

Supplemental data: overview tables

Table Is. Expression characteristics of the *PAL* gene family in *Arabidopsis*.

Data from *Arabidopsis* literature, ESTs, and our semi-quantitative RT-PCR are given in the table as +/- for low, + for moderate, ++ for high, and – for decreasing expression. Because of different PCR dynamics of fragments of different size and separate RNA gel blots, data can be compared only among the different tissues, but not between genes or experiments. In case of chimeric promoter-GUS constructs, only those of *Arabidopsis* promoters analyzed in *Arabidopsis* were included. Data from GUS and immunohistochemistry were included whenever available. Shaded fields without a number indicate that the tissue/condition was studied, but no expression detected. ESTs are given in absolute (EST) as well as in relative (EST rel) numbers to account for the different sizes of EST classes and to estimate overrepresentation of ESTs in a particular condition. To this end, the number of ESTs for a particular gene in a given class was divided by the total number of ESTs in this class and multiplied by 100,000 to yield a comparable relative number in ESTs/100,000 ESTs (rounded to the nearest whole number). See Materials and Methods for the full description of classification and total numbers in the different classes. Shaded fields without a number indicate that no ESTs were found in the tissue or condition. Abbreviations: ER, endoplasmic reticulum; ER-anchored, localization in the ER membrane through the membrane anchor of P450 enzymes; mRNA, RNA gel blots; A, A box; AC, AC-unified element; AT, AT-rich element; E, E box; G+H, G box in conjunction with H box; GCC, GCC box; H, H box; S, S box; SARE, salicylic acid-responsive element. When an element occurs more than once in a particular promoter, the number is given within parentheses after the respective element. Promoter elements searched for, but not found in any of the 34 genes involved in monolignol biosynthesis are: As-1 box in conjunction with an OBP-1 binding site, the jasmonate- and ethylene-responsive element (JERE), the FP56, and the hypersensitive-response element (HSRE). See Materials and Methods for the respective random occurrences of the elements in the *Arabidopsis* genome.

| Gene | other names | AGI number | signals for localization | expression | expression | | | | | | | | | | | | | | regulatory elements | | | | | | | | | | | | | | | | | | | | | |
|--------------------------|-------------------------|------------|--------------------------|-------------------|------------|----------|--------------------|-------------|--------------------|-------|--------|--------|----------------|--------------------|-----|-----|-----|------|---------------------|-------------|-------|---------|----------------|--------------------|------------------|-----------------|---------|--|--|--|--|--|--|--|--|--------|-----|-----|--|--|
| | | | | | method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | siliques, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns | | | | | | | | | | | | | |
| <i>Arath:PAL1</i> | <i>PAL1^a</i> | At2g37040 | | RT-PCR | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | AC | | | | |
| | | | | EST (41)* | 2 | | 1 | 1 | 13 | | | | | | | | | | | | | | | | | | | | | | | | | | | S | | | | |
| | | | | EST rel (25.5)* | 62 | | 3 | 6 | 64 | | | | | | | | | | | | | | | | | | | | | | | | | | | H | | | | |
| | | | | mRNA ^a | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^c | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^d | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^e | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^g | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^h | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| mRNA ⁱ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| mRNA ^j | + | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| AIPAL1::GUS ^a | + _{a2} | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| AIPAL1::GUS ^d | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| AIPAL1::GUS ^f | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath:PAL2</i> | <i>PAL2^e</i> | At3g53260 | | RT-PCR | ++ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | AC (2) | | | | |
| | | | | EST (50) | | | 2 | 2 | 17 | | | | | | | | | | | | | | | | | | | | | | | | | | | | S | | | |
| | | | | EST rel (31.1) | | | 6 | 11 | 84 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^b | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^c | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^g | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^h | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| mRNA ⁱ | + | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RT-PCR ^k | + _{k1} | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath:PAL3</i> | <i>PAL3^e</i> | At5g04230 | | RT-PCR | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | E | | | | |
| | | | | EST (1) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | GCC | | |
| | | | | EST rel (0.6) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^a | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^g | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | | mRNA ^h | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| mRNA ⁱ | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| RT-PCR ^e | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath:PAL4</i> | | At3g10340 | | RTPCR | + | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | A | | | | |
| | | | | EST (28) | | | 2 | 1 | 5 | | | | | | | | | | | | | | | | | | | | | | | | | | | | G+H | | | |
| | | | | EST rel (17.4) | | | 6 | 6 | 25 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

