Transposase-Derived Transcription Factors Regulate Light Signaling in Arabidopsis

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siRNA candidates were fluorescently tagged at the 5′ end of sense and antisense strands and transfected. Cell-capacitance measurements on mouse β cells transfected with fluorescently tagged siRNA were recorded by using the perforated patch-clamp technique. Inhibition of IP6K1, but not of IP6K2, reduced the exocytotic capacity (Fig. 4D), and the effect of silencing was again most pronounced on the first pulse, reflecting depletion of the RRP of granules (Fig. 4, B and C). Furthermore, addition of 5-IP_7 in the presence of siRNA to IP6K1 restored a normal exocytotic response (Fig. 4E). Thus, endogenous IP_7 generated by IP6K1, but not IP6K2, appears to account for the enhanced exocytotic capacity in β cells. The discrepancy between our exogenous versus endogenous systems may reflect a differential distribution or cellular associations of the two kinases in vivo. IP6K1 associates with proteins involved in exocytosis but IP6K2 does not (*22*). Studies on IP6K2 have also revealed a discrepancy between overexpression studies and gene silencing (*23*).

IP6K1 siRNA did not alter number of L-type Ca^{2+} channels per patch or channel open probability, mean closed time, or mean open time (fig. S7). Hence, in contrast to IP_6, IP_7 appears not to affect L-type Ca^{2+} channel activity (*13*).

We find that the pancreatic β cell maintains high concentrations of IP_7. This apparently functions in the insulin secretory process by regulating the RRP of insulin-containing granules, thereby maintaining the immediate exocytotic capacity of the β cell. It is noteworthy that a putative disruption of the IP6K1 gene in a family with type 2 diabetes (*24*) and reduced plasma insulin levels in mice in which the IP6K1 gene has been deleted (*25*). This may be of interest in the context of understanding the molecular mechanisms underlying the development of diabetes.

References and Notes

1. M. J. Berridge, *Ann. N.Y. Acad. Sci.* **766**, 31 (1995).
2. B. Vanhaesebroeck *et al.*, *Annu. Rev. Biochem.* **70**, 535 (2001).
3. T. Takenawa, T. Itoh, *Biochim. Biophys. Acta* **1533**, 190 (2001).
4. M. Bennett, S. M. Onnebo, C. Azevedo, A. Saiardi, *Cell. Mol. Life Sci.* **63**, 552 (2006).
5. R. F. Irvine, M. J. Schell, *Nat. Rev. Mol. Cell Biol.* **2**, 327 (2001).
6. S. B. Shears, *Biochem. J.* **377**, 265 (2004).
7. A. Saiardi, R. Bhandari, A. C. Resnick, A. M. Snowman, S. H. Snyder, *Science* **306**, 2101 (2004).
8. X. Pesesse, K. Choi, T. Zhang, S. B. Shears, *J. Biol. Chem.* **279**, 43378 (2004).
9. A. Saiardi, E. Nagata, H. R. Luo, A. M. Snowman, S. H. Snyder, *J. Biol. Chem.* **276**, 39179 (2001).
10. C. J. Barker, J. Wright, P. J. Hughes, C. J. Kirk, R. H. Michell, *Biochem. J.* **380**, 465 (2004).
11. Y. S. Lee, S. Mulugu, J. D. York, E. K. O'Shea, *Science* **316**, 109 (2007).
12. C. J. Barker, I. B. Leibiger, B. Leibiger, P.-O. Berggren, *Am. J. Physiol. Endocrinol. Metab.* **283**, E1113 (2002).
13. O. Larsson *et al.*, *Science* **278**, 471 (1997).
14. A. M. Efanov, S. V. Zaitsev, P.-O. Berggren, *Proc. Natl. Acad. Sci. U.S.A.* **94**, 4435 (1997).
15. M. Høy, P.-O. Berggren, J. Gromada, *J. Biol. Chem.* **278**, 35168 (2003).
16. M. Høy *et al.*, *Proc. Natl. Acad. Sci. U.S.A.* **99**, 6773 (2002).
17. Materials and methods are available as supporting material on *Science* Online.
18. P. Rorsman, E. Renström, *Diabetologia* **46**, 1029 (2003).
19. K. D. Gillis, R. Mossner, E. Neher, *Neuron* **16**, 1209 (1996).
20. C. S. Olofsson *et al.*, *Pfluegers Arch.* **444**, 43 (2002).
21. E. Renström, L. Eliasson, K. Bokvist, P. Rorsman, *J. Physiol.* **494**, 41 (1996).
22. H. R. Luo *et al.*, *Neuron* **31**, 439 (2001).
23. E. Nagata *et al.*, *J. Biol. Chem.* **280**, 1634 (2005).
24. J. Kamimura *et al.*, *J. Hum. Genet.* **49**, 360 (2004).
25. Lexicon knockout mouse NIH-0750, Mouse Genome Database (MGD), Mouse Genome Informatics Web Site, www.informatics.jax.org/external/ko/lexicon/1223.html (18 July 2006).
26. We thank S. H. Snyder for constructs, C. B. Wollheim for both INS-1E cells and hGH constructs, S. Seino for MIN6m9 cells and I. B. Leibiger for discussion. This work was supported by grants from Karolinska Institutet, Novo Nordisk Foundation, the Swedish Research Council, the Swedish Diabetes Association, EFSD, The Family Erling-Persson Foundation, Berth von Kantzow's Foundation, Robert A. Welch Foundation, NIH (GM31278), EuroDia (LSHM-CT-2006-518153), and the U.K. Medical Research Council.

