differentiation. During *P. patens* regeneration, all differentiated cells undergo division, giving rise to protonemata. As our results indicate that PpFIE is involved in maintaining the undifferentiated state of apical cells, we examined whether PpFIE protein accumulation correlates with the regeneration process. To induce this process, leaves from *PpFIE-GUS* transgenic lines were detached from mature gametophores and placed on BCD media for different periods of time up to 88 hours and subsequently stained for GUS (Fig. 4). Following detachment, we monitored the regeneration process at the surface of the distal leaf region, rather than the proximal marginal region of the incision site where wounding might affect FIE expression. Forty-eight hours after induction, single scattered cells expressing PpFIE-GUS were observed on the leaflets (Fig. 4C,I). At 72 hours some of the GUS-expressing cells were observed to

PpFIE-GUS protein accumulation patterns reveal that the protein is present in all meristematic cells and gametophytic cells undergoing fate transition. The complex pattern of PpFIE-GUS localization suggests that it is involved in various developmental processes restricted to the haploid tissue during the *P. patens* life cycle.
undergo cell division (Fig. 4K, arrows). After 88 hours protonema filaments emerged from cells in which GUS staining was visible (Fig. 4L, arrowhead).

In order to examine whether PpFIE transcription is upregulated during the regeneration process, wild-type leaves were detached and incubated as described above. RNA was purified from approximately 1000 leaves collected at time ‘0’ and 72 hours after detachment. Quantitative RT-PCR analysis showed that the FIE transcript is upregulated at least twofold 72 hours after leaf detachment, as compared with time ‘0’ (Fig. 4M).

PpFIE upregulation and the spatial and temporal pattern of accumulation of the protein during the regeneration process indicate that the epigenetic machinery is involved during cell reprogramming and acquisition of pluripotency.

A. thaliana FIE is able to complement P. patens FIE

To determine whether FIE protein function is conserved between bryophytes and angiosperms, we performed a cross-species complementation assay. To this end, transgenic P. patens lines were generated, in which the endogenous PpFIE was replaced via homologous recombination with an AtFIE cDNA driven by the native moss PpFIE promoter (designated AtFIE-co). Four independent P. patens AtFIE-co lines were isolated expressing AtFIE (see Fig. S1B and Fig. S2B in the supplementary material). All four AtFIE-co lines partially complemented the lack of the endogenous PpFIE (Fig. 3K-M, Fig. 5B). Similar to ΔPpFIE mutant lines, AtFIE-co lines exhibited abnormal buds with multiple primordial leaves at the early phase of growth (Fig. 3K). However, in contrast to ΔPpFIE plants, AtFIE-co lines were able to develop mature gametophores (Fig. 3L,M), although AtFIE-co lines exhibited distinct abnormal phenotypes. The distance between leaves along the gametophore was shorter, resulting in a denser appearance as compared with wild-type gametophores (compare Fig. 5A and 5B). At the apex of mature gametophores, clusters of shoot apices developed, bearing juvenile leaves (Fig. 5C, arrows). This phenomenon was also observed in lateral shoot apices (data not shown). Under reproduction-inducing conditions (Hohe et al., 2002), AtFIE-co lines failed to produce sex organs. The PpFIE-GUS accumulation pattern overlapped with the sites in which the above mentioned abnormalities were observed. The failure of AtFIE to support the proper development of reproductive organs could be due to the inability of AtFIE to recognize additional subunits present in the PcG complex at this particular P. patens developmental stage. These results demonstrate that FIE has been functionally conserved through evolution, thus allowing partial rescue of the ΔPpFIE mutant using AtFIE.
PpFIE partially complements the gametophytic lesion of the A. thaliana fie mutant

The ability of AtFIE to rescue P. patens plants lacking PpFIE indicates that AtFIE can functionally recognize components of the P. patens PcG complex. Thus we performed the reciprocal experiment and analyzed whether PpFIE can functionally complement the absence of AtFIE in the A. thaliana PcG complex.

