The genome of Aechmea fasciata provides insights into the evolution of tank epiphytic habits

and ethylene-induced flowering

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Supplementary Figure 1 Genome size estimation using GenomeScope.



Supplementary Figure 2 Hi-C heatmap of each pseudo-chromosome.



Supplementary Figure 3 Heat map of LTR distribution in each chromosome.



Supplementary Figure 4 Dot plot of synteny alignment between *A. comosus* and the ancestral genome.



Supplementary Figure 5 Dot plot of synteny alignment between *A. bracteatus* and the ancestral genome.



Supplementary Figure 6 Phylogenetic analysis of *Ricesleeper2* gene families.



Supplementary Figure 7 Phylogenetic analysis of *TPS10* gene families.

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Supplementary Figure 8 Multiple alignment of *GID1C* proteins. Os, *Oryza sativa subsp. Japonica*; Ms, *Musa acuminata subsp. malaccensis*; Acb, *A. bracteatus*; Acc, *A. comosus*; Af, *A. fasciata*.



Supplementary Figure 9 Gene expression analysis of two *GID1C-like* genes in *A. fasciata*. Af03916, *AfGID1C-like1*; Af03917, *AfGD11C-like2*.

а pfam03514 GRAS Pssm-ID: 397536 Cd Length: 374 Bit Score: 442.88 E-value: 5.43e-152 50 20 30 40 60 70 10 80 Cdd:pfam03514 1 LVHLLLACAEAVSSGDLSLAQAILARLNQLASPAGDPMQRLAAYFTEALAARLARsgssiysaLPPRPTSPSDSIERISA 80 90 100 110 120 130 140 150 160 gi 1147553370 317 H—FYEASPCLKFAHFTANQAILEAFAGCRRVHVVDLGVRQGLQWPALLQALALRPGGAPSFRLTAVGPP—ASGDALRE 392 Cdd:pfam03514 81 Yk1FYEVSPYLKFGHFTANQAILEAFEGEERVHIIDFDIGQGLQWPSLIQALASRPGGPPHLRITGIGDPqfSSAEELEE 160
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 aaaaaaaaaeveeeeeeaaaeEAVAVNAVLELHQVLAQLGAAE
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 Cdd:pfam03514 161 TGDRLAQFADSLGVPFEFNPLVAKRLEDLDLEMLDvRPG------EALAVNCVFALHRLLDESVSLE 221
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 K——VLGTVRALRPRVFTVVEQEANLINAGSFRDFTEALHYYSTVFDSLEGCGSAGSSDR-VMAEAYVGREIANVVGCE
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 Cdd:pfam03514 222 SprdtFLRLVRSLNPKVVTLVEQEANHNSAPFLNRFVEALHYYSALFDSLEATLPRDSEERrKVERELLGREIVNVACE 301 360 330 340 350 370 380 390 gi 1147553370 547 GPERTERHETLAQWRGRMGRAGFHPVPIGSDAFKQASTLLALFSgggGGGFRVEEREGCLTLGWHTRPLIATSAWR 622 Cdd:pfam03514_302_GAERVERHETFGKWRERMRRAGFRPVPLSEFAVKQAKLLLRLYY----VDGYTVEEDNGSLVLGWKGRPLVAASAWR_374 b DELLA pfam12041 Pssm-ID: 403308 Cd Length: 68 Bit Score: 118.26 E-value: 3.76e-32 20 30 40 50 70 С pfam03514 GRAS Pssm-ID: 397536 Cd Length: 374 Bit Score: 448.65 E-value: 2.46e-154 30 50 10 20 40 60 70 80 Query 9724 Cdd:pfam03514 1 LVHLLLACAEAVSSGDLSLAQAILARLNQLASPAGDPMQRLAAYFTEALAARLARsgssiysaLPPRPTSPSDSIERISA 80 100 Query 9724 Cdd:pfam03514 81 Yk1FYEVSPYLKFGHFTANQAILEAFEGEERVHIIDFDIGQGLQWPSLIQALASRPGGPPHLRITGIGDPqfSSAEELEE 160 Query_9724 Cdd:pfam03514 161 TGDRLAQFADSLGVPFEFNPLVAKRLEDLDLEMLDvRPG-----------EALAVNCVFALHRLLDESVSLESprd 225 260 270 280 290 300 250 310 320
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 DELLAVLGYKVRSSDMADVAQKLEQLEWVMG—NAQEDGISHLA-----SDTVHVPSDLSSWVESMLSELN
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Supplementary Figure 10 Domain analysis of *AcSLR1-like* and *AfSLR1-like* based on searches of the NCBI Conserved Domain Database. a, alignment of *AcSLR1-like* at the GRAS domain; b, alignment of *AcSLR1-like* at the DELLA domain; d, alignment of *AfSLR1-like* at the GRAS domain; d, alignment

of *AfSLR1-like* at the DELLA domain.