- a* Ohl *et al.*, 1990
a1 induction by HgCl₂
a2 in all tissues except the root tip and the shoot apical meristem
a3 except the root tip, strong in vascular tissue
a4 in vascular tissue
a5 in sepals, anthers and carpels, not in petals, very strong in pollen
a6 GUS transcript
b Wanner *et al.*, 1993
b1 *Pseudomonas* infection
c Deikman and Hammer, 1995
c1 cytokinin induction
d Leyva *et al.*, 1995
d1 low temperature
d2 very strong GUS activity in protoxylem cells
d3 GUS transcript, upon *Pseudomonas* infection
d4 at low temperatures, GUS activity in the cortical cells (photosynthetically active) of the inflorescence stem
e Wanner *et al.*, 1995
f Mauch-Mani and Slusarenko, 1996
f1 in vascular tissue
f2 *Peronospora* infection
g Lee *et al.*, 1997
h Mizutani *et al.*, 1997
i Ehling *et al.*, 1999
i1 *Peronospora* infection
j Ruegger *et al.*, 1999
k Jin *et al.*, 2000
k1 in seedling leaves
*** 1 EST is unclassified

Table IIs. Expression characteristics of the *C4H* gene in Arabidopsis.

See Table 1 for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | regulatory elements | | | | | | | | | | | | | | | | | |
|------------------|-------------------------------------|-------------|--------------------------|--|---------------------|--------|---------------|--------------------|-----|-----|-----|------|-------|-------------|-------|---------|----------------|--------------------|------------------|-----------------|---------|---|
| expression | | | | | | | | | | | | | | | | | | | | | | |
| method | | | | | | | | | | | | | | | | | | | | | | |
| seedling | elicited seedling | whole plant | aboveground organs | roots | leaves | flower | silique, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns | |
| Class I | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath:C4H</i> | CYP73A5 <i>REF3</i> ⁱ | At2g30490 | ER-anchored | RT-PCR EST (29) EST rel (18.0) mRNA ^a mRNA ^b mRNA ^c mRNA ^d mRNA ^e mRNA ^f mRNA ^g RT-PCR ^g <i>AIC4H::GUS</i> ^a <i>AIC4H::GUS</i> ^h | + | | | + | + | + | + | ++ | ++ | | | | | | | | | H |
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- ^a Bell-Lelong *et al.*, 1997
^{a1} GUS in primary leaves, cotyledons, strongest in root
^{a2} highest expression in roots
^{a3} restricted to veins in mature leaves
^{a4} weak throughout the flower, including vasculature of sepals, with stronger staining at the stigma
^{a5} GUS stronger in older siliques than in younger ones
^{a6} restricted to xylem
^b Lee *et al.*, 1997
^c Mizutani *et al.*, 1997
^d Meyer *et al.*, 1998
^e Ehling *et al.*, 1999
^{e1} *Peronospora* infection
^f Ruegger *et al.*, 1999
^g Jin *et al.*, 2000
^{g1} in seedling leaves
^h Nair *et al.*, 2002
^{h1} expression highest in roots, all cell types
^{h2} in the vascular tissue of stem, petiole, leaf, and silique wall
^{h3} overall staining in the flower, unlike *C3H::GUS*
^{h4} strong in seed, unlike *C3H::GUS*
ⁱ C. Chapple, personal communication

Table III. Expression characteristics of the 4CL gene family in Arabidopsis.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | regulatory elements | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----------------------|-------------------|------------|--------------------------|--|---------------------|----------|--------------------|-------------|--------------------|-------|--------|--------|---------------|--------------------|-----|-----|-----|------|-------|-------------|-------|---------|----------------|--------------------|------------------|-----------------|---------|---|---|---|---|----|---|--------|-----|--|--|--|
| | | | | | method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | silique, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns | | | | | | | | | | | |
| Class I | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL1 | 4CL1 ^a | At1g51680 | | RT-PCR EST (8) EST rel (5.0) mRNA ^a mRNA ^b mRNA ^c mRNA ^d mRNA ^e RT-PCR ^f | | + | | | | + | + | +/- | + | | + | + | + | ++ | ++ | ++ | | | | + | | | + | 4 | 9 | | | AC | | | | | | |
| Arath;4CL2 | 4CL2 ^d | At3g21240 | | RT-PCR EST (13) EST rel (8.1) mRNA ^d | | + | | | | | | + | + | + | + | +/- | + | + | ++ | ++ | ++ | | | | + | | | + | 2 | 4 | | 2 | 4 | AC (2) | AC* | | | |
| Arath;4CL4 | | At3g21230 | | RT-PCR EST (2) EST rel (1.2) | | | | | | | | | | | | | | | | | + | + | | | | | | | | | 2 | 4 | | AT | AC* | | | |
| Class II | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL3 | 4CL3 ^d | At1g65060 | | RT-PCR EST (8) EST rel (5.0) RT-PCR ^d RT-PCR ^f | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | H | | | |
| Class 4CL-like | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 1 | | At1g20510 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 2 | | At1g20500 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 3 | | At1g20490 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 4 | | At1g20480 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 5 | | At1g62940 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 6 | | At4g19010 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 7 | | At4g05160 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 8 | | At5g63380 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Arath;4CL-like 9 | | At5g38120 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

