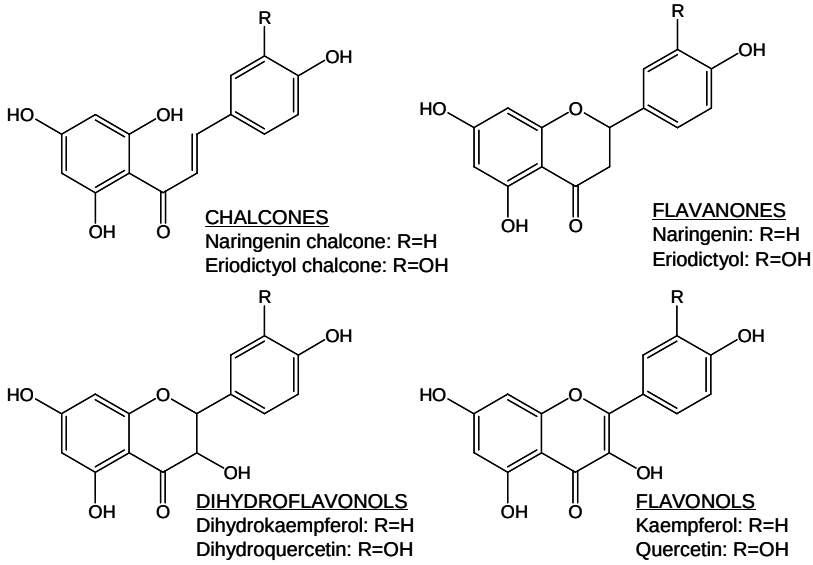
A



SUBSTRATES	ENZYME ACTIVITY
Naringenin chalcone	N.D.
Eriodictyol chalcone	N.D.
Naringenin	38.1 ± 0.6
Eriodictyol	50.7 ± 0.3
Dihydrokaempferol	N.D.
Dihydroquercetin	N.D.
Kaempferol	N.D.
Quercetin	N.D.

B

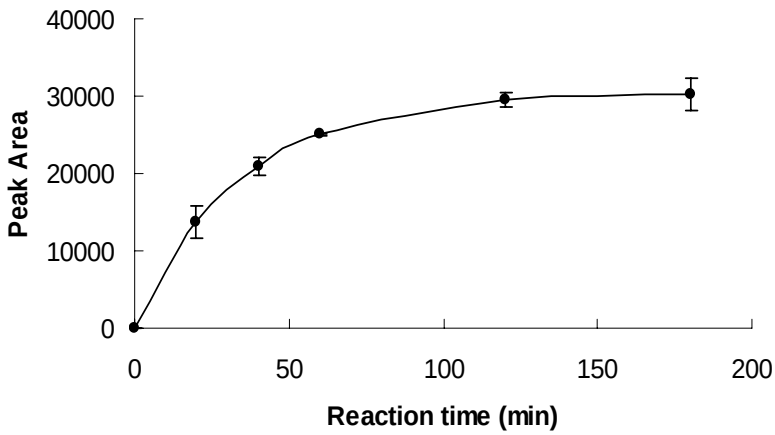


Fig. S1. A. Enzyme activities of CYP93G2-expressing yeast microsomes toward different flavonoid substrates. Data are mean ± SD of triplicate measurements and expressed in nmol product min^{-1} mg $protein^{-1}$. N.D. = not detected. B. Production of 2-hydroxyeriodictyol from eriodictyol in reactions catalyzed by CYP93G2-expressing yeast microsomes.

