

Table 1 Suppl. *SWEET* family genes from *Arabidopsis* and rice genomes.

Name	Accession No.	Name	Accession No.
<i>AtSWEET1</i>	AT1G21460	<i>OsSWEET1a</i>	Os01g65880
<i>AtSWEET2</i>	AT3G14770	<i>OsSWEET1b</i>	Os05g35140
<i>AtSWEET3</i>	AT5G53190	<i>OsSWEET2a</i>	Os01g36070
<i>AtSWEET4</i>	AT3G28007	<i>OsSWEET2b</i>	Os01g50460
<i>AtSWEET5</i>	AT5G62850	<i>OsSWEET3a</i>	Os05g12320
<i>AtSWEET6</i>	AT1G66770	<i>OsSWEET3b</i>	Os01g12130
<i>AtSWEET7</i>	AT4G10850	<i>OsSWEET4</i>	Os02g19820
<i>AtSWEET8</i>	AT5G40260	<i>OsSWEET5</i>	Os05g51090
<i>AtSWEET9</i>	AT2G39060	<i>OsSWEET6a</i>	Os01g42110
<i>AtSWEET10</i>	AT5G50790	<i>OsSWEET6b</i>	Os01g42090
<i>AtSWEET11</i>	AT3G48740	<i>OsSWEET7b</i>	Os09g08440
<i>AtSWEET12</i>	AT5G23660	<i>OsSWEET7c</i>	Os12g07860
<i>AtSWEET13</i>	AT5G50800	<i>OsSWEET11</i>	Xa13/Os8N3
<i>AtSWEET14</i>	AT4G25010	<i>OsSWEET12</i>	Os03g22590
<i>AtSWEET15</i>	AT5G13170	<i>OsSWEET13</i>	Os12g29220/Xa25
<i>AtSWEET16</i>	AT3G16690	<i>OsSWEET14</i>	Os11g31190/Os11N3
<i>AtSWEET17</i>	AT4G15920	<i>OsSWEET15</i>	Os02g30910
		<i>OsSWEET16</i>	Os03g22200

Table 2 Suppl. Relative expression of 16 *PeSWEET* genes in four tissues of *Phalaenopsis equestris*.

Clade	Gene	Flower	Leaf	Stem	Root
I	<i>PeSWEET4</i>	240.54	64.86	138.34	47.79
	<i>PeSWEET5a</i>	6.69	7.21	3.87	2.07
	<i>PeSWEET5b</i>	5.86	0.80	1.30	0.00
	<i>PeSWEET6</i>	19.54	4.13	13.66	0.78
	<i>PeSWEET7a</i>	0.06	0.00	0.00	0.00
	<i>PeSWEET7b</i>	0.00	0.00	0.00	0.00
	<i>PeSWEET7c</i>	0.06	0.00	0.31	0.00
	<i>PeSWEET7d</i>	0.00	0.00	0.00	0.00
III	<i>PeSWEET9</i>	0.06	0.00	0.19	0.00
	<i>PeSWEET10</i>	11.73	0.00	0.16	0.00
	<i>PeSWEET11</i>	51.65	145.03	32.97	29.03
	<i>PeSWEET12</i>	0.09	0.00	0.04	0.11
	<i>PeSWEET13</i>	281.45	97.85	110.37	19.44
	<i>PeSWEET14</i>	0.00	0.00	0.00	0.00
	<i>PeSWEET15</i>	14.41	1.45	0.08	0.00
IV	<i>PeSWEET16</i>	2.02	0.64	0.43	29.77