To this end, we tested whether PpFIE can rescue the aborted embryo of A. thaliana plants in which the female gametophyte contributes a fie mutant allele (Ohad et al., 1996; Ohad et al., 1999; Chaudhury et al., 1997). To test this possibility we established six independent transgenic lines expressing PpFIE under the A. thaliana FIE native promoter (ProAtFIE:PpFIE) as described by Kinoshita et al. (Kinoshita et al., 2001). To establish the complementation assay, we first crossed ProAtFIE:PpFIE A. thaliana lines as female recipients with pollen from heterozygous FIE/fie plants. F1 progenies from the six parents were selected for kanamycin resistance as an indication for the presence of the ProAtFIE:PpFIE transgene. These lines were then screened for the presence of the fie allele as determined by seed abortion (Ohad et al., 1996). In addition, the same heterozygous F1 plants (FIE/fie) hemizygous for the transgene (PpFIE/~; plant genotype designated as FIE/fie.PpFIE/~) were tested by DNA restriction analysis for the presence of the fie mutant allele, monitoring for the unique DraI polymorphic site (see Fig. S3C in the supplementary material). The expression of the PpFIE transgene in these lines was confirmed by RT-PCR analysis (see Fig. S3B in the supplementary material). F2 progenies were collected and germinated, out of which FIE/fie,PpFIE/~ plants were selected as described above. Complementation was assessed by scoring F3 progeny seed abortion ratio in siliques from individual F2 plants, derived from self pollination.

In the case that PpFIE would fully complement the fie mutant allele, one would expect that F2 plants carrying both alleles would display 25% seed abortion in the F3 generation (Ohad et al., 1999), in contrast to the 50% seed abortion if no complementation occurs. Out of six independent lines, two displayed abortion of approximately 45% (Table 2, rows 1 and 2), which is significantly lower than 50% (χ² test, P<0.001), in which the morphology of aborted embryos was not different from FIE/fie aborted embryos. These results indicate that the bryophyte FIE protein partially complements for the absence of a functional FIE allele in the flowering plant female gametophyte, thus supporting early seed development and allowing embryo rescue.

An additional genetic approach was employed to determine whether PpFIE is able to complement the A. thaliana fie allele. The A. thaliana fie mutant allele causes embryo lethality when transmitted through the female parent, with 100% penetration (Ohad et al., 1996). Thus, the fie mutant allele is not transmitted by the female parent but only through the male. A cross between a FIE/fie female with a wild-type male will result in 100% wild-type F1 plants (Table 2, row 6). However, if PpFIE can compensate for A. thaliana fie lack of function in the female

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**Fig. 4.** PpFIE expression and protein accumulation in detached, somatic leaves. GUS staining of detached leaves from the gametophore, incubated in BCD medium for time intervals of 24, 48, 57, 72 and 88 hours. (A-F) PpFIE-GUS staining of gametophore leaves. (G-L) Magnification of the respective images. Dividing cells are marked with an arrow, differentiated protonema grown on the leaf in L is marked with an arrowhead. (M) Quantitative RT-PCR analysis of PpFIE expression at time ‘0’ and 72 hours after leaf detachment. Scale bars: 0.1 mm.

**Fig. 5.** Morphological analysis of mature gametophores from wild type and plants in which PpFIE is replaced by the AtFIE gene. (A) Wild-type adult gametophore. (B) Adult AtFIE-co gametophore exhibiting clusters of shoot apices bearing juvenile leaves at the shoot apex. (C) Magnification of an AtFIE-co apex (box in B). Arrows mark the leaflets that formed on the proliferated apex. The images were taken by light stereo-microscopy. Scale bars: 1 mm in A,B; 0.1 mm in C.
gametophyte, then a heterozygous \textit{FIE/fie} female carrying the \textit{PpFIE} transgene is expected to transmit the \textit{A. thaliana fie} mutant allele to the next generation.