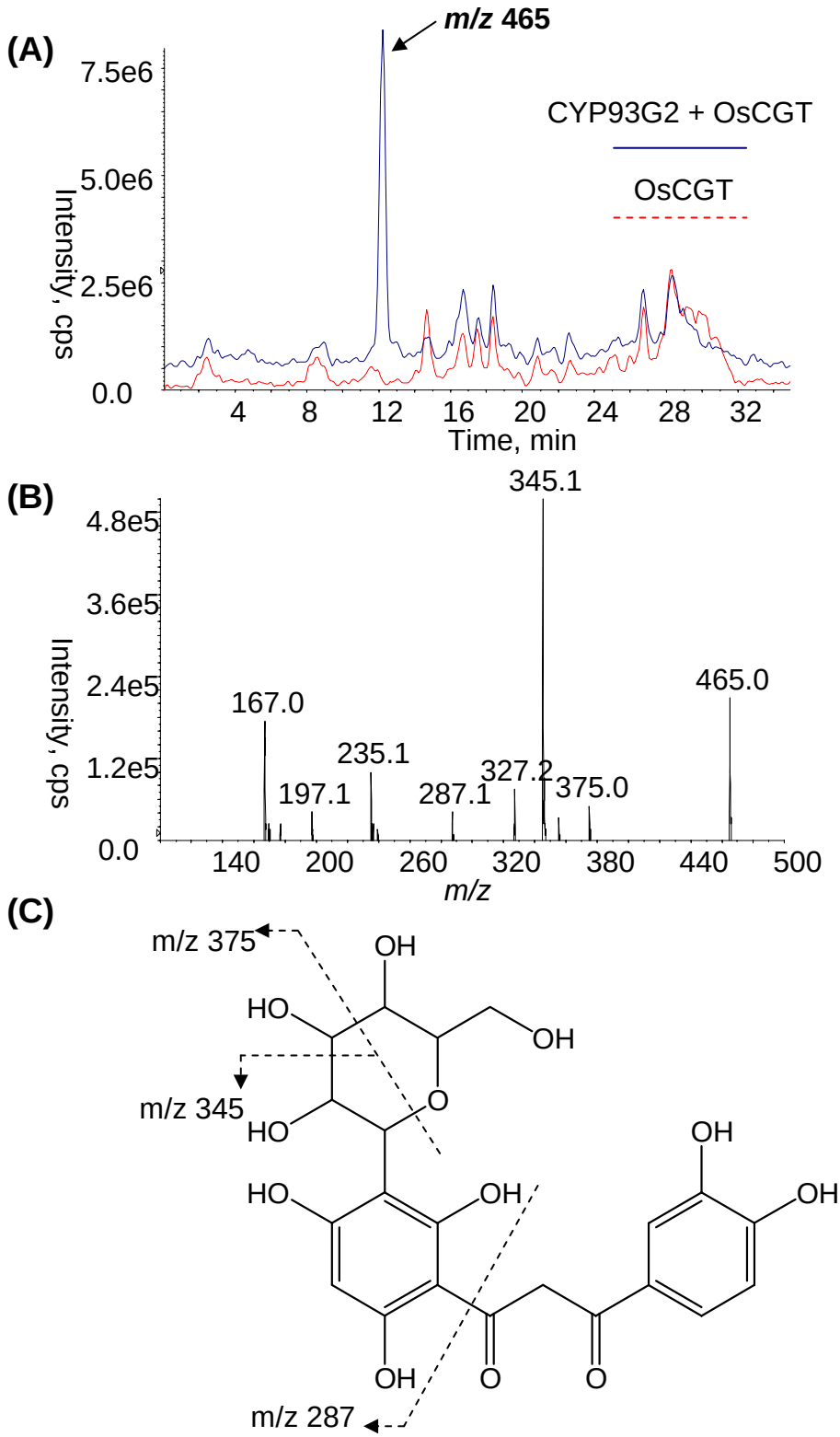


Fig S2. Accumulation of *C*-glucosyl-2-hydroxyneriodictyol in transgenic Arabidopsis co-expressing CYP93G2 and OsCGT. (A) Detection of a distinct peak producing a $[M-H]^-$ ion at m/z 465 in the double transformant sample. (B) MS/MS spectrum of the m/z 465 ion revealed the fragmentation pattern consistent with that reported for *C*-glucosyl-2-hydroxyflavanone in the open chain form as shown in (C).