^a Lee *et al.*, 1995
^{a1} *Pseudomonas* infection
^b Lee *et al.*, 1997
^c Mizutani *et al.*, 1997
^d Ehling *et al.*, 1999
^{d1} *Peronospora* infection
^{d2} UV irradiation
^{d3} 4CL3 expression not affected by *Peronospora* or wounding
^e Ruegger *et al.*, 1999
^f Jin *et al.*, 2000
^{f1} in seedling leaves
^{f2} 4CL1 transcript unaffected by sucrose
^{*} in the first intron

Table Vs. Expression characteristics of the C3H gene family in Arabidopsis.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | | | | | | | | | | | | | | | | | | regulatory elements | | | |
|----------------------|-------------------------------------|------------|--------------------------|---|----------|--------------------|-------------|--------------------|-------|--------|--------|---------------|--------------------|-----|-----|-----|------|-------|-------------|-------|---------|---------------------|----------------|--------------------|------------------|
| | | | | method | seedling | eriolated seedling | whole plant | aboveground organs | roots | leaves | flower | silique, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | | wounded leaves | pathogen infection | various stresses |
| Class I | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> ;C3H1 | CYP98A3 <i>REF8</i> ^b | At2g40890 | ER-anchored | RT-PCR EST (36) EST rel (22.4) mRNA ^a mRNA ^b mRNA ^c <i>AtC3H::GUS</i> ^c C3H ^a C3H ^c | + | | | | | | | | | | | | | | | | | | | | AC |
| | | | | | | 5 | 3 | 5 | | | 7 | | | | | | | | | | | 2 | 14 | | |
| | | | | | | 14 | 17 | 25 | | | 28 | | | | | | | | | | | 283 | 32 | | |
| | | | | | | | | + | +/- | +/- | + | ++ | | | | | | | | | | + | | | |
| | | | | | + | | | ++ | + | + | + | ++ | | | | | | | | | | | | | |
| | | | | | + | | | ++ | +c1 | +c2 | +c3 | + | + | | | | | | | | | + | | | |
| | | | | | | | | +a1 | | | | | + | + | | | | | | | | | | | |
| | | | | | | | | +c4 | | | | | | | | | | | | | | | | | |
| | | | | | | | | | | | | | | + | + | + | + | + | + | | | | | | |
| Class II | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> ;C3H2 * | CYP98A8 | At1g74540 | | RT-PCR EST (1) EST rel (0.6) | | | | | + | | + | | | | | | | | | | | | | | A |
| | | | | | | 1 | | | | | | | | | | | | | | | | | | | |
| | | | | | | 3 | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> ;C3H3 * | CYP98A9 | At1g74550 | | RT-PCR EST (0) EST rel (0) | + | | | | + | + | + | | | + | + | | | | | | | | | | |
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^a Schoch *et al.*, 2001
^{a1} immunolocalization using a polyclonal anti-CYP98A3 antibody; mainly in differentiating xylem, also in secondary phloem in the cortical zone of mature root
^{a2} immunolocalization using a polyclonal anti-CYP98A3 antibody; very strong in differentiating xylem
^b Franke *et al.*, 2002a
^c Nair *et al.*, 2002
^{c1} expression highest in roots, expressed in stele and endodermis; not expressed in root apical meristem, epidermis and cortex
^{c2} in the vascular tissue of stem, petiole, leaf, petal, sepal, anther, stigma
^{c3} in the vascular tissue of the silique wall, not in seed
^{c4} immunolocalization using a polyclonal anti-CYP98A3 antibody; in stele
^{c5} immunolocalization using a polyclonal anti-CYP98A3 antibody; in meta- and protoxylem cells in the young stem, strongest in lignified interfascicular fibers and xylem vessels of older stem
* *C3H2* and *C3H3* are single exon genes