F\textsubscript{1} progeny resulting from a cross between a \textit{FIE/fie,PpFIE/~} female and a wild-type male (see Fig. S4A,B, column P and Fig. S4C,D in the supplementary material) carrying a GFP marker were screened by RFLP analysis for the presence of the \textit{fie} mutant allele (see Fig. S4A,B, column F\textsubscript{1} in the supplementary material). In addition, progenies obtained from self-fertilization of the above F\textsubscript{1} plants were tested morphologically for seed abortion (see Fig. S4E in the supplementary material). Out of 67 F\textsubscript{1} progenies, four carried the \textit{fie} allele, whereas in the control experiment in which a \textit{FIE/fie} female was crossed with the same wild-type male donor, all 192 resulting plants were homozygous for the \textit{FIE} wild-type allele as expected. The presence of the GFP marker provided by the male donor assured that the outcrossing occurred properly.

Although \textit{PpFIE} was able to facilitate the transmission of the female \textit{A. thaliana fie} allele, none of the F\textsubscript{3} progenies in the complementation experiment was homozygous for \textit{A. thaliana fie}. Since the paternal \textit{AtFIE} allele is apparently not expressed until late embryogenesis (Yadegari et al., 2000), we suggest that under the experimental conditions we have used \textit{PpFIE} complementation is delimited to the early phase, during which \textit{PpFIE} is provided maternally.

Based on our findings that \textit{PpFIE} can partially complement the \textit{A. thaliana fie} lesion at particular developmental stages, and that \textit{AtFIE} can replace \textit{PpFIE} at the bud stage, we conclude that there has been partial functional conservation of \textit{FIE} during land plant evolution.

\textbf{PpFIE and \textit{AtFIE} PcG proteins interact in planta}

In \textit{A. thaliana}, \textit{FIE} and SET domain proteins were shown to interact directly (Katz et al., 2004), as in the case for the homologous PcG proteins in \textit{D. melanogaster}, \textit{Mus musculus}, and \textit{H. sapiens} (reviewed by Berger and Gaudin, 2003; Hsieh et al., 2003; Simon and Tamkun, 2002). To test whether \textit{PpFIE} and \textit{PpCLF} are able to interact, as expected from their proposed function, we used the BiFC assay (Bracha-Drori et al., 2004). To this end we cloned the full-length cDNAs of \textit{PpFIE} and \textit{PpCLF}, each fused to either the N-terminal (YN) or C-terminal (YC) fragments of the YFP encoding protein. YFP fluorescence from single confocal sections is overlaid with Nomarsky differential interference contrast (DIC) images. Scale bars: 50 \textmu m.

**Table 2. Abortion rates of wild type, \textit{A. thaliana fie} mutants and \textit{A. thaliana fie} mutants complemented with \textit{PpFIE}**

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Abortion ratio</th>
<th>Abortion average ratio</th>
<th>( \chi^2 )</th>
<th>( P ) value ( /H_0 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>( PpFIE/\sim,FIE/fie ) line 1</td>
<td>469:586, 1:1</td>
<td>44.45</td>
<td>13.00</td>
<td>0.003 (50%)*</td>
</tr>
<tr>
<td>( PpFIE/\sim,FIE/fie ) line 17</td>
<td>611:728, 1:1</td>
<td>45.59</td>
<td>10.4</td>
<td>0.001 (50%)*</td>
</tr>
<tr>
<td>( FIE/fie )</td>
<td>879:804, 1:1</td>
<td>52.22</td>
<td>3.34</td>
<td>0.068 (50%)</td>
</tr>
<tr>
<td>( PpFIE/\sim,FIE/FIE )</td>
<td>3:1162, 0:1</td>
<td>0.002</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>( FIE/FIE ) - wild type</td>
<td>3:1328, 0:1</td>
<td>0.002</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>F\textsubscript{1} of ( FIE/FIE ) female × ( FIE/fie ) male</td>
<td>2:880, 0:1</td>
<td>0.002</td>
<td>–</td>
<td>–</td>
</tr>
</tbody>
</table>