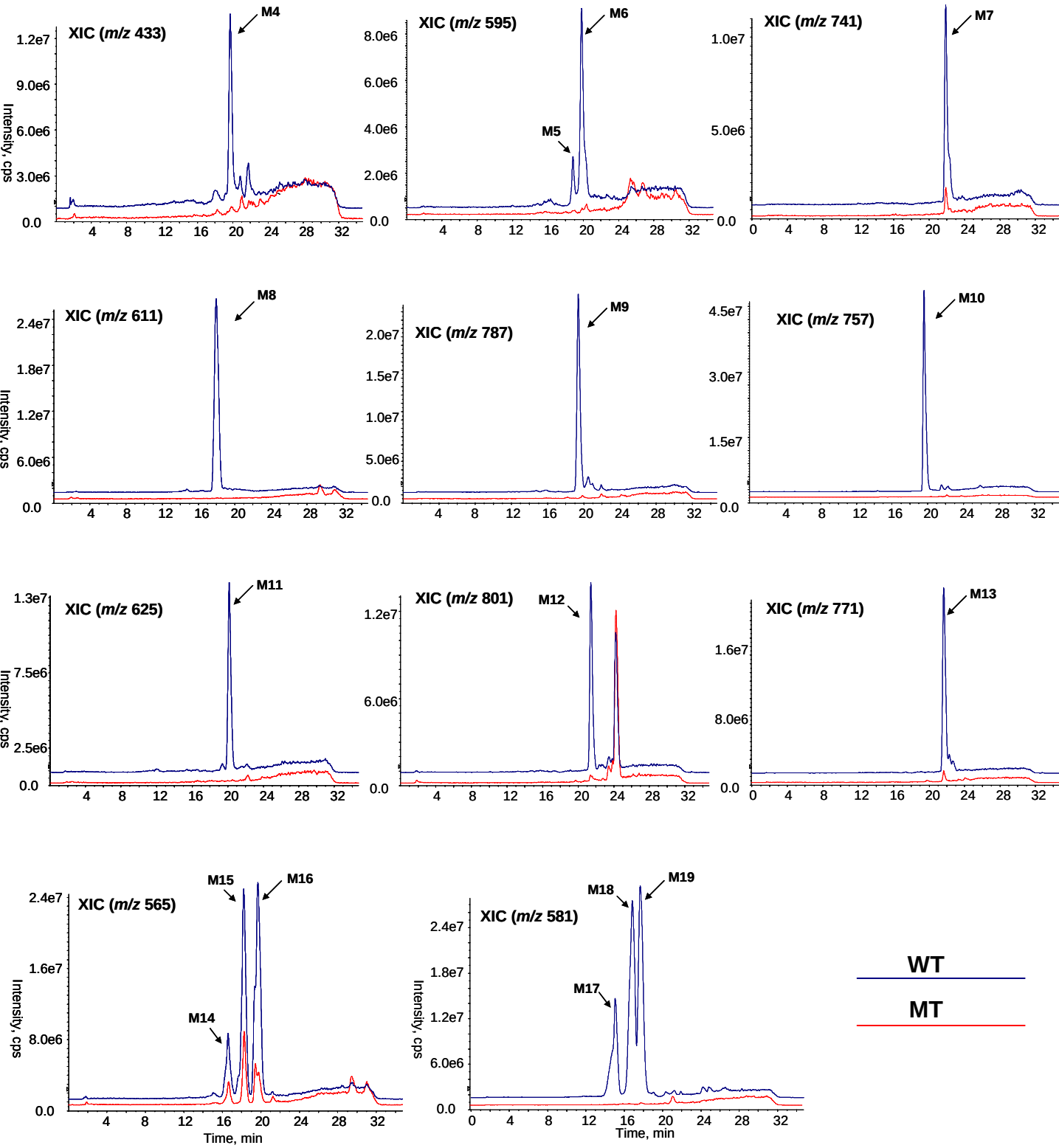


Fig. S3. Representative extracted ion chromatograms (XICs) for the *C*-hexosyl-flavone derivatives (M4 – M19, Table 1) in the rice wild-type (WT) and the CYP93G2 mutant (MT) non-hydrolyzed methanol samples.