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Transposase-Derived Transcription Factors Regulate Light Signaling in *Arabidopsis*

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Plants use light to optimize growth and development. The photoreceptor phytochrome A (phyA) mediates various far-red light–induced responses. We show that *Arabidopsis FHY3* and *FAR1*, which encode two proteins related to *Mutator*-like transposases, act together to modulate phyA signaling by directly activating the transcription of *FHY1* and *FHL*, whose products are essential for light-induced phyA nuclear accumulation and subsequent light responses. FHY3 and FAR1 have separable DNA binding and transcriptional activation domains that are highly conserved in *Mutator*-like transposases. Further, expression of *FHY3* and *FAR1* is negatively regulated by phyA signaling. We propose that FHY3 and FAR1 represent transcription factors that have been co-opted from an ancient *Mutator*-like transposase(s) to modulate phyA-signaling homeostasis in higher plants.

Plants constantly monitor their light environment in order to grow and develop optimally, using a battery of photoreceptors. Phytochromes are a family of photoreceptors that monitors the incident red [(R), 600 to 700 nm] and far-red [(FR), 700 to 750 nm] light wavelengths by switching reversibly between the R light–absorbing, biologically inactive Pr form and the FR light–absorbing, biologically active Pfr form (*1*, *2*). Upon photoactivation, phyA, the primary photoreceptor for FR light, is translocated from the cytoplasm into the nucleus to induce FR light–responsive gene expression that is required for various photoresponses, such as seed germination, seedling de-etiolation, FR light–preconditioned blocking of greening, and flowering (*3*). Genetic studies have identified two pairs of homologous genes essential for phyA signaling: (i) *FAR1* (far-red–impaired response 1) and *FHY3* (far-red–elongated hypocotyl 3) and (ii) *FHY1* (far-red–elongated hypocotyl 1) and *FHL* (*FHY1*-like) (*4*–*7*). FHY1 and FHL have been implicated in mediating the light-dependent nuclear accumulation of phyA (*8*, *9*). However, the biochemical function of FHY3 and FAR1 remains to be elucidated.

FHY3 and FAR1 share extensive sequence homology with MURA, the transposase encoded by the maize *Mutator* element, and with the predicted transposase of the maize mobile element *Jittery* (*10*, *11*). Both of these transposons are members of the superfamily of *Mutator*-like elements (MULEs) (*12*). Database mining and phylogenetic analysis revealed that FHY3/FAR1-like sequences are present in various angiosperms and fall into several phylogenetic clusters intermingled with MULE transposases (*13*) (table S1 and fig. S1). These proteins share an N-terminal C2H2-type zinc-

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chelating motif of the WRKY-GCM1 family, a central putative core transposase domain, and a C-terminal SWIM motif (*14*, *15*), with highly conserved predicted secondary and tertiary structures (figs. S2 and S3). To investigate the molecular function of FHY3 and FAR1, we generated transgenic plants expressing FHY3 and FAR1 proteins fused with a glucocorticoid receptor (GR) to control their nuclear localization (*16*). Both the *FHY3p::FHY3-GR* and *FAR1p::FAR1-GR* transgenes conferred a dexamethasone (DEX)–dependent rescue of the respective mutant phenotype (fig. S4), indicating that FHY3 and FAR1 act in the nucleus.