Table VIa. Expression characteristics of the *CCoAOMT* gene family in *Arabidopsis*.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | | | | | | | | | | | | | | | regulatory elements | | | | | | | | |
|--------------------------------|-----------------------------|------------|--------------------------|--|-----------------------------|----------|--------------------|-------------|--------------------|---------------|----------------|--------|---------------|--------------------|---------|----------|-----|---------|---------------------|-------------|---------|---------|----------------|--------------------|------------------|-----------------|-------------|
| | | | | | method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | silique, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns |
| Class I | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> : <i>CCoAOMT1</i> | <i>CCoAOMT</i> ^c | At4g34050 | | RT-PCR EST(45) EST rel (28.0) mRNA ^c | ++ 1 31 +/- | | | | | ++ 4 11 | ++ 19 93 | + | ++ 1 | ++ 9 | ++ 1 | ++ 36 | + | ++ + | ++ + | ++ + | ++ + | ++ + | | | 1 42 | 9 21 | AC (2) H |
| Class II | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> : <i>CCoAOMT2</i> | | At1g24735 | | RT-PCR EST(0) EST rel (0) | +/- | | | | | +/- | + | + | + | + | + | + | +/- | +/- | + | + | + | | | | | H | |
| <i>Arath</i> : <i>CCoAOMT3</i> | | At3g61990 | ER | RT-PCR EST(6) EST rel (3.7) | + | | | | | + | ++ | | | | | | | | + | + | ++ | | | | | S | |
| <i>Arath</i> : <i>CCoAOMT4</i> | | At3g62000 | | RT-PCR EST(2) EST rel (1.2) | + | | | | | + | | | | | | | +/- | +/- | + | + | + | + | | | | | |
| <i>Arath</i> : <i>CCoAOMT5</i> | | At1g67990 | | RT-PCR EST(1) EST rel (0.6) | +/- | | | | | + | + | + | + | | | | + | + | + | + | + | + | | | | | |
| <i>Arath</i> : <i>CCoAOMT6</i> | <i>CCoAOMT</i> ^a | At1g67980 | | RT-PCR EST(2) EST rel (1.2) RT-PCR ^b | + ^{b1} | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> : <i>CCoAOMT7</i> | | At4g26220 | | RT-PCR EST(4) EST rel (2.5) | ++ | | | | | + | ++ | +/- | + | | | | + | + | + | ++ | ++ | ++ | | | | | 1 2 |

^a Zou and Taylor, 1994

^b Jin *et al.*, 2000

^{b1} in seedling leaves

^c Goujon *et al.*, 2003a

^{c1} highly expressed in the basal portion as compared to the apical portion of the inflorescence stem

Table VII. Expression characteristics of the CCR gene family in Arabidopsis.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | | | | | | | | | | | | | | | | regulatory elements | | | | | | | | |
|-------------------------|---|------------|--------------------------|------------|--------|----------|--------------------|-------------|--------------------|-------|--------|--------|---------------|--------------------|-----|-----|-----|------|-------|---------------------|-------|---------|----------------|--------------------|------------------|-----------------|---------|--|
| | | | | | method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | siliqua, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns | |
| Class I | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR1 | CCR1 ^{ab} IRX4 ^a | At1g15950 | | RT-PCR | ++ | | | | | | | | | | | | | | | | | | | | AC | | | |
| | | | EST (43) | | | 6 | 8 | 8 | | 2 | 8 | 1 | | | | | | | | | | | | | | | | |
| | | | EST rel (26.7) | | | 17 | 45 | 39 | | 29 | 72 | 32 | | | | | | | | | | | | | | | | |
| | | | mRNA ^b | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | mRNA ^c | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR2 | CCR2 ^{ab} | At1g80820 | | RT-PCR | + | | | | | | | | | | | | | | | | | | | | | | | |
| | | | EST (4) | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | EST rel (2.5) | | | | | | | | | | | | | | | | | | | | | | | | | |
| | | | mRNA ^b | | | | | | | | | | | | | | | | | | | | | | | | | |
| Class CCR-liks | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR-like1 | | At1g76470 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR-like2 | | At2g02400 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR-like3 | | At2g33590 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR-like4 | | At2g33600 | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath</i> :CCR-like5 | | At5g58490 | | | | | | | | | | | | | | | | | | | | | | | | | | |

^a Jones *et al.*, 2001^b Lauvergeat *et al.*, 2001^{b1} *Xanthomonas* infection^{b2} induced by *Xanthomonas* infection and salicylic acid^{b3} not induced by methyl jasmonate or ethylene^c Goujon *et al.*, 2003b^{c1} moderately expressed in the basal part of the inflorescence stem, highly expressed in the apical part of the inflorescence stem