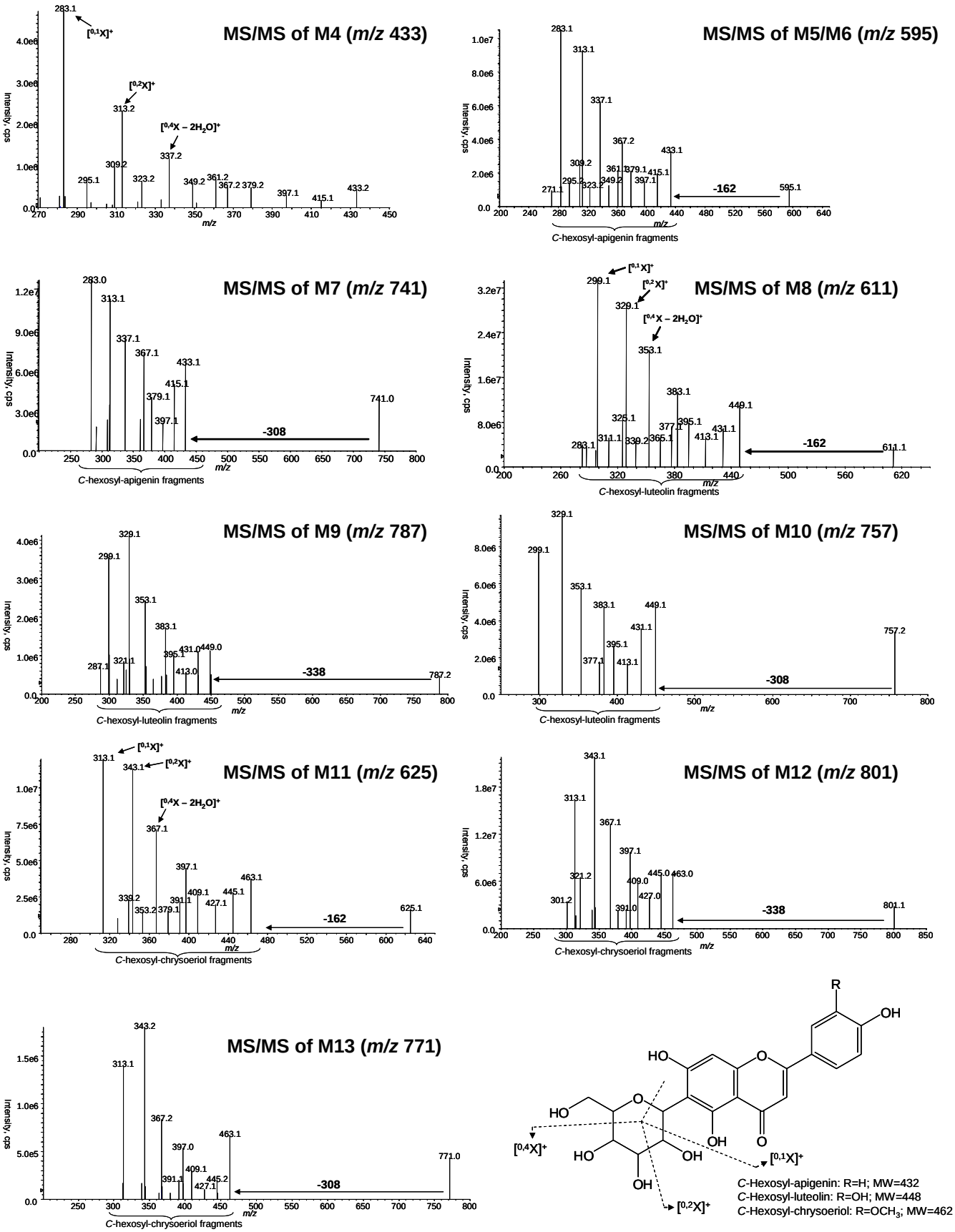


Fig. S4. MS/MS spectra for M4-M13 (*C*-hexosyl-flavone *O*-glycosylated derivatives). Fragmentation pattern for selected ions observed in the spectra is shown based on the structure of a 6*C*-hexosyl-flavone.