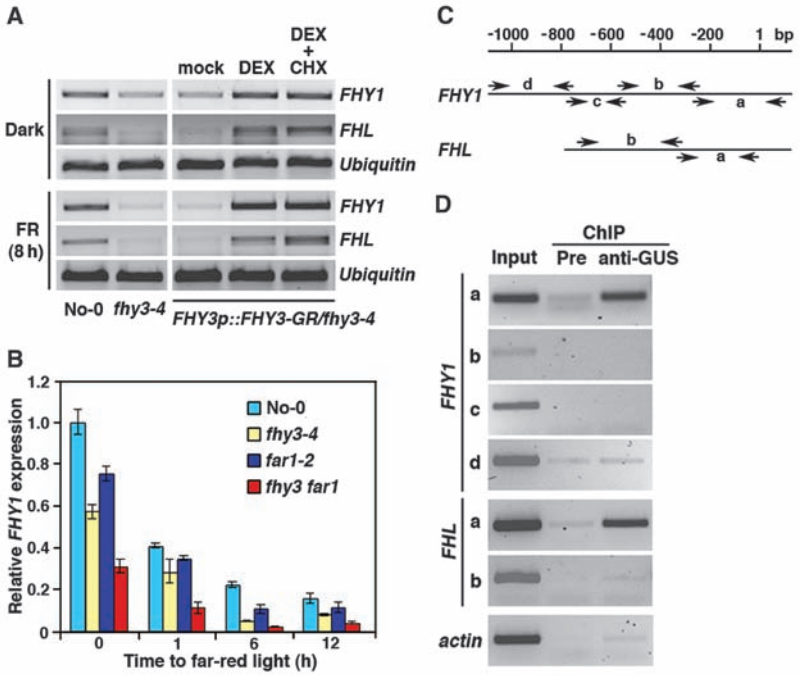

Fig. 1. FHY3 and FAR1 directly up-regulate *FHY1* and *FHL* expression. (**A**) Both *FHY1* and *FHL* are up-regulated by DEX or DEX plus CHX treatment in the *FHY3p::FHY3-GR/fhy3-4* transgenic plants. Seedlings were grown in darkness for 4 days and were then kept in darkness or transferred to FR light for 8 hours (h) before analysis. Expression of a *Ubiquitin* gene was shown as a control. No-0, wild-type No-0 ecotype. (**B**) Reduced expression of *FHY1* in the *fhy3-4*, *far1-2*, and *fhy3 far1* double mutants, as compared with that in the wild-type No-0 plants. Error bars represent SDs of triplicate experiments. (**C**) Diagram of the promoter fragments of *FHY1* and *FHL*. The locations of PCR primers used for the enrichment test are indicated (arrows). "1" indicates the putative transcription initiation site. (**D**) Enrichment of the "a" fragments of the *FHY1* and *FHL* promoters from the anti-GUS ChIP samples. Pre, preimmune.

Previous studies suggested that FHY3 is required for maintaining proper expression levels of *FHY1* and *FHL* in a light-independent manner (*7*, *10*). Semiquantitative reverse transcription polymerase chain reaction (RT-PCR) analysis showed that DEX or DEX plus cycloheximide [(CHX), a protein synthesis inhibitor (*17*) (fig. S5)] treatment, but not mock treatment, restored the expression levels of *FHY1* and *FHL* in both dark-grown and FR light–grown *FHY3p::FHY3-GR/fhy3-4* transgenic seedlings (Fig. 1A). This observation suggests that FHY3 activates *FHY1* and *FHL* expression. In addition, quantitative RT-PCR showed that *FHY1* expression was also reduced in the *far1-2* mutant and was much further reduced in the *fhy3 far1* double mutant, as compared with that in the wild-type seedlings (Fig. 1B). This result suggests that FHY3 and FAR1 act together to up-regulate *FHY1* expression.