Supplementary Figure 11 Root tip chromosome karyotype analysis of *A. fasciata*.

Туре	Length (bp)	Count
N10	9050129	6
N20	7538727	12
N30	6962080	19
N40	5533891	28
N50	4689950	38
N60	2670604	53
N70	967756	86
N80	509414	166
N90	213451	329
Min.	45520	-
Max.	11307573	_
Ave.	792203	-
Total	529983447	669

Supplementary Table 1 Summary of genome assembly.

Supplementary Table 2 Summary of protein-coding genes in *A. fasciata*.

Protein coding gene number	26,216		
Total length of protein coding gene (bp)	108,991,579		
Average length of protein coding gene (bp)	4157		
Total exon length (bp)	28,099,890		
Average length of exon (bp)	198		
Total intron length (bp)	80891689		
Average length of intron (bp)	712		

Supplementary Table 3 Summary of BUSCO analysis of protein-coding genes from *A. fasciata* geome (93.4%).

397	Complete BUSCOs (C)								
348	Complete and single-copy BUSCOs (S)								
49	Complete and duplicated BUSCOs (D)								
19	Fragmented BUSCOs (F)								
9	Missing BUSCOs (M)								
425	Total BUSCO groups searched								

Supplementary Table 4 Summary of BUSCO analysis of *A. fasciata* geome (98.4%).

418	Complete BUSCOs (C)
410	Complete and single-copy BUSCOs (S)
8	Complete and duplicated BUSCOs (D)
5	Fragmented BUSCOs (F)
2	Missing BUSCOs (M)
425	Total BUSCO groups searched

Supplementary Table 5 Summary of repeat sequences in the *A. fasciata* genome.

		Number	Length	% of	% of
			(bp)	repeats	geneome
	Repeats total	499787	214719703	100	61.72471
LTR	Gypsy	18790	83223889	38.75932	23.92408
Retrotransposon	Copia	5445	13830252	6.441073	3.975734
	unknown	14837	18093919	8.426762	5.201395
Retrotransposon	LINE	5398	3349713	1.56004	0.9629301
	SINE	4	236	1.099107e-	6.784208e-
				04	05
Unclassified	Unknown	143904	83787245	39.02168	24.08602

retroelement					
DNA transposon	Helitron	174	199246	0.09279353	0.05727654
	Academ-1	1	60	2.794341e-	1.724799e-
				05	05
	MuLE-MuDR	921	1586369	0.7388092	0.4560279
	PIF-	123	100598	0.04685085	0.02891855
	Harbinger'				
	hAT-Tip100	39	49081	0.02285817	0.01410914
	hAT-Tag1	114	249706	0.01162939	0.0717821
TE total		189750	204470314	95.22662	58.77836
	Simple_repeat	310037	10249389	4.773381	2.946356

Supplementary Table 6 ChIP-qPCR analysis of the binding of *AfEIL1-like* to *AfFTL2*.

	Primer: 448-1: F, TAACGCACTCTCCCCTCAA; R, TCATTTATTCACGCCCTCTG.													
		CT	AVE.	VOL(ul)	IDF	$\triangle CT$	\triangle CT (DNA normalized)	%INPUT	$\Delta\Delta Ct$ [ChIP/NIS]	Fold Enrichment				
		22.45												
	IN 448-1	22.38	22.33	2				0.006891234		4.16				
		22.16			101	7 16666667	12 02407015							
	ID 449 1	29.45			101	/.1000000/	15.82487815							
	IP 440-1 EIN2	28.41	29.49666667	200										
EXP	EINS	30.63							2 0575 4710					
									-2.03754719					
	IgG 448-1		32.54	100										
		32.54			5 1	10.21	15 00010521	0.00165544						
		22.45			51	10.21	13.00242534	0.00105544						
	IN 448-1	22.38	22.33	2										
		22.16												

	Primer: 448-2:F, TCAAACAAAGAAATACCCCG; R, CCAACGAATCTGACGGCAT.													
		СТ	AVE.	VOL(ul)	IDF	$\triangle CT$	\triangle CT (DNA normalized)	%INPUT	$\Delta\Delta Ct$ [ChIP/NIS]	Fold Enrichment				
EVD		21.96												
EAP	IN 448-1	21.99	22.03666667	2	101	6.57	13.22821148	0.010421052	-2.07754719	4.22				
		22.16												

IP 448-1	28.69								
EIN ₂	28.7	28.60666667	200	ł					
EINS	28.43								
	32.05								
IgG 448-1	31.55	31.67	100				0.002468022		
	31.41			51	0 622222222	15 20575969			
	21.96	22.036666667			51	9.633333333	13.30373808	0.002408925	
IN 448-1	21.99		2						
	22.16								