\( \chi^2 \) test was used to determine whether the \( H_0 \) hypothesis of 50% seed abortion fit with the different genetic categories. Lines marked with * exhibit a significantly lower statistical rate of seed abortion than the expected 50%.
sequence. Members of each protein pair were transiently coexpressed via Agrobacterium tumefaciens-mediated transformation in leaf epidermal cells of Nicotiana benthamiana. YFP fluorescence was observed in cells expressing both YC-PpFIE and YN-PpCLF (Fig. 6A). No fluorescence was observed when expressing YC-PpFIE with YN only (Fig. 6E) or YN-PpCLF with YC only (Fig. 6K), both serving as negative controls. Interaction between both proteins was localized in the nucleus, which is in agreement with the known functions of the PcG in regulating chromatin structure (Dingwall et al., 1995; Francis et al., 2004; Paro and Hogness, 1991). The above result supports the hypothesis that PpFIE and PpCLF interact in vivo to form the core of a PcG complex.

The complementation tests described above suggest that both P. patens and A. thaliana FIE proteins interact with the respective PcG complex subunits in the other species. We next tested whether FIE proteins from either P. patens or A. thaliana were able to interact with their counterpart SET domain proteins. Using the BiFC assay we show that PpFIE can interact with AtCLF and AtSWN (Fig. 6B and 6D), but fails to interact with AtMEA (Fig. 6C). All interactions occurred in the nucleus. Whereas the interaction between PpFIE and PpCLF gave rise to a reconstitution of the YFP in almost all cells, the interaction with AtSWN appeared only sporadically. As negative controls, neither the SET domain proteins nor PpFIE or AtFIE interacted with the half-complementing counterpart YFP protein alone (Fig. 6K,N,E,J, respectively). In addition, we observed an interaction between AtFIE and PpCLF (Fig. 6F). These cross-species protein interactions are in agreement with the genetic complementation assays described above. P. patens FIE could interact only with A. thaliana CLF or SWN, which are SET domain proteins that have evolved earlier during plant evolution compared with AtMEA, the most recently derived gene among the A. thaliana SET domain family (Spillane et al., 2007).

**DISCUSSION**

**PcG function has been conserved during plant evolution**

The Polycomb group (PcG) complex controls gene expression profiles epigenetically. In this study we identified P. patens single-copy orthologs to the A. thaliana PcG complex core (FIE) and SET domain catalytic (CLF) subunits. Two lines of evidence indicate that PpFIE is a true functional ortholog of the PcG core subunit. First, even though the reciprocal complementation assays between P. patens and A. thaliana were limited to specific developmental stages, they demonstrate that the FIE genes have maintained their function during evolution. Second, our BiFC experiments show that PpFIE interacts with two A. thaliana SET domain PcG proteins, AtCLF and AtSWN.

Further studies will reveal the extent of functional conservation of PpFIE as a member of a transcriptional repressor complex (PRC2) alongside the A. thaliana life cycle. To this end, the ability of PpFIE to regulate AtFIE target genes, evident by either ChIP assay or the analysis of marker genes in vivo, could be applied.

Interestingly, PpFIE did not interact with AtMEA, which is the most recently diverged member in the SET domain protein family present in flowering plants (Chanvivattana et al., 2004; Spillane et al., 2007). Although all three A. thaliana SET domain proteins are expressed in the ovule (Chanvivattana et al., 2004; Goodrich et al., 1997; Grossniklaus et al., 1998; Wang et al., 2006; Xiao et al., 2003), MEA has a more prominent function in regulating central cell development (Grossniklaus et al., 1998; Kiyosue et al., 1999; Wang et al., 2006). The lack of interaction between PpFIE and AtMEA in the BiFC assay agrees with the partial complementation in A. thaliana by PpFIE, which could result from the inability of PpFIE and AtMEA to form a complex in the central cell. Consistent with this hypothesis, it was recently shown that the apomictic Hieracium (H. piloselloides) and non-apomictic Hieracium (H. pilosella) FIE proteins differentially bind members of the PcG complex, thus limiting their later function. The inability to bind particular partners was attributed to specific modifications at the protein level, which may lead to structural changes between the two proteins (Rodrigues et al., 2008).