We next performed a chromatin immunoprecipitation (ChIP) assay to test for a direct interaction of FHY3 with the *FHY1* and *FHL* promoters in vivo, using the *35S::GUS-FHY3/fhy3-4* transgenic plants (*5*). Multiplex PCR revealed enrichment for the "a" fragments [365 and 353 base pairs (bp), respectively] of the *FHY1* and *FHL* promoters in the anti-GUS ChIP samples, as compared with that in the ChIP samples prepared with preimmune antisera and the *Actin* gene control (Fig. 1, C and D). This

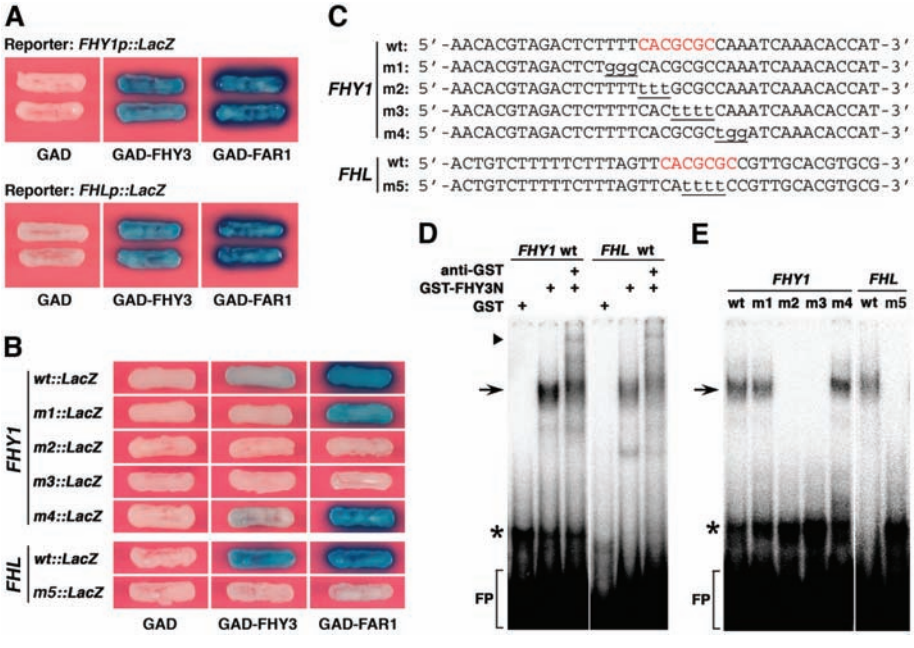

Fig. 2. FHY3 and FAR1 directly bind to the *FBS* motif present in the *FHY1* and *FHL* promoters via the N-terminal zinc finger motif. (**A**) GAD-FHY3 and GAD-FAR1, but not GAD itself, strongly activate expression of the *LacZ* reporter genes driven by the *FHY1* and *FHL* promoters in yeast. (**B**) GAD-FHY3 and GAD-FAR1 activate the *LacZ* reporter genes driven by the wild-type 39-bp subfragments of *FHY1* and *FHL* promoters (*wt::LacZ*) in yeast. Mutations in the *FBS* motif (m2, m3, and m5) abolish activation of the *LacZ* reporter gene expression. (**C**) Diagram of the wild-type and mutant *FHY1* and *FHL* subfragments used to drive the *LacZ* reporter gene expression and as probes in EMSA. The wild-type *FBS* motif is shown in red. Nucleotide substitutions in the mutant fragments are underlined. (**D** and **E**) EMSA assay showing that GST-FHY3N protein, but not GST by itself, specifically binds to the *FHY1* and *FHL* wild-type probes (D) but not to the m2, m3, and m5 mutant probes (E). Arrows indicate the up-shifted bands. The triangle indicates the supershifted DNA-protein-antibody complex when incubated with antibodies to GST. Asterisks indicate nonspecific binding. FP, free probe.

result indicates that FHY3 directly occupies the *FHY1* and *FHL* promoters in vivo. Moreover, constitutive overexpression of *FHY1* suppressed the phenotypes of the *fhy3-4*, *far1-2*, and *fhy3 far1* double mutants (fig. S6). Further, in response to FR light treatment, the nuclear accumulation of phyA–green fluorescent protein (phyA-GFP) is modestly reduced in the *fhy3-4* mutant (reduced to about 60% of the wild-type levels) but is essentially abolished in the *fhy3 far1* double mutant (fig. S7). Together, these findings suggest that FHY3 and FAR1 act together to regulate phyA nuclear accumulation through direct activation of *FHY1* and *FHL* expression.