Table VIII. Expression characteristics of the *F5H* gene family in *Arabidopsis*.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | silique, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | regulatory elements |
|-------------------|------------------------------------|------------|--------------------------|--|----------|--------------------|-------------|--------------------|-------|--------|--------|---------------|--------------------|-----|-----|-----|------|-------|-------------|-------|---------|----------------|--------------------|------------------|-----------------|---------------------|
| | | | | | | | | | | | | | | | | | | | | | | | | | | introns |
| <i>Arath:F5H1</i> | CYP84A1 <i>FAH</i> ^a | At4g36220 | ER-anchored | RT-PCR EST (2)* EST rel (1.2) mRNA ^b mRNA ^c mRNA ^e mRNA ^f RT-PCR ^d | ++ | | 1 3 | + | + | ++ | + | + | + | + | + | + | ++ | ++ | ++ | | | | | | H | |
| <i>Arath:F5H2</i> | CYP84A4 | At5g04330 | ER-anchored | RT-PCR EST (0) EST rel (0) | + | | | | +/– | | +/– | | | + | + | + | + | +/– | +/– | | | | | G+H | | |

^aChapple *et al.*, 1992^bMeyer *et al.*, 1998^cRuegger *et al.*, 1999^dJin *et al.*, 2000^{d1}

in seedling leaves

^eNair *et al.*, 2002^fGoujon *et al.*, 2003a^{ff}

highly expressed in the basal portion as compared to the apical portion of the inflorescence stem

*

1 EST is unclassified

Table IXs. Expression characteristics of the *COMT* gene in Arabidopsis.

See Table I for the full explanation of table and abbreviations.

| Gene | other names | AGI number | signals for localization | expression | method | seedling | etiolated seedling | whole plant | aboveground organs | roots | leaves | flower | siliques, seed | inflorescence stem | 1cm | 3cm | 5cm | 10cm | 15 cm | fully grown | light | sucrose | wounded leaves | pathogen infection | various stresses | upstream region | introns | regulatory elements | |
|--------------------------------|-------------------|------------|--------------------------|---|--------|----------|--------------------|-------------|--------------------|-------|---------------|---------------|----------------|--------------------|-----|-----|-----|------|-------|-------------|-------|---------|----------------|--------------------|------------------|-----------------|---------|---------------------|---|
| | | | | | | + | ++ | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | + | | + |
| <i>Arath;COMT</i> | OMT1 ^a | At5g54160 | myristoylation | RT-PCR EST (99) EST rel (61.6) mRNA ^a mRNA ^b mRNA ^d RT-PCR ^c <i>AtCOMT::GUS</i> ^d | | ++ | | | | + | ++ | + | + | | + | + | + | ++ | ++ | ++ | | | | 2 | 18 | | | SARE* | |
| | | | | | | + | | | | + | | + | | | | | | | | | | | | 85 | 41 | | | | |
| | | | | | | + | + | | | | | | | | | | | | | | | | | | | | | | |
| | | | | | | | ^{c1} | | | | ^{d3} | ^{d4} | ^{d5} | ^{d6} | | | | | | | | | | | | | | | |
| | | | | | | | ^{d2} | | | | | | | | | | | | | | | | | | | | | | |
| Class <i>COMT</i>-likes | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 1</i> | | At1g21100 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 2</i> | | At1g21110 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 3</i> | | At1g21120 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 4</i> | | At1g21130 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 5</i> | | At1g33030 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 6</i> | | At1g51990 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 7</i> | | At1g63140 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 8</i> | | At1g76790 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 9</i> | | At1g77520 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 10</i> | | At1g77530 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 11</i> | | At3g53140 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 12</i> | | At5g37170 | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| <i>Arath;COMT-like 13</i> | | At5g53810 | | | | | | | | | | | | | | | | | | | | | | | | | | | |

^a Zhang *et al.*, 1997^b Ruegger *et al.*, 1999^c Jin *et al.*, 2000^{c1} in seedling leaves^d Goujon *et al.*, 2003a^{d1} moderately expressed in the basal part of the inflorescence stem, highly expressed in the apical part of the inflorescence stem^{d2} constitutive in 3d-old-seedlings, very high in vascular tissues in 12d-old tissues^{d3} basal GUS activity in leaf blade of young leaves, in vascular tissues of mature leaves^{d4} only in the sepal veins^{d5} only in the lignified ends of siliques^{d6} very high in xylem, differentiating fibers and mature phloem

*

in the first intron

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