

Supplemental Data. Tuteja et al. (2009). Endogenous, tissue-specific short interfering RNAs silence the chalcone synthase gene family in *Glycine max* seed coats

Supplemental Table 1. Percentage Genomic Sequence Similarity of Pair Wise Alignments of the Nine Members of the *CHS* Gene Family.

	<i>CHS1</i>	<i>CHS2</i>	<i>CHS3</i>	<i>CHS4</i>	<i>CHS5</i>	<i>CHS6</i>	<i>CHS7</i>	<i>CHS8</i>	<i>CHS9</i>
<i>CHS1</i>	100								
<i>CHS2</i>	95	100							
<i>CHS3</i>	98	95	100						
<i>CHS4</i>	98	95	97	100					
<i>CHS5</i>	98	95	97	99	100				
<i>CHS6</i>	93	93	92	92	92	100			
<i>CHS7</i>	82	82	82	81	81	81	100		
<i>CHS8</i>	83	82	83	82	81	81	97	100	
<i>CHS9</i>	97	95	97	97	97	93	82	82	100

The values given in this table are the percentage sequence similarity between the genes at top of columns and the genes to the left of the rows. The percent values corresponding to the empty spaces are a mirror image of those below the 100 values. The same result is obtained no matter in which order the pairs of genes are compared.

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Supplemental Table 2. Unique Small RNA Signatures from the Williams Seed Coat Library (*i*) with 100% Identity to *CHS* Genes in a Pair Wise Comparison.

	<i>CHS1</i>	<i>CHS2</i>	<i>CHS3</i>	<i>CHS4</i>	<i>CHS5</i>	<i>CHS6</i>	<i>CHS7</i>	<i>CHS8</i>	<i>CHS9</i>
<i>CHS1</i>	953								
<i>CHS2</i>	545	740							
<i>CHS3</i>	909	541	960						
<i>CHS4</i>	881	532	892	960					
<i>CHS5</i>	881	533	893	960	961				
<i>CHS6</i>	410	379	397	377	377	494			
<i>CHS7</i>	123	178	145	149	149	113	1118		
<i>CHS8</i>	165	201	186	190	190	103	917	1067	
<i>CHS9</i>	782	510	801	805	805	358	126	166	850

The values given in this table are the number of siRNA signatures that are 100% identical to the genes at top of columns and the genes to the left of the rows. The percent values corresponding to the empty spaces are a mirror image of those below the numbers highlighted in blue. The same result is obtained no matter in which order the pairs of genes are compared. The numbers highlighted in blue are the reference numbers used to calculate the percentages values presented in Supplemental Table 3.

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Supplemental Table 3. Percentage of Unique *CHS*-siRNAs From the Williams (*l*) Seed Coat Library Aligning to *CHS* Sequences with 100% Identity that Are Shared Between different *CHS* Genes.

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GENE	<i>CHS1</i>	<i>CHS2</i>	<i>CHS3</i>	<i>CHS4</i>	<i>CHS5</i>	<i>CHS6</i>	<i>CHS7</i>	<i>CHS8</i>	<i>CHS9</i>
<i>CHS1</i>	100	57	95	92	92	43	13	17	82
<i>CHS2</i>	74	100	73	72	72	51	24	27	69
<i>CHS3</i>	95	56	100	93	93	41	15	19	83
<i>CHS4</i>	92	55	93	100	100	39	15	20	84
<i>CHS5</i>	92	55	93	100	100	39	15	20	84
<i>CHS6</i>	83	77	80	76	76	100	23	21	72
<i>CHS7</i>	11	16	13	13	13	10	100	82	11
<i>CHS8</i>	15	19	17	18	18	10	86	100	16
<i>CHS9</i>	92	60	94	95	95	42	15	19	100

^a Reference genes to which all others were compared to determine the percent of shared *CHS*-siRNA signatures are those listed in column one.

The reference numbers used to calculate the percentage values presented in this Supplemental Table 3 are those shaded in blue in Supplemental Table 2. For example, to determine the percent of *CHS* unique signatures with 100% identity to *CHS1* that also were 100% identical to *CHS2*, we multiplied the number of signatures that have 100 identity to *CHS1* and *CHS2* (545 from Supplemental Table 2) by 100 and divide by the total number of signatures with identity to *CHS1* (953, the reference number in blue in Supplemental Table 2). This was equal to 57. The percentage values given in row one were calculated with the reference number 953. Row two values were calculated using reference number 740, which is the total number of signatures with 100% identity to *CHS2*. The values in the ensuing rows were calculated using the reference numbers highlighted in blue for each individual row in Supplemental Table 2.

The light-blue and pink shaded columns and rows highlight the lower percentage values corresponding to the more divergent sequences (*CHS7* and *CHS8*).