We next used a yeast one-hybrid assay to delineate the DNA sequences to which FHY3 and FAR1 bind. GAL4 transcriptional activation domain–FHY3 (GAD-FHY3) or GAD-FAR1 fusion proteins, but not GAD alone, activated the *LacZ* reporter genes driven by the *FHY1* and *FHL* promoters (Fig. 2A). Deletion analysis narrowed down the FHY3/FAR1 binding site to a 39-bp promoter subfragment located on the "a" fragment for both *FHY1* and *FHL* (Fig. 2B). Notably, these subfragments share a stretch of consensus sequence: 5′-TTCACGCGCC-3′ (Fig. 2C). Mutating the core sequence "CACGCGC" of this motif (m2 and m3 for *FHY1* and m5 for *FHL*) abolished the reporter gene activation by both GAD-FHY3 and GAD-FAR1. Mutating the flanking sequences (m1 and m4) did not obviously affect the reporter gene activation by GAD-FAR1 but clearly reduced activation by GAD-FHY3 (Fig. 2B). Thus, "CACGCGC" likely defines a cis-element that confers specific binding for FHY3 and FAR1 and is named *FBS* for FHY3/FAR1 binding site.

Domain deletion analysis revealed that the N-terminal fragments of FHY3 and FAR1 are necessary and sufficient for activating the *LacZ* reporter genes driven by the *FHY1* and *FHL* promoters (fig. S8). Consistent with this finding, electrophoretic mobility shift assay (EMSA) showed that recombinant GST-FHY3N fusion protein (glutathione *S*-transferase fused with the first 200 amino acids of FHY3, including the zinc finger motif) caused an up-shift of the radiolabeled wild-type *FHY1* and *FHL* probes (Fig. 2D) but not of the m2, m3, and m5 mutant probes (Fig. 2E). Moreover, the addition of antibodies to GST caused a supershift of the wild-type probes (Fig. 2D). Further, preincubation of the GST-FHY3N fusion proteins with two metal chelators, 1,10-*o*-phenanthroline or EDTA, effectively reduced DNA binding activity (fig. S9). Thus, we conclude that FHY3 binds directly to the *FBS* motif by the N-terminal zinc finger motif. Genome-wide analysis by means of the PatMatch program (*18*) against an *Arabidopsis* promoter database (http://stan.cropsci.uiuc.edu/sift/index.php) revealed that the *FBS* motif is also present in the promoters of hundreds of other genes, including the R light photoreceptor *PHYTOCHROME B* (*PHYB*), *CIRCADIAN CLOCK–ASSOCIATED 1* (*CCA1*), and *EARLY FLOWERING 4* (*ELF4*). Yeast one-hybrid assay showed that GAD-FHY3 and GAD-FAR1 are capable of activating the *LacZ* reporter genes driven by *PHYB*, *ELF4*, and *CCA1* promoter fragments containing the wild-type *FBS* motif but not a mutated *FBS* motif (fig. S10). This observation is consistent with a reported role of FHY3 in gating R light signaling to the circadian clock (*19*).

To test whether FHY3 has an intrinsic transcriptional regulatory activity, we fused a full-length FHY3 with the LexA DNA binding domain. The LexA-FHY3 fusion protein, but not