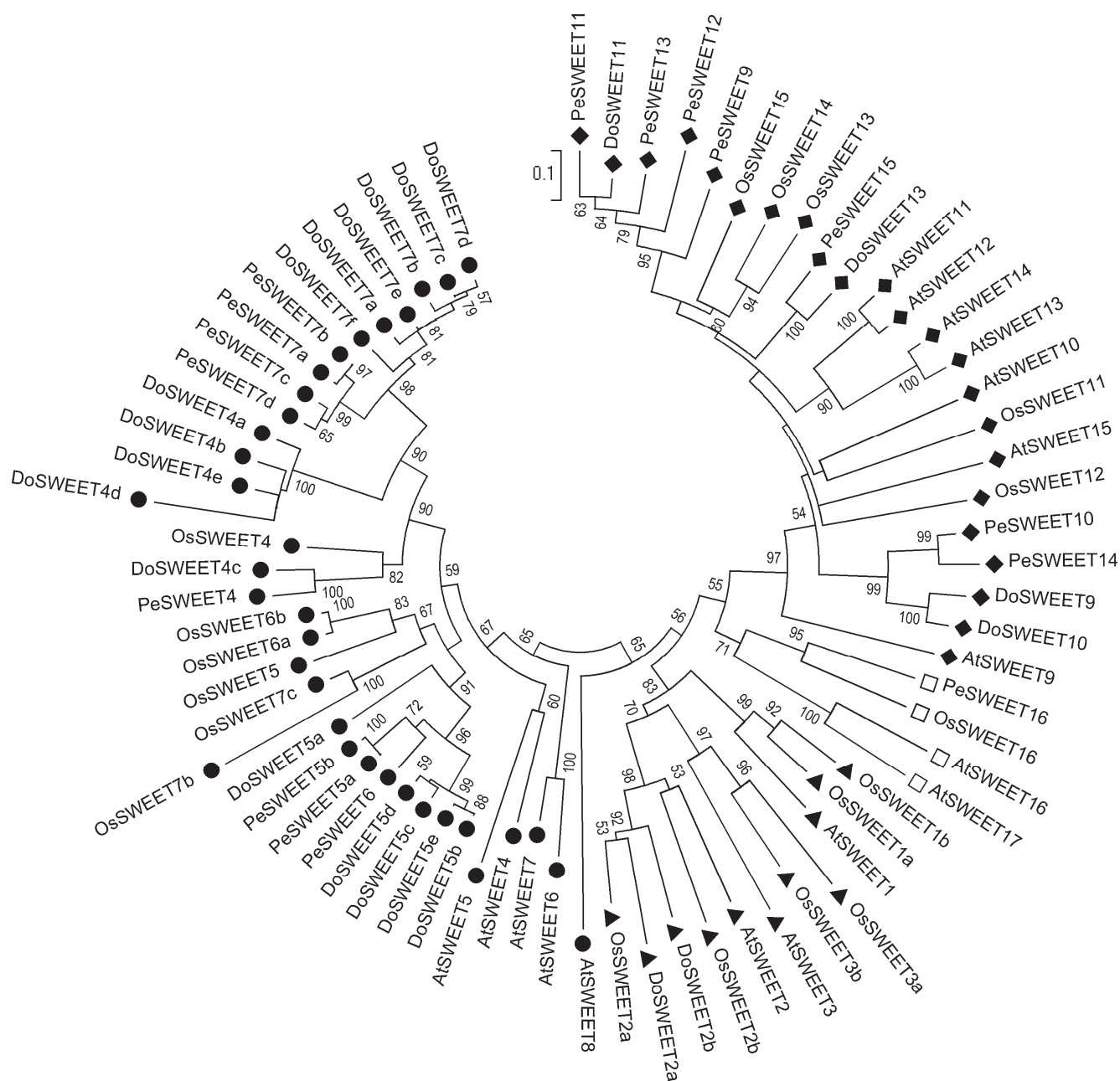
Table 3 Suppl. The primers for real-time qPCR used in this study. F - forward, R - reverse, Tm - melting temperature, E - amplification efficiency of primer pairs, R - correlation coefficient.

