

CORRECTION

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# Correction: Identification of SSR markers linked to the abscission of cotton boll traits and mining germplasm in Cotton

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**Correction: J Cotton Res 7, 20 (2024)**  
<https://doi.org/10.1186/s42397-024-00180-3>

Following publication of the original article (Shui et al. 2024), the author found 5 errors in the published article.

1. One of the author's name has been corrected from Gou Chunping to Guo Chunping.
2. The reference (Zhao SQ. 2016) in Table 2 has been updated to: Zhao SQ. Analysis on the major gene

and multigene mixed inheritance and QTL mapping for early maturity traits in upland cotton. *Chin Acad Agric Sci.* 2016. <https://doi.org/10.3969/j.issn.20160501>. (in Chinese with English abstract).

3. In 'Results' part, 'Phenotype analysis of 238 cotton boll abscission among cotton accessions' paragraph, the phenotype analysis of AR1 ranging from 19.27%–63.79%, which was wrongly written as 19.27%–63.97%.
4. The '2018KRL' is modified to '2018KEL' in Table 1.

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The original article can be found online at <https://doi.org/10.1186/s42397-024-00180-3>.

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Table 1 has been updated from:

**Table 1** Phenotypic statistics of cotton boll abscission traits

Trait	Env	Min	Max	Mean	SD	CV%	Skewness	Kurtosis	H <sup>2</sup>
AR1 /%	2018KRL	2.11	31.32	10.45	4.58	43.83	0.90	1.73	0.60
	2018SHZ	0.43	41.45	14.72	9.39	63.79	0.58	-0.57	
	2019KEL	21.22	63.30	41.03	7.91	19.27	0.12	-0.43	
	2019SHZ	1.65	34.68	13.51	6.73	49.81	0.71	0.27	
AR2 /%	2018KRL	23.01	73.89	43.31	9.25	21.36	0.50	0.38	0.60
	2018SHZ	11.67	58.65	33.74	10.87	32.22	0.53	-0.49	
	2019KEL	35.15	74.94	55.54	6.81	12.26	-0.12	-0.04	
	2019SHZ	15.64	60.17	38.91	7.94	20.41	0.01	-0.07	
FP /d	2018KRL	77.85	88.65	83.85	2.15	2.56	-0.27	-0.40	0.75
	2018SHZ	66.25	85.90	77.77	4.72	6.07	-0.58	-0.65	
	2019KEL	69.00	80.00	73.22	2.24	3.06	-0.58	-0.09	
	2019SHZ	72.80	91.00	82.17	4.09	4.98	-0.53	-0.67	
WGP /d	2018SHZ	132.55	148.00	140.37	3.64	2.59	0.41	-0.39	0.32
	2019KEL	111.50	145.00	132.04	4.65	3.52	-0.39	1.28	
	2019SHZ	135.55	159.50	147.40	4.54	3.08	0.30	-0.05	

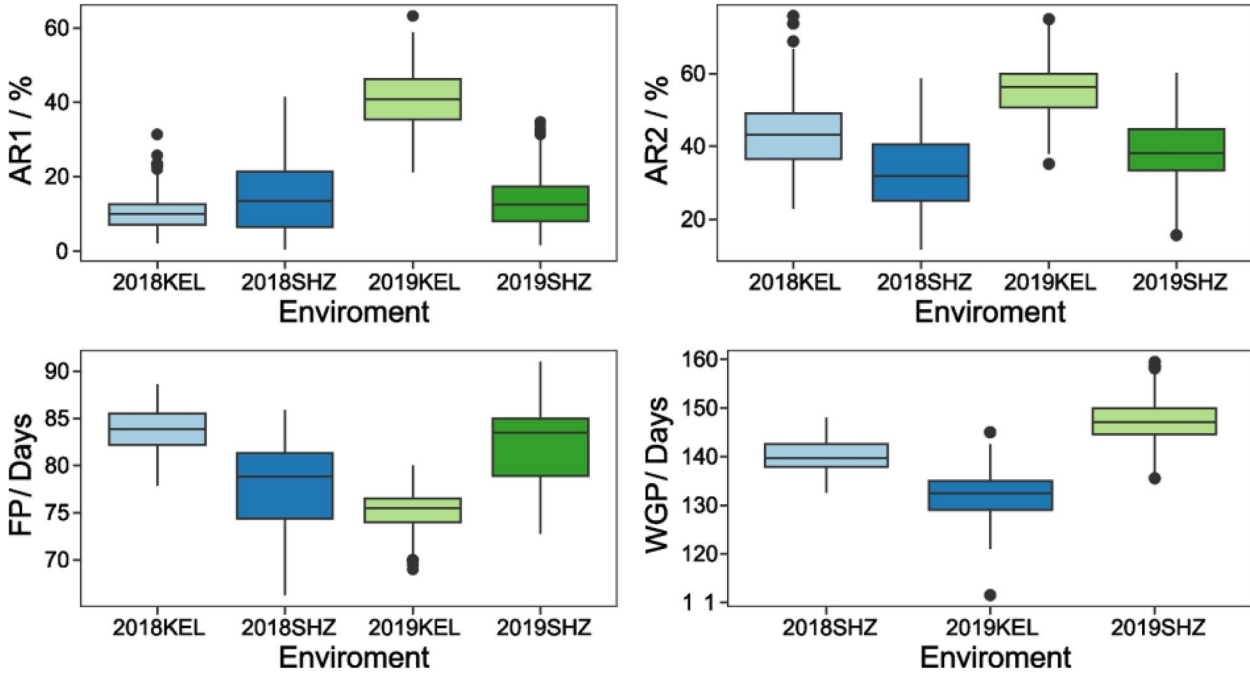
To:

**Table 1** Statistics of cotton the abscission of cotton boll traits in cotton

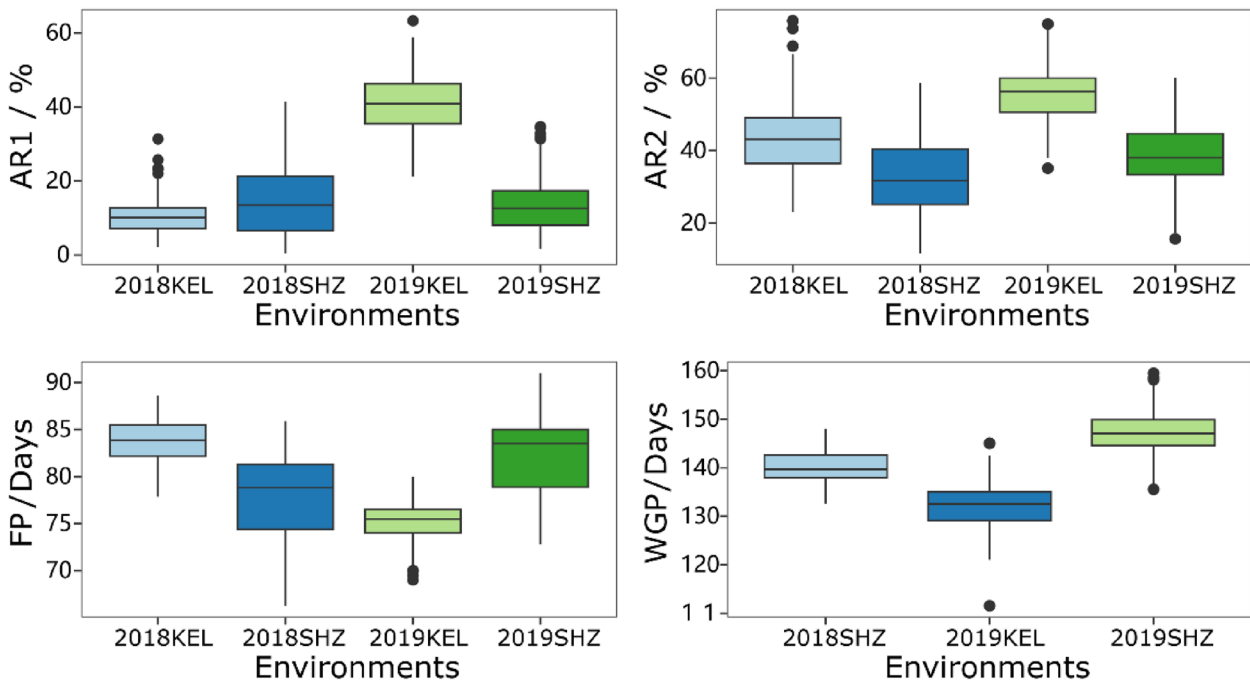
Trait	Env	Min	Max	Mean	SD	CV%	Skewness	Kurtosis	H <sup>2</sup>
AR1 /%	2018KEL	2.11	31.32	10.45	4.58	43.83	0.90	1.73	0.6
	2018SHZ	0.43	41.45	14.72	9.39	63.79	0.58	-0.57	
	2019KEL	21.22	63.30	41.03	7.91	19.27	0.12	-0.43	
	2019SHZ	1.65	34.68	13.51	6.73	49.81	0.71	0.27	
AR2 /%	2018KEL	23.01	73.89	43.31	9.25	21.36	0.50	0.38	0.6
	2018SHZ	11.67	58.65	33.74	10.87	32.22	0.53	-0.49	
	2019KEL	35.15	74.94	55.54	6.81	12.26	-0.12	-0.04	
	2019SHZ	15.64	60.17	38.91	7.94	20.41	0.01	-0.07	
FP /d	2018KEL	77.85	88.65	83.85	2.15	2.56	-0.27	-0.40	0.75
	2018SHZ	66.25	85.90	77.77	4.72	6.07	-0.58	-0.65	
	2019KEL	69.00	80.00	73.22	2.24	3.06	-0.58	-0.09	
	2019SHZ	72.80	91.00	82.17	4.09	4.98	-0.53	-0.67	
WGP /d	2018SHZ	132.55	148.00	140.37	3.64	2.59	0.41	-0.39	0.32
	2019KEL	111.50	145.00	132.04	4.65	3.52	-0.39	1.28	
	2019SHZ	135.55	159.50	147.40	4.54	3.08	0.30	-0.05	

5. The four X-axes is modified to Environments in Fig. 1.

Fig. 1 has been updated from:



To:



The original article (Shui et al. 2024) has been updated.

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#### Reference

- Shui G, Lin H, Ma X, et al. Identification of SSR markers linked to the abscission of cotton boll traits and mining germplasm in Cotton. *J Cotton Res.* 2024;7:20. <https://doi.org/10.1186/s42397-024-00180-3>.
- Zhao SQ. Analysis on the major gene and multigene mixed inheritance and QTL mapping for early maturity traits in upland cotton. *Chin Acad Agric Sci.* 2016. <https://doi.org/10.3969/j.issn.201600501>. (in Chinese with English abstract).