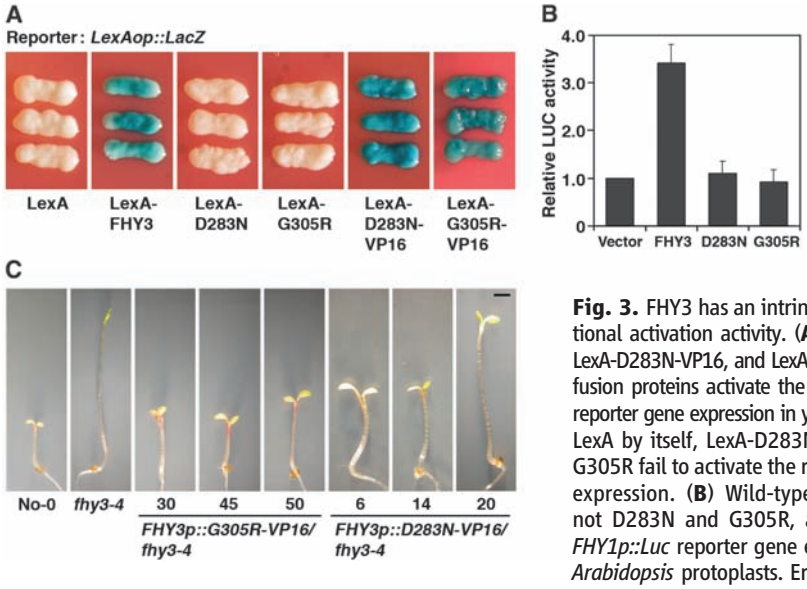

Fig. 3. FHY3 has an intrinsic transcriptional activation activity. (**A**) LexA-FHY3, LexA-D283N-VP16, and LexA-G305R-VP16 fusion proteins activate the *LexAop::LacZ* reporter gene expression in yeast, whereas LexA by itself, LexA-D283N, and LexA-G305R fail to activate the reporter gene expression. (**B**) Wild-type FHY3, but not D283N and G305R, activates the *FHY1p::Luc* reporter gene expression in *Arabidopsis* protoplasts. Error bars represent SDs of triplicate experiments. LUC, luciferase. (**C**) Images of 4-day-old FR light–grown seedlings of multiple independent lines, showing that the *FHY3p::D283N-VP16* and *FHY3p::G305R-VP16* fusion genes confer complete or partial rescue of the *fhy3-4* mutant phenotype. Scale bar, 2 mm.

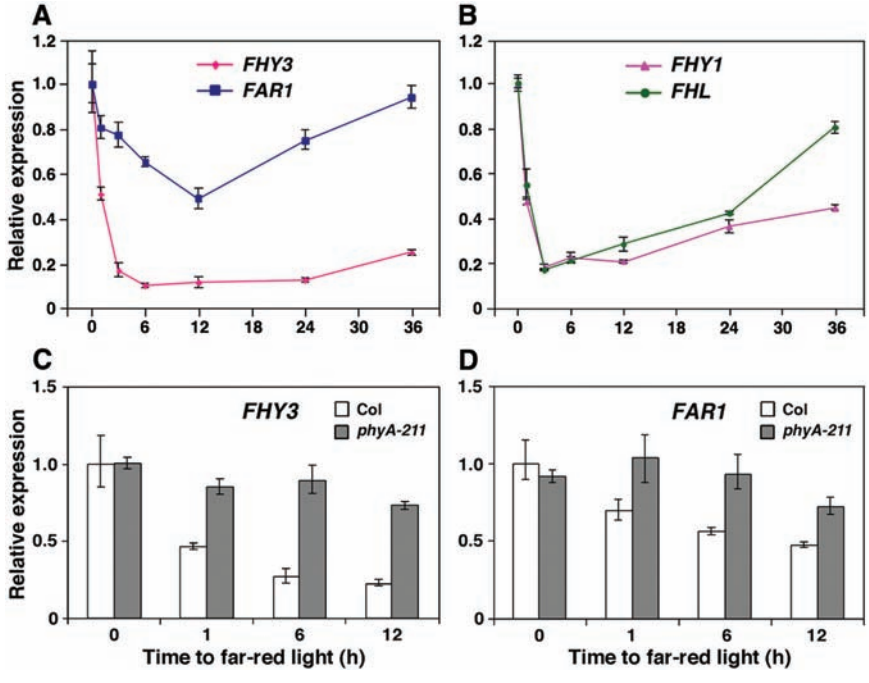

Fig. 4. Down-regulation of *FHY3*, *FAR1*, *FHY1*, and *FHL* by phyA signaling. (**A** and **B**) The transcript levels of *FHY3* and *FAR1* (A) and *FHY1* and *FHL* (B) are down-regulated by FR light. (**C** and **D**) The transcript levels of *FHY3* (C) and *FAR1* (D) remain relatively stable in the *phyA-211* mutant, as compared with levels in the Columbia wild-type (Col) background. The expression levels in dark-grown wild-type plants were set as 1. Error bars in (A) to (D) represent SDs of triplicate experiments.