In mammals, the PcG complex exerts its function by methylating H3K27 via the SET domain of the enhancer of zeste subunit (Czermin et al., 2002; Muller et al., 2002). Our analysis shows that PpFIE and the SET domain protein PpCLF interact in vivo (Fig. 6), which supports the possibility that in P. patens these proteins form a complex to perform a similar biochemical function as in mammals. This hypothesis is supported by the conservation of the catalytic PcP SET domain protein in P. patens, as this is also present in A. thaliana, H. sapiens and D. melanogaster (see Fig. S5 in the supplementary material).

**FIE function in P. patens**

During wild-type bud formation the apical cell divides, giving rise to a subset of three-faced apical daughter cells. After several consecutive cell divisions some of the peripheral cells along the surface of the young bud give rise to either leaf primordia (Schumaker and Dietrich, 1997) or meristematic cells that subsequently develop into lateral shoots. PpFIE-GUS protein levels are correlated with organ differentiation, as they gradually decline from the bud apex towards the region where leaf initials emerge, until the fusion protein can no longer be observed. Bud initiation in ΔPpFIE mutants is indistinguishable from wild type (Fig. 3A,F), thus PpFIE is not essential for the initiation of the three-faced apical cell. However, soon after the ΔPpFIE three-faced apical cell gives rise to several daughter cells, secondary buds are initiated, forming multiple apices in a repeatable pattern (Fig. 3G). These secondary buds initiate leaf primordia only after they grow further apart from the center of the main bud cluster (Fig. 3I).

Taking the PpFIE protein expression pattern and ΔPpFIE mutant phenotype together, we hypothesize that in wild-type P. patens FIE functions to maintain an undifferentiated state of meristematic cells within the apex. These cells are designated to become lateral shoots, probably by the epigenetic repression of gene expression. This repression can be relieved by as yet unknown signals, thus allowing the initiation of lateral shoot formation, as the apex is pushed upwards by its daughter cells. Thus the ΔPpFIE mutant phenotype might result from failure of the PcG complex to repress such meristematic cells from pursuing their default program to differentiate into lateral buds in due time.

Whereas in the wild type each bud gives rise to individual gametophores bearing leaves, ΔPpFIE mutants develop multiple bud apices that fail to form leafy gametophores. However, mutant buds continue to proliferate, until marginal buds generate undeveloped leaf primordia, thus being relieved from the repressed state they were in. These results indicate that the potential to develop leaves exists in these mutant apices (Fig. 3J, see insertion).

This phenomenon might not necessarily derive directly from the absence of PpFIE. Rather, it might result from the presence of multiple apices, leading to either overproduction of a signal inhibiting leaf differentiation, or it might be due to the dilution of a required signal consumed by the overproliferating buds situated within close vicinity.
The proposed role of PpFIE, as revealed from the ΔPpFIE phenotype and PpFIE expression pattern, is to maintain the pluripotency of the three-faced apical daughter cell. This fits well with the known function of PcG proteins during stem cell differentiation (for reviews, see Kanno et al., 2008; Pietersen and van Lohuizen, 2008). Mammalian EED and ESC PcG proteins, homologs of FIE and CLF, respectively, take part in the maintenance of stem cells by preventing their differentiation (Boyer et al., 2006; Bracken et al., 2006; Lee et al., 2006). Mutant stem cells lacking EED cannot maintain their pluripotency and are prone to differentiate (Boyer et al., 2006; O’Carroll et al., 2001). Similarly, in the A. thaliana fie mutant the central cell, serving as a stem cell, proliferates and differentiates precociously into juvenile endosperm without fertilization (Chaudhury et al., 1997; Ingouff et al., 2005; Ohad et al., 1996; Ohad et al., 1999), demonstrating that the PcG complex represses the central cell from differentiating to endosperm prior to fertilization.

Thus, the role of FIE in bryophyte development, as revealed in this study, agrees with the basic function of the PcG complex to regulate self-renewal and inhibit differentiation. This developmental role is conserved in both the plant and the animal kingdom.

