Table S1. Generation and assessment of *pid* and *enp* genotype combinations

Genotype	Test/procedure applied to assess the genotype
+[1] +/+ + (L*er*)	Progeny (12 plants) of the L*er* line used in this study was crossed with *pid-2/15* alleles. The resulting F1 plants did not segregate *laterne* seeds (however, see Table S3).
+ *enp*/+ +	Plants with this genotype were produced by cross of L*er* with *enp*/*enp* plants. These F1 plants have rare floral defects.
+ *enp*/+ *enp*	Isolated line from the original *laterne* segregating line. All *pid* alleles used in this study were crossed with the progeny (15 plants) of this *enp* homozygote. From the resulting F1 97 plants were scored for *laterne* segregation. All produced *laterne* seeds.
+ *enp*/*pid*-15 *enp*	The genotype of this line was confirmed by crossing with *pid*-15 homozygotes. This led to 50% F1 plants with a *pid* phenotype (genotype: *pid-15 +/pid-15 enp*) and 50% almost wild-type plants (*pid-15 +/+ enp*). The *pid*-15 *enp*/+ *enp* plants produced ~ 25% *laterne* seeds.
pid-x[2] *enp*/*pid*-x *enp*	Homozygous double mutants, which are produced by selfing of *pid*-x +/+ *enp* or *pid-x enp*/+ *enp* lines. Seeds with the typical *laterne* appearance make 6,25% and 25% of the progeny of the former and the latter respectively.
pid-2/15 enp/*pid-2/15* +	Produced by crossing of *pid*-2/15 *enp*/+ *enp* with *pid*-2/15 homozygotes. This results in ~1:1 *pid* to wt[3] plants. All *pid* plants are either sterile or segregate rarely *laterne* (at least 20% reduction; 30 plants analysed).
pid-x +/+ *enp*	Produced by crossing *pid*-x homozygotes with *enp* homozygotes. All F1 plants segregate *laterne.*
pid-x +/*pid*-x +	Selfing of *pid* homozygous lines produces *pid*-plants with allele-specific phenotypic strength.
pid-x +/+ +	Produced by crossing *pid*-x with wild-type plants. F1 plants segregate *pid*-phenotypes and wild types.

+[1], wild-type allele; x[2], any *pid* allele; wt[3], wild-type phenotype.

Table S2. Penetrance of *laterne* seed phenotype

Line	Genotype	Genetic background	% *laterne* expected	% *laterne* seeds observed (mutant/total)
R1	*pid-15 enp*/+ *enp*	L*er*	25	26.2 (28/107)
R2	*pid-15 enp*/+ *enp*	L*er*	25	28 (30/107)
R120802	*pid-15 enp*/+ *enp*	L*er*	25	21.4 (135/631)
III2E4a	*pid-15 enp*/+ *enp*	L*er*	25	23.3 (24/103)
III2A82	*pid-15 enp*/+ *enp*	L*er*	25	22.2 (36/162)
				Mean: 24.22±2.79
R55A	*pid-15* +/+ *enp*	L*er*	6.25	6.7 (96/1443)
R99A	*pid-15* +/+ *enp*	L*er*	6.25	8.5 (72/847)
				Mean: 7.6±1.27
211x8a	*pid-8* +/+ *enp*	WS-2/L*er*	6.25	5.3 (42/794)
211x8b	*pid-8* +/+ *enp*	WS-2/Ler	6.25	5.4 (25/461)
211x8c	*pid-8* +/+ *enp*	WS-2/L*er*	6.25	5.3 (23/430)
212x8a	*pid-8* +/+ *enp*	WS-2/L*er*	6.25	5.2 (19/366)
212x8b	*pid-8* +/+ *enp*	WS-2/L*er*	6.25	6.0 (18/300)
212x8c	*pid-8* +/+ *enp*	WS-2/L*er*	6.25	7.4 (40/542)
				Mean: 5.77±0.85
211x92a	*pid-9* +/+ *enp*	Col/L*er*	6.25	7.2 (35/484)
211x92b	*pid-9* +/+ *enp*	Col/L*er*	6.25	7.2 (47/656)
211x92c	*pid-9* +/+ *enp*	Col/L*er*	6.25	7.7 (38/491)
212x91a	*pid-9* +/+ *enp*	Col/L*er*	6.25	7.3 (29/400)
212x91e	*pid-9* +/+ *enp*	Col/L*er*	6.25	6.7 (23/343)
212x91f	*pid-9* +/+ *enp*	Col/L*er*	6.25	6.7 (31/460)
				Mean: 7.13±0.38
latAx21	*pid-2* +/+ *enp*	L*er*	6.25	5.1 (7/137)
latAx22	*pid-2* +/+ *enp*	L*er*	6.25	6.5 (21/322)
latAx23	*pid-2* +/+ *enp*	L*er*	6.25	6.8 (13/190)
latAx24	*pid-2* +/+ *enp*	L*er*	6.25	6.4 (21/326)
latAx25	*pid-2* +/+ *enp*	L*er*	6.25	5.0 (8/159)
				Mean: 5.96±0.84

Table S3. Frequency of 'leaky' *laterne* seeds in different backgrounds

Number of lines scored	Genotype	Genetic background	*laterne* seed/total number of seeds
6	*pid-15* +/+ +	L*er*	2/2423
2	*pid-2* +/+ +	L*er*	0/440
15	*pid-2* +/*pid-2* +	L*er*	1/700
3	*pid-8* +/*pid-8* +	Ws	5/1500
5	*pid-9* +/+ +	Col	4/3200
7	*pid-15* +/+ +	L*er*/Nd	3/5200
7	*pid-15* +/+ +	L*er*/Col	23/5700

Table S4. Auxin transport measurements in wild-type (L*er*), *pinoid* and *laterne* plants

Genotype	Number of analysed plants	% ^{14}C-IAA*
Wild type (++/++)	*n*=10	100±46%
pinoid total (*pid-15* +/*pid-15* +)	*n*=48	35±31%
pinoid with flowers	*n*=25	42±32%
pinoid without flowers	*n*=23	28±29%
laterne (*pid-15 enp*/*pid-15 enp*)	*n*=50	34±33%

*Average transport in wild type as reference. Relative concentrations of ^{14}C-IAA transported to the basal 4 mm of 2.5 cm stem fragments within 24 hours.