LexA alone, activated a *LacZ* reporter gene driven by the *LexA* operator (Fig. 3A). Two amino acid–substituted FHY3 proteins corresponding to the *fhy3-9* Gly^{305}→Arg^{305} (G305R) and *fhy3-10* Asp^{283}→Asn^{283} (D283N) mutant alleles (*5*) failed to activate the *LacZ* reporter gene (Fig. 3A), despite comparable levels of expression for the wild-type and mutant FHY3 fusion proteins. In addition, wild-type FHY3 protein, but not the G305R or D283N mutant proteins, activated a luciferase reporter gene driven by the *FHY1* promoter in *Arabidopsis* protoplasts (Fig. 3B). Further, fusion with the VP16 activation domain of herpes simplex virus restored the transcriptional activation activity of G305R and D283N (Fig. 3A), and the fusion proteins conferred a complete or partial rescue of the *fhy3-4* mutant phenotype (Fig. 3C). These results suggest that the intrinsic transcriptional activation activity of FHY3 is essential for its biological function. Domain deletion analysis revealed that the C-terminal region of FHY3 and FAR1 that lacks the N-terminal zinc finger motif is necessary and fully capable of activating the reporter gene expression in yeast, whereas their N-terminal DNA binding domains are unable to activate the reporter gene (fig. S11). These observations suggest that FHY3 and FAR1 have separable DNA binding and transcriptional activation domains.

Finally, we examined how FR light regulates the expression of *FHY3* and *FAR1* using quantitative RT-PCR. In a wild-type background, the transcript levels of *FHY3* declined rapidly after exposure to FR light. Expression of *FAR1* was also down-regulated by FR light, although with slower kinetics and to a lesser degree (Fig. 4A). Expression of *FHY1* and *FHL* displayed a pattern similar to that of *FHY3* (Fig. 4B), which is consistent with their being the direct target genes of *FHY3* and *FAR1*. In contrast, expression of *FHY3* and *FAR1* remained high in the *phyA-211* mutant under FR light (Fig. 4, C and D). These results indicate that expression of *FHY3* and *FAR1* is subject to a negative feedback regulation by phyA signaling and suggest that FHY3 and FAR1 act at a focal point of a feedback loop that maintains the homeostasis of phyA signaling (fig. S12).

Our phylogenetic and functional analyses support a scenario whereby one or several related MULE transposases gave rise to the *FHY3/FAR1*-related genes during the evolution of angiosperms through a process termed "molecular domestication" (*20*), with concomitant loss of the ability to transpose (*21*) (fig. S13). Similar to this, DAYSLEEPER, an *Arabidopsis hAT*-like transposase, has been shown to act as a DNA binding protein and is essential for plant development (*22*). However, it is not known whether this protein can directly regulate gene expression. Our results demonstrate that a transposase-derived protein can bind to a promoter region and directly stimulate the transcription of that gene. Innovation of phyA, which occurred before the origin of angiosperms, has been hypothesized to confer an adaptive advantage to the successful colonization of the first angiosperms on Earth (*23*). The domestication of FHY3 and FAR1 from an ancient transposase(s) might mark an event in the evolution of angiosperms serving to meet the challenges of changing light environments. Our results also provide functional evidence to support the proposition that transposable elements, which are prevalent throughout the genomes of many plants and animals, can serve as a source of new transcription factors that allow populations to adapt and species to evolve (*24*).