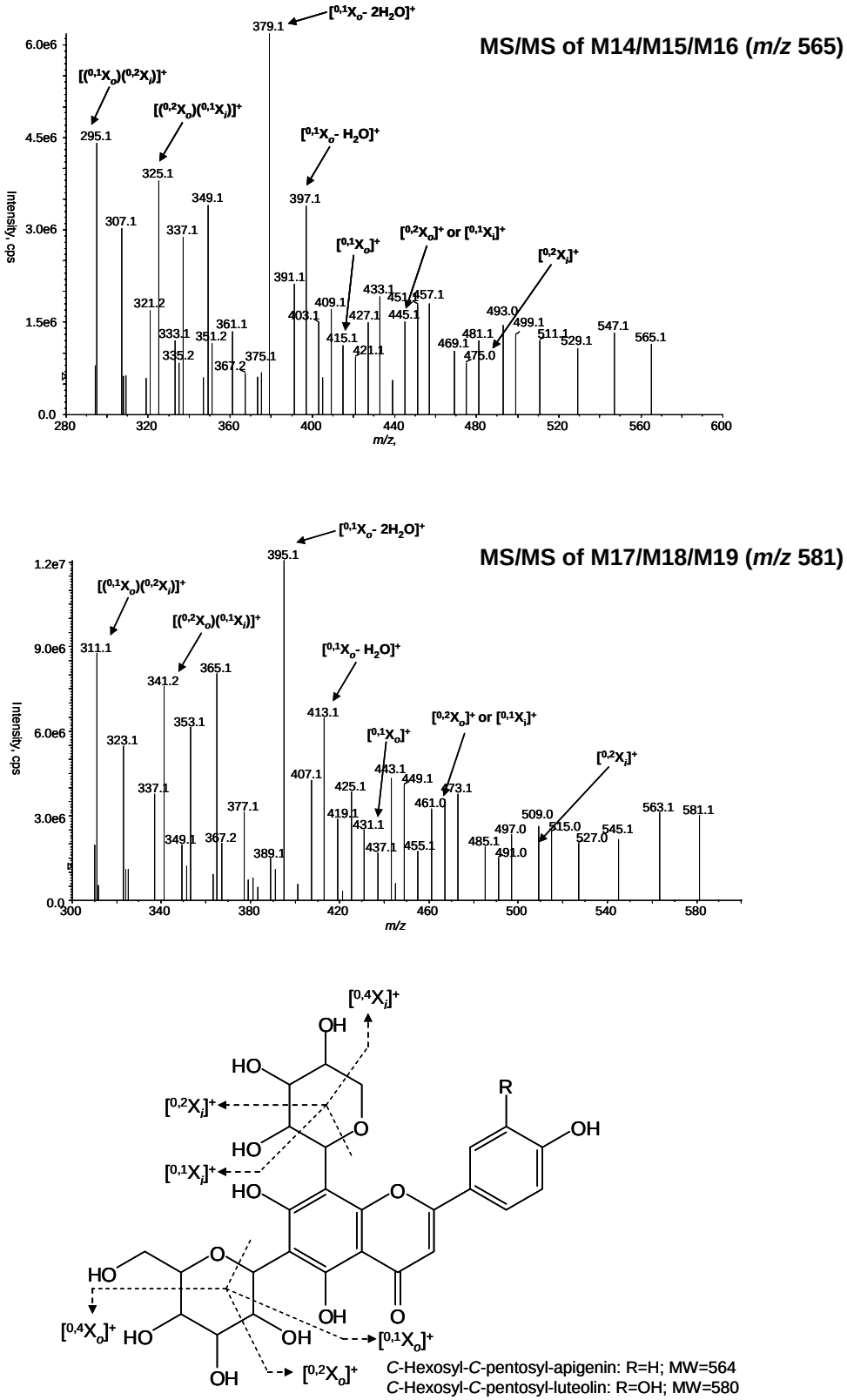


Fig. S5. MS/MS spectra and fragmentation patterns for M14 – M19 (*C*-hexosyl-*C*-pentosyl flavones). Fragmentation pattern for selected ions observed in the spectra is shown based on the structure of a 6*C*-heoxyl-8*C*-pentosyl flavone.

Table S1. List of 2-hydroxyflavanone *O*-glycosides identified in Arabidopsis overexpressing CYP93G2. Metabolites were identified in non-acid hydrolyzed extracts by LC-MS. The identities of the [2-hydroxyflavanone+H]$^+$ ions (bold) had been confirmed by their MS^3 spectra

Precursor ion $[M+H]^+$	Retention time (min)	MS/MS ions	Compound assignment
613	12.8	451, **289**	2-hydroxy-naringenin di-*O*,*O*-hexosides
451	17.1,18.5	**289**	2-hydroxy-naringenin *O*-hexosides
629	12.9	467, **305**	2-hydroxy-eriodictyol di-*O*,*O*-hexosides
467	16.1, 16.8	**305**	2-hydroxy-eriodictyol *O*-hexosides

Table S2. List of primers used in this study

Gene		Forward Primer		Reverse Primer	Purpose
CYP93G2	CL543	5’-ACTATGGAGGAAGGCGTCGTCGGTG	CL544	5’-GGAGTAGAAGGAAGGGAGCGGTTGG	Full-length cDNA cloning for yeast expression
	CL993	5’-GCGTCTAGAATGGAGGAAGGCGTCGT	CL994	5’-CGCGAGCTCTCAGGAGTAGAAGGAAGG	Full-length cDNA cloning for Arabidopsis over-expression
	CL1216	5’-GCTGGAGACCATCATCGAG	CL1256	5’-TGAAGAAGACCTGGGTGTCG	Genomic PCR and RT-PCR
OsCGT	CL1316	5’-GATGGATCCATGCCGAGCTCTG	CL1317	5’-ACCCTCGAGTCAATTAGTGCG	Full-length cDNA cloning for Arabidopsis over-expression
	CL1329	5’-CTCTCCCTCTGCGCCTACTT	CL1330	5’-GATCTTTTGCCTGGTTGCTC	Genomic PCR and RT-PCR