

Convergent loss of awn in two cultivated rice species *Oryza sativa* and *Oryza glaberrima* is caused by mutations in different loci

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		1 st exon		2 nd exon			
<i>O. glaberrima</i>	1	MNP		TTAAAADQPSKPS	AAAARKRKSSAKPKASSSSLP	TATAATNASPKRSKVAAGAGDD	59
<i>O. sativa</i>	1	MNP		TTAAAADQPSKPS	AAAAARKRKSSAKPKASSSSLP	TATAATNASPKRSKVAAGAGDD	60
			Ins(GCC)		Sub(GCG -> ACG)		
					3 rd exon	4 th exon	
<i>O. glaberrima</i>	60	GDG	DADAAEEKPEPAKDYIHVRARRGQATDSHSLAERVRRERISERMKLLQSLVPGCNKI				119
<i>O. sativa</i>	61	GD	DADAAEEKPEPAKDYIHVRARRGQATDSHSLAERVRRERISERMKLLQSLVPGCNKI				120
			Sub(GGC -> GCC)				
				5 th exon	6 th exon		
<i>O. glaberrima</i>	120	TGKALMLDEI	INYVQSLQRQVEFLSMKCLATMNPQLDFDSHYMP	SKDMSHMPVPAYPS	GDP		179
<i>O. sativa</i>	121	TGKALMLDEI	INYVQSLQRQVEFLSMKCLATMNPQLDFDSHYMP	SKDMSHMPVPAYP	SSDP		180
				Sub(GGC -> AGC)			
<i>O. glaberrima</i>	180	TTTTAF	SYTGSPATADPFTVYNCWELDLHTAMQMGATT	GLSQDGP	IATMAPSPSPLPHH		239
<i>O. sativa</i>	181	TTTTAF	SYTGSPATADPFTVYNCWELDLHTAMQMGATT	GLSQDGP	IATMAPSPSPLPHH		239
				7 th exon	Del(TCG)		
<i>O. glaberrima</i>	240	PPLHGFYGGQQQQG	TTVNHMKAEP				263
<i>O. sativa</i>	240	PPLHGFYGGQQQQG	TTVNHMKAEP				263

Figure S1 Amino acid sequences of RAE1/An-1 in *O. glaberrima* and *O. sativa*

Amino acid sequences of RAE1/An-1 in *O. glaberrima* and *O. sativa* are aligned by ClustalW. Mutations in the DNA sequence are shown below the mutation sites. The thick gray bar under the aligned sequences represents a conserved bHLH domain. The thin black bars and gray bars above the aligned sequences indicate the region of exons.

Table S1 Primers used in this study

Primers for linkage analysis of <i>RAE1</i>		
RAE1-38F	AGATTGGTTTAGGCTGCAGG	SSR
RAE1-38R	AAGGGCAGCAAATCAGGTAC	
RAE1-54F	TCACTAGCACAATCCTCCTC	SSR
RAE1-54R	GGCAAAGAACTTGTTTTGATGTTGTGAAG	
RAE1-78F	TTCTAGCACTACTAGAAAACACGTTTCTGC	dCAPS(PstI)
RAE1-78R	ATATTTTTGCAGGCGGGTGG	
RAE1-63F	GCTACAGTCCACGCCGCAACCCTCCGGTAC	dCAPS(KpnI)
RAE1-63R	CGTGCAATGTTTTAATCCGCC	
RAE1-69F	GAAGGGCAGGAAAACAAGAG	SSR
RAE1-69R	TTGTGTCCGGTGAGATTTGG	
RAE1-86F	TGTATGAAATGTTACAGAACTTGCTCTCGA	dCAPS(XhoI)
RAE1-86R	GTCATATGCGTGCACCTTGAC	
RAE1-53F	TTGGAAAACACAGTGCCGTC	SSR
RAE1-53R	CGATGGAGCAGTAGTTAGAG	
RAE1-44F	AGCGTTCAACGTTTGGATGG	SSR
RAE1-44R	TCAGAGACAGAGTCAAGTGC	
Primers for linkage analysis of <i>RAE3</i>		
RM341-F	CAAGAAACCTCAATCCGAGC	SSR
RM341-R	CTCCTCCCGATCCCAATC	
RM6346-F	ACTTTGATCGATCAGCCACC	SSR
RM6346-R	AGGTGGTGGAGATGAAGCAG	
RM20699-F	CCCGAGCCAGACAACATTCC	SSR
RM20699-R	GAGGTGTGAGGTGAGGAAGATGC	
6KG27612-F	TAGGTAGGAGTAGGCCGGAT	Indel
6KG27612-R	GCATGCACATATGTCACTGTGTAA	
6KG28331-F	CGATCTCCTTTGCATCTTTC	Indel
6KG28331-R	GGTGGTTAGCACCTTTGTGT	
6KG28941-F	CTCCTCTGATCACCTCGCT	Indel
6KG28941-R	GGAGAGGAGCAGCTTCTTG	
6KG29384-F	GTTTTGCTCAGGCAAATGAT	Indel
6KG29384-R	GCACCCAAGATTTTATTGGA	
6KG29722-F	ATGTTAGCCTTTTTCCTCCA	Indel
6KG29722-R	GGTCTTCGTTAGTCTTATGCATCT	
6KG30196-F	CTTGTTTCCATTTTGTGGG	Indel
6KG30196-R	GGAGGAAGAAGAGGACGAAG	