

Additional file 3

Supplemental Table 2. A list of 30 loci showing early and later mutations in Asian rice.

Rice locus ^a	Number of mutations shared between <i>Indica</i> and <i>Japonica</i> ^b		Number of mutations specific to <i>Indica</i> ^c		Number of mutations specific to <i>Japonica</i> ^c	
	5'	Coding	5'	Coding	5'	Coding
<i>SH4</i>	<u>6</u>	<u>1</u> (nons)		1(nons)	1(idl)	
<i>An-1(Awn-1)</i>		<u>2</u> (1 non,idl:1 aa)	1(idl)	<u>2</u> (idl:>3 aa)	<u>3</u> (1 idl)	<u>7</u> (2 nons, 3 idl:>3 aa)
<i>An-2(Awn-2)</i>	<u>4</u>			<u>1</u> (idl:>3 aa)		
<i>Hd5(Gdh8)</i>		1(idl:1 aa)	<u>4</u> (1 idl)	1(idl:1 aa)	<u>2</u> (1 idl)	
<i>GL3.2</i>	<u>7</u> (3 idl)	3(1 nons)	<u>11</u> (3 idl)		<u>3</u>	
<i>GIF1</i>	<u>2</u> (idl)	2(2 nons)	<u>7</u> (2 idl)	5(1 nons, 1 idl:2 aa)	<u>2</u> (2 idl)	2
<i>AGO2</i>	<u>3</u> (3 idl)	1(1 nons)	<u>2</u>	4(3 nons)	<u>7</u> (2 idl)	19(9 nons)
<i>GS5</i>	1(idl)	1(idl:1 aa)	<u>7</u> (2 idl)	4(3 nons)	<u>2</u>	3(1 nons, <u>1</u> idl:2 aa)
<i>PROG1</i>	<u>2</u> (1 idl)	1	1			
<i>TCP19</i>	<u>2</u> (1 idl)				<u>2</u> (2 idl)	
<i>CKX2</i>		1(idl:2 aa)	<u>4</u>	1(idl:2 aa)	<u>3</u> (1 idl)	3(3 nons)
<i>Hd3a</i>	<u>4</u> (1 idl)					<u>3</u> (3 nons)
<i>Hd1</i>	1	<u>3</u> (2 nons,1 idl:2 aa)	<u>2</u> (1 idl)	<u>2</u> (1 nons, 1 idl:>3 aa)	1(idl)	1(nons)
<i>Hd6</i>	<u>2</u> (1 idl)					<u>1</u> (idl: stop codon)
<i>C1</i>	<u>2</u> (1 idl)					1(nons)
<i>CHI</i> [#]		1(nons)	1		1	
<i>DFR</i>	<u>2</u> (1 idl)		<u>4</u> (2 idl)	2(1 nons)	<u>6</u> (2 idl)	2(1 nons)
<i>ANS1</i>		1(nons)		1(nons)	1(idl)	6(3 nons)
<i>Os04g47040</i>		<u>1</u> (idl:5 aa)		<u>1</u> (idl:5 aa)	<u>2</u>	2(1 nons, <u>1</u> idl:6 aa)
<i>Rc</i> [#]	<u>3</u> (1 idl)	2(1 nons, <u>1</u> idl:stop codon)	1(idl)	<u>1</u> (idl:>3aa)		
<i>MYB3</i>		2(1 nons, <u>1</u> idl:3 aa)				
<i>MYB15</i>	<u>3</u> (1 idl)	3(<u>2</u> idl:5 aa)			1	
<i>SK2</i>	1		<u>8</u> (1 idl)		<u>8</u> (2 idl)	
<i>DAHPS2</i>	<u>4</u>	1			1(idl)	
<i>PK1</i>	1(idl)		<u>3</u> (1 idl)		<u>6</u> (2 idl)	
<i>EPSPS</i>	<u>3</u> (1 idl)		1(idl)			
<i>ME</i>	<u>3</u>	1(idl:2 aa)		3(1 idl:2 aa)		1(nons)
<i>Os12g34860.1</i>		2(1 nons, <u>1</u> idl:stop codon)	<u>4</u> (1 idl)	1(nons)		
<i>RAE2</i>	<u>3</u>	<u>1</u> (idl:stop codon)				<u>2</u> (2 idl:2 aa)
<i>SPL16</i>	1(idl)		1	2(1 nons)	<u>3</u> (2 idl)	1 (idl:1 aa)
Subtotal	60	31	62	32	55	54

^a Loci in bold were detected under positive selection during Phase I.

^b Mutations contributed to positive selection were underlined, including nonsynonymous substitutions (nons) and indels (idl). Amino acid (aa) changes introduced by each indel was listed after comma. Synonymous substitutions (syn) were not shown for simplicity but included in the mutation number.

^c Underlined mutations are under positive selection in Phase II.

[#] Genes of shorter sequences