Primer	Sequence	Tm [°C]	E [%]	R ²
PeSWEET5-F	5'-TTCCTCTACGCCCCTAAAAACC-3'	79.6	96.05	0.990
PeSWEET5-R	5'-GACTATGACCCACCGTGAGCACAAAC-3'			
PeSWEET7b-F	5'-GAGCTTTGTTATGTCATCCTCTACC-3'	74.4	97.45	0.991
PeSWEET7b-R	5'-TCTGCATCATATCAAATAAGATGAC-3'			
PeSWEET11-F	5'-TACAAAGACACCAAAGTGCCCCAA-3'	79.4	98.34	0.997
PeSWEET11-R	5'-GCCACCATCAACCACCTTCATAAC-3'			
PeSWEET12-F	5'-CTCTGTCACCGTATTTGCTGCTC-3'	77.5	102.5	0.992
PeSWEET12-R	5'-ATTTTCCTTCCACTTCCAACCTCT-3'			
PeSWEET13-F	5'-GCTTTCTCCGTCAGCGTTTTTGC-3'	82.3	95.5	0.991
PeSWEET13-R	5'-ATGTTCTGGCAGCTTGTTCCCC-3'			
PeSWEET15-F	5'-TAATCTTATTATTGGACGGGGGA-3'	81.0	103	0.998
PeSWEET15-R	5'-CAGGTAAATGGCATGAATTCCACG-3'			
PeSWEET16-F	5'-TGCCATTGGATTTGTTCTGGGTTTC-3'	79.4	99.1	0.993
PeSWEET16-R	5'-TCTTCTTCTGCTGCTGCTTTTTCT-3'			
PeActin4-F	5'-GTATTCCTAGCATTGTTGGT-3'	83.2	100	0.997
PeActin4-R	5'-CAGAGTGAGAATACCTCGTTTG-3'			

Table 4 Suppl. *DoSWEET* and *PeSWEET* genes identified in this study and their predicted protein structural characteristics. The number of transmembrane domains (TDM) was predicted by *TMHMM Server v2.0* (<http://www.cbs.dtu.dk/services/TMHMM/>). aa - amino acids, * - the sequence was non-full length, - the intron was not analyzed.

Gene name	Gene ID	Intron	aa	TMD
<i>DoSWEET2a</i>	Dendrobium_GLEAN_10059880	5	258	7
<i>DoSWEET2b</i>	Dendrobium_GLEAN_10079392	5	237	7
<i>DoSWEET4a</i>	Dendrobium_GLEAN_10017333	3	240	7
<i>DoSWEET4b</i>	Dendrobium_GLEAN_10039063	3	237	7
<i>DoSWEET4c</i>	Dendrobium_GLEAN_10083274	5	263	7
<i>DoSWEET4d</i>	Dendrobium_GLEAN_10088029	2	218	7
<i>DoSWEET4e</i>	Dendrobium_GLEAN_10093399	5	527	7
<i>DoSWEET5a</i>	Dendrobium_GLEAN_10017234	4	229	7
<i>DoSWEET5b*</i>	Dendrobium_GLEAN_10039399	--	199	5
<i>DoSWEET5c</i>	Dendrobium_GLEAN_10108766	6	244	7
<i>DoSWEET5d</i>	Dendrobium_GLEAN_10120618	5	236	7
<i>DoSWEET5e</i>	Dendrobium_GLEAN_10120619	4	243	7
<i>DoSWEET7a</i>	Dendrobium_GLEAN_10013906	3	259	7
<i>DoSWEET7b</i>	Dendrobium_GLEAN_10047874	4	295	7
<i>DoSWEET7c</i>	Dendrobium_GLEAN_10049867	3	259	7
<i>DoSWEET7d</i>	Dendrobium_GLEAN_10058387	3	259	7
<i>DoSWEET7e</i>	Dendrobium_GLEAN_10058388	3	259	7
<i>DoSWEET7f</i>	Dendrobium_GLEAN_10058390	5	255	7
<i>DoSWEET9</i>	Dendrobium_GLEAN_10041475	5	240	7
<i>DoSWEET10</i>	Dendrobium_GLEAN_10058756	5	252	7
<i>DoSWEET11</i>	Dendrobium_GLEAN_10016975	6	366	7
<i>DoSWEET13</i>	Dendrobium_GLEAN_10125587	5	261	7
<i>PeSWEET4</i>	PEQU_36366	4	248	7
<i>PeSWEET5a</i>	PEQU_21727	4	236	7
<i>PeSWEET5b</i>	PEQU_36396	4	236	7
<i>PeSWEET6</i>	PEQU_02746	6	235	7
<i>PeSWEET7a</i>	PEQU_22452	3	258	7
<i>PeSWEET7b</i>	PEQU_26391	3	267	7
<i>PeSWEET7c</i>	PEQU_34901	3	258	7
<i>PeSWEET7d</i>	PEQU_34903	3	258	7
<i>PeSWEET9</i>	PEQU_33680	5	259	7
<i>PeSWEET10</i>	PEQU_14684	5	252	7
<i>PeSWEET11</i>	PEQU_03343	5	261	7
<i>PeSWEET12</i>	PEQU_08115	5	262	7
<i>PeSWEET13</i>	PEQU_38598	5	265	7
<i>PeSWEET14</i>	PEQU_14645	5	257	7
<i>PeSWEET15</i>	PEQU_12442	5	261	7
<i>PeSWEET16</i>	PEQU_05481	5	298	7