References and Notes

1. M. M. Neff, C. Fankhauser, J. Chory, *Genes Dev.* **14**, 257 (2000).
2. P. H. Quail, *Nat. Rev. Mol. Cell Biol.* **3**, 85 (2002).
3. F. Nagy, S. Kircher, E. Schäfer, *Semin. Cell Dev. Biol.* **11**, 505 (2000).
4. M. Hudson, C. Ringli, M. T. Boylan, P. H. Quail, *Genes Dev.* **13**, 2017 (1999).
5. H. Wang, X. W. Deng, *EMBO J.* **21**, 1339 (2002).
6. T. Desnos, P. Puente, G. C. Whitelam, N. P. Harberd, *Genes Dev.* **15**, 2980 (2001).
7. Q. Zhou *et al.*, *Plant J.* **43**, 356 (2005).
8. A. Hiltbrunner *et al.*, *Curr. Biol.* **15**, 2125 (2005).
9. A. Hiltbrunner *et al.*, *Plant Cell Physiol.* **47**, 1023 (2006).
10. M. E. Hudson, D. R. Lisch, P. H. Quail, *Plant J.* **34**, 453 (2003).
11. R. Lin, H. Wang, *Plant Physiol.* **136**, 4010 (2004).
12. D. Lisch, *Trends Plant Sci.* **7**, 498 (2002).
13. The accession numbers for *Arabidopsis* PHYA, FHY3, FAR1, FHY1, FHL, and the maize MURA and the predicted transposase of *Jittery* are NP_172428, NP_188856, NP_567455, NP_181304, AAC23638, AAA21566, and AAF66982, respectively.
14. M. M. Babu, L. M. Iyer, S. Balaji, L. Aravind, *Nucleic Acids Res.* **34**, 6505 (2006).
15. K. S. Makarova, L. Aravind, E. V. Koonin, *Trends Biochem. Sci.* **27**, 384 (2002).
16. D. Wagner, R. W. M. Sablowski, E. M. Meyerowitz, *Science* **285**, 582 (1999).
17. The effectiveness of CHX treatment in inhibiting protein synthesis was shown by blocking HY5 protein accumulation in FR light–treated *Arabidopsis* seedlings (fig. S5). A full description of the materials and methods are available as supporting material on *Science* Online.
18. T. Yan *et al.*, *Nucleic Acids Res.* **33**, W262 (2005).
19. T. Allen *et al.*, *Plant Cell* **18**, 2506 (2006).
20. W. J. Miller, J. F. McDonald, D. Nouaud, D. Anxolabéhère, *Genetica* **107**, 197 (1999).
21. We observed partial synteny conservation of *Arabidopsis FHY3* and *FAR1* with their orthologs in *Brassica* and *Populus*, suggesting that the genomic locations of these genes have been fixed in the eudicots (fig. S13).
22. P. Bundock, P. Hooykaas, *Nature* **436**, 282 (2005).
23. S. Mathews, *J. Hered.* **96**, 197 (2005).
24. C. Biémont, C. Vieira, *Nature* **443**, 521 (2006).

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Supporting Online Material

www.sciencemag.org/cgi/content/full/318/5854/1302/DC1
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References

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Social Comparison Affects Reward-Related Brain Activity in the Human Ventral Striatum

K. Fliessbach,[1] B. Weber,[1] P. Trautner,[1] T. Dohmen,[2] U. Sunde,[2] C. E. Elger,[1] A. Falk[3]*

Whether social comparison affects individual well-being is of central importance for understanding behavior in any social environment. Traditional economic theories focus on the role of absolute rewards, whereas behavioral evidence suggests that social comparisons influence well-being and decisions. We investigated the impact of social comparisons on reward-related brain activity using functional magnetic resonance imaging (fMRI). While being scanned in two adjacent MRI scanners, pairs of subjects had to simultaneously perform a simple estimation task that entailed monetary rewards for correct answers. We show that a variation in the comparison subject's payment affects blood oxygenation level–dependent responses in the ventral striatum. Our results provide neurophysiological evidence for the importance of social comparison on reward processing in the human brain.

The absolute consumption level, or alternatively the absolute level of income, is the most important determinant of individual well-being in traditional economic models of decision-making. These models typically assume that social comparisons, and therefore relative income, play no role. This view has long been challenged by social psychologists and anthropologists, who have argued that comparison with other individuals

ERRATUM

Post date 21 December 2007

Reports: "Transposase-derived transcription factors regulate light signaling in *Arabidopsis*" by R. Lin *et al*. (23 November 2007, p. 1302). In the sixth sentence of the third paragraph on page 1304, an incorrect Web site was referenced. The correct Web site should be The *Arabidopsis* Information Resource (www.arabidopsis.org). Also, in reference 13 on page 1305, the accession numbers for *Arabidopsis* FAR1, FHY1, and FHL (AAD51282, AAL35819, and CAB82993, respectively) were mistyped as NP_567455, NP_181304, and AAC23638.