Supplementary information

Dynamics of plant DNA replication based on PCNA visualization

Ryohei Yokoyama¹, Takeshi Hirakawa¹, Seri Hayashi¹, Takuya Sakamoto¹ and Sachihiro Matsunaga^{1*}

¹Department of Applied Biological Science, Faculty of Science and Technology, Tokyo University of Science, 2641 Yamazaki, Noda, Chiba 278-8510, Japan.

*For correspondence.

Sachihiro Matsunaga

Department of Applied Biological Science, Faculty of Science and Technology, Tokyo University of Science, 2641 Yamazaki, Noda, Chiba 278-8510, Japan.

Phone: +81-4-7124-1501 Fax: +81-4-7122-9104 E-mail:sachi@rs.tus.ac.jp



Supplementary Figure S1.

(a) Meristematic epidermal cells were used in AtPCNA1-EdU co-localization analyses (n = 307 nuclei from three plants).

(b) Confirmation of the AtPCNA1-EGFP line as a useful marker line for visualization of S-phase progression. The ratio of the number of nuclei showing AtPCNA1 dotted and speckled patterns to total nuclei was calculated and compared with a previous report using EdU incorporation⁶.



Supplementary Figure S2.

Relative root elongation of pAtPCNA1::AtPCNA1-EGFP on the control medium and medium supplemented with 12 μ g/mL aphidicolin. Root length was measured 24 h after transfer to each medium.

Туре	AtPCNA1 signals	EdU signals	
Ι	whole	whole	
II	whole	speckled	
III	whole	negative	
IV	dotted	whole	
V	speckled	whole	
VI	speckled	mixed	
VII	speckled	speckled	

Supplementary Table S1. Classification of the pattern of AtPCNA1 and EdU signals in Fig 4.

Supplementary Table S2. PCR primers used in this study.

No.	Name	Purpose	Sequence	Tm(℃)
1	AtPCNA1_forward_pENTR_PCR	Cloning	CACCGGGCAAAGTCGGTTTTGGA	64
2	AtPCNA1_reverse_pENTR_PCR	Cloning	GGGATTAGTGTCTTCTTCTTCTTCA	56
3	AtPCNA1 seqence1	Sequencing	GGGCTCGTTGTTGAAGAAGGTTCTA	61
4	AtPCNA1 seqence2	Sequencing	GTAAAACGACGGCCAG	51
5	AtPCNA1 seqence3	Sequencing	GGAAACAGCTATGACCATG	51