**PpFIE function during reproductive development**

ΔPpFIE mutants were unable to develop gametophores, thus remaining infertile. However, PpFIE-GUS was detected during sex organ and gamete formation, yet was excluded from the zygote once fertilization took place, implying that it has a possible function during sexual development. Furthermore, when replacing the native PpFIE with AtFIE, the resulting transgenic plants were able to develop gametophores. However, the apical cells of these plants failed to produce sex organs, and developed multiple apices on top of the gametophore apex instead. It is possible that at this developmental stage, AtFIE, in contrast to PpFIE, fails to recognize particular P. patens PcG subunits, which are crucial for proper development. Taken together, the above results indicate that PpFIE takes part in regulating the transition from the vegetative to the reproductive phase.

In support of the above we found that ΔPpFIE mutants form cone-like structures resembling young sporophytes. These mutants also express the sporophytic marker genes MKN2 and MKN5 (Sakakibara et al., 2008). Thus, these results indicate that PpFIE controls the transition of particular developmental stages along the P. patens life cycle, including the transition from the gametophytic to the sporophytic stage. This function of the PcG complex has been retained for more than 450 million years of plant evolution.

**PpFIE function during redifferentiation**

PpFIE is present mainly in apical meristematic cells but is absent from cells that have already differentiated, such as in mature leaves. Our data show that PpFIE expression and protein accumulation precede the regeneration processes in which leaf somatic cells are about to regenerate, giving rise to protomers (Fig. 4), as well as in wounded tissue (data not shown), and further support the proposed function in establishing self-renewal and pluripotency. We predict that leaf regeneration first requires de-differentiation of leaf cells, allowing them to pass through a meristematic state before they can acquire a new identity. Upregulation of PpFIE might allow the cell to enter into a reprogrammable state facilitated by chromatin remodeling, as expected from PcG function.

So far the analysis of plant cell de-differentiation and regeneration has been performed mainly with protoplasts (for a review, see Grafi, 2004). Our results now show that the PpFIE protein might serve as a novel molecular marker, highlighting cells that are about to divide and differentiate, thus serving as a tool to monitor these processes during the development of the entire plant and leaf regeneration.

**Evolution of the PcG role in development**

PpFIE is mainly expressed in gametophytic tissues. The transition of land plants from haploid dominancy to diploid dominancy may have evolved either by utilizing established developmental pathways acting within the gametophyte (the ‘homologous’ theory) or via novel genes and networks that arose specifically to support this process (the ‘antithetic’ theory) (Bennici, 2005). Support for the homologous model was suggested in the case of PpRSL1 and PpRSL2, which control gametophytic rhizoid formation in P. patens, whereas their orthologs AtrRSL1 and AirRHD6 control sporophytic root hair development in A. thaliana (Menand et al., 2007). Our results show that the PRC2 epigenetic machinery, in which FIE is included, was maintained through the evolution of land plants, repressing the differentiation of meristematic cells in the gametophyte. This is supported by the observation that PpFIE-GUS was detected only in haploid tissues.

During the evolution of land plants the PcG machinery was recruited to regulate the proper development of sporophytic programs, such as transition from the vegetative to the reproductive phase, flowering time and flower organ formation (for reviews, see Guitton and Berger, 2005; Hsieh et al., 2003; Kohler and Makarevich, 2006). This was accomplished by the diversification of the SET domain in P. patens to a gene family in A. thaliana, allowing the formation of diverse PcG complexes, as seen in the case of MEA, which is specialized in regulating endosperm development (Kawabe et al., 2007; Miyake et al., 2009; Spillane et al., 2007).

Thus, the findings described here highlight an example whereby, instead of harnessing pre-existing transcription factors, higher-order epigenetic machinery was recruited to regulate the expression of particular gene sets to control evolving developmental programs.

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**Supplementary material**

Supplementary material for this article is available at http://dev.biologists.org/cgi/content/full/136/14/2433/DC1

**References**