A



B

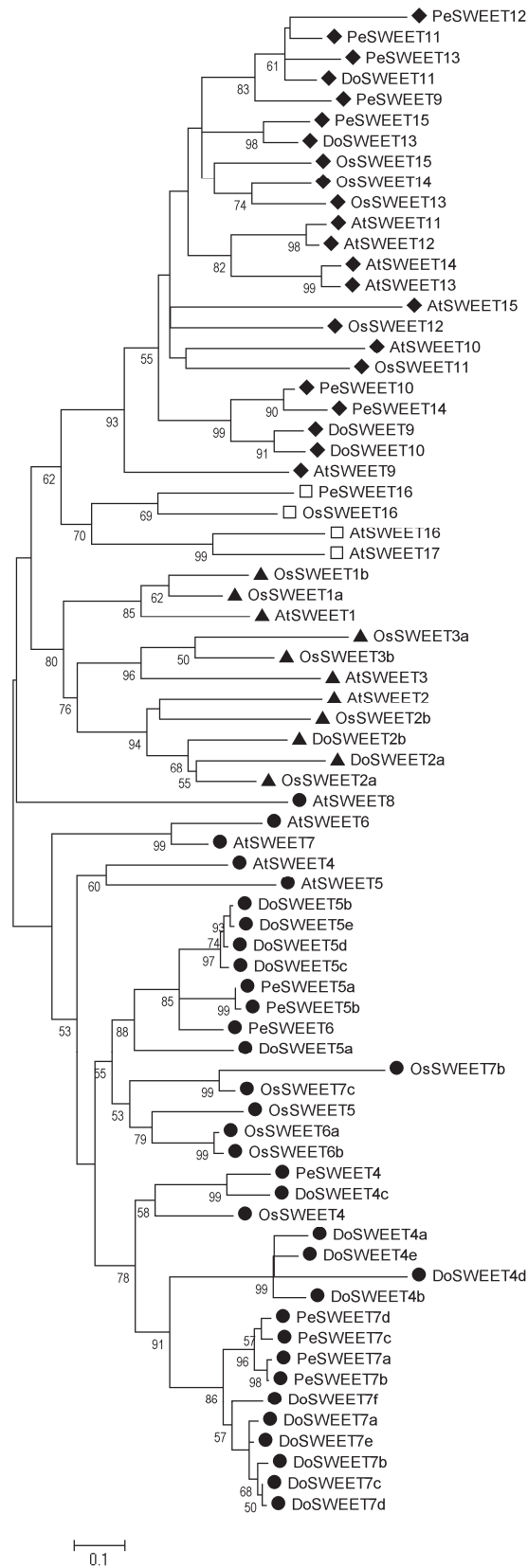


Fig. 1 Suppl. Unrooted phylogenetic tree of predicted SWEET proteins from *Dendrobium officinale*, *Phalaenopsis equestris*, *Arabidopsis thaliana*, and *Oryza sativa* by using Minimum Evolution (A) and Maximum Likelihood (B) methods with poisson model and complete deletion missing data treatment. The numbers at the nodes represent bootstrap percentage values based on 1 000 replications. The scale bar represents 0.1 substitutions per amino acid position. The shapes represents different classes. AtSWEET and OsSWEET protein sequences were used as references to categorize the DoSWEETs and PeSWEET.

