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published in
Plant Physiology
2001

DOI (link to publisher)
10.1104/pp.126.4.1519

document version
Publisher's PDF, also known as Version of record

Link to publication in VU Research Portal

citation for published version (APA)

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Enhanced Copper Tolerance in *Silene vulgaris* (Moench) Garcke Populations from Copper Mines Is Associated with Increased Transcript Levels of a 2b-Type Metallothionein Gene


Department of Ecology and Ecotoxicology of Plants, Faculty of Biology, Vrije Universiteit, De Boelelaan 1087, 1081 HV Amsterdam, The Netherlands (N.A.L.M.v.H., H.W.J.H., K.F.B., H.S., J.A.C.V., W.H.O.E.); and Department of Biochemistry, University of Kuopio, P.O. Box 1627, 70211 Kuopio, Finland (V.H.H., S.O.K., A.I.T.)

*Silene vulgaris* (Moench) Garcke has evolved populations with extremely high levels of copper tolerance. To evaluate the role of metallothioneins (MTs) in copper tolerance in *S. vulgaris*, we screened a cDNA library derived from a highly copper-tolerant population using Arabidopsis-based MT probes and identified an MT2b-like gene. When expressed in yeast, this gene, *SvMT2b*, restored cadmium and copper tolerance in different hypersensitive strains. Northern-blot analysis and quantitative reverse transcriptase-PCR showed that plants from the copper-tolerant *S. vulgaris* populations had significantly higher transcript levels of *SvMT2b* than plants from the copper-sensitive populations, both in roots and shoots and with and without copper exposure. Southern-blot analysis suggested that the higher expression of the latter allele was caused by gene amplification. Segregating families of crosses between copper-sensitive and copper-tolerant plants exhibited a 1 to 3 segregation for *SvMT2b* expression. Allele-specific PCR showed that low-expression F$_3$ plants were homozygous for the allele inherited from the copper-sensitive parent, whereas high-expression plants possessed at least one allele from the tolerant parent. *SvMT2b* expression did not cosegregate with copper tolerance in crosses between sensitive and tolerant plants. However, a significant cosegregation with copper tolerance did occur in families derived from crosses between moderately tolerant F$_3$ plants with different *SvMT2b* genotypes. Thus, overexpression of *SvMT2b* conferred copper tolerance although only within the genetic background of a copper tolerant plant.

The Bladder Campion, *Silene vulgaris* (Moench) Garcke, has evolved strongly heavy metal-tolerant populations at sites with high heavy metal concentrations in the soil (Ernst, 1974; Schat et al., 1996). The mechanisms underlying such high-level tolerance are largely metal specific (Schat and Vooijs, 1997). High-level copper tolerance in *S. vulgaris*, as suggested by the segregation patterns in crosses between plants from copper-sensitive and copper-tolerant populations, may be controlled by two primary tolerance genes (major genes) and some hypostatic “modifiers” (Schat and Ten Bookum, 1992b; Schat et al., 1993, 1996). The nature and physiological functions of these genes have not been identified yet.

Metallothioneins (MTs) might be involved in copper tolerance. MTs are low molecular weight, Cys-rich cytoplasmic metal-binding proteins that could protect cells against the toxic effects of copper by chelating this heavy metal. Genes encoding MTs occur in animals, higher plants, eukaryotic microorganisms, and in some prokaryotes. There are different MT families, subfamilies, subgroups, and isoforms. A review of MTs in plants and their characteristics is given by Rauser (1999). Several plant species contain large MT gene families, consisting of different MT gene types, and/or multiple MT genes of one type (Zhou and Goldsbrough, 1995; Hudspeth et al., 1996). The similarity between MT genes within one species is often very high. Moreover, three MT genes are situated within 20 kb of the same chromosome in cotton (Hudspeth et al., 1996). Likewise, two type 1 MT genes are found within 3 kb in Arabidopsis (Zhou and Goldsbrough, 1995). These findings strongly suggest that gene amplification is involved in the evolution of MT genes.

The functions of MTs in plants are still unclear (Rauser, 1999). However, Murphy and Taiz (1995) found that MT2 expression was the primary determinant of ecotypic differences in the copper tolerance of Arabidopsis seedlings. Moreover, heavy metal tolerance in plants can be improved by (over) expression of yeast MT genes (Hasegawa et al., 1997), and plant MT genes can restore metal tolerance in MT-deficient yeast (Zhou and Goldsbrough, 1994). For these rea-

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1 This work was supported by the European Community (Environment Research Program: Environment and Climate, contract no. ENV 4–CT95–0083 [Phytorehab]).

* Corresponding author; e-mail hschat@bio.vu.nl; fax 31–20–4447123.
sons, it is conceivable that MTs might play a role in copper tolerance in *S. vulgaris*.

This study was performed to isolate and characterize MT genes from *S. vulgaris*, and to investigate their role in copper tolerance in different populations of this species. The latter was done by heterologous expression in hypersensitive yeast, as well as by analyzing the co-segregation of MT expression and copper tolerance in segregating families of crosses between copper-sensitive and -tolerant plants.

**RESULTS**

**MT Sequences**

A cDNA library was prepared from leaves of untreated copper-tolerant plants (population Imsbach). Of the Arabidopsis-based MT probes tested (*MT1a*, *MT2a*, *MT2b*, *MT3*), only *MT2b* yielded hybridizing plaques. The corresponding *S. vulgaris* cDNA (*SvMT2b*; GenBank accession no. AF101825) showed a high amino acid sequence identity with Arabidopsis MT2b (Zhou and Goldsbrough, 1995; GenBank Accession no. U11256) and *Mesembryanthemum crystallinum* MT (GenBank accession no. AF000935), particularly in the Cys-rich N-terminal and C-terminal parts (Fig. 1). The *SvMT2b* gene sequences were also determined in two other populations of *S. vulgaris*. The *SvMT2b* cDNA sequence of plants from Amsterdam differed at 7-bp positions from the Imsbach cDNA. These resulted in three amino acid substitutions in the spacer region (Ser for Asn, Gly for Ala, and Met for Lys, at the positions 18, 32, and 46 of the predicted protein). The cDNA of plants from Marsberg differed at 5-bp positions from the Imsbach cDNA, resulting in one amino acid substitution (Met for Lys at position 46).

**Yeast Complementation**

A copper-sensitive yeast, DBY746, transformed with *SvMT2b*-pAJ401 was able to grow at 5 mM CuSO₄, whereas the untransformed DBY746 mutant grew up to 1 mM copper. Copper tolerance of the copper-sensitive yeast was thus approximately 5-fold increased. The MT-deficient copper-sensitive yeast *cup1* mutant DM771–6C transformed with *SvMT2b* grew at 1 mM CuSO₄, but the untransformed mutant did not grow at 0.5 mM copper.

A cadmium-sensitive yeast, JWY53 (vacuolar membrane ABC transporter mutant *ycf1*), transformed with *SvMT2b*-pAJ401 was able to grow at 0.1 mM CdSO₄, whereas the original yeast mutant with or without pAJ401 plasmid grew up to 0.01 mM CdSO₄ (Fig. 2).

**SvMT2b mRNA Expression Analysis in Parental Ecotypes**

Both northern-blot hybridization and quantitative RT-PCR showed much higher levels of *SvMT2b* mRNA in the roots (Fig. 3) and leaves (data not shown) of the plants from the copper-tolerant populations Imsbach and Marsberg than in those from three copper-sensitive populations Amsterdam (Fig. 3), Wijlre and Gaschurn (data not shown). *SvMT2b* expression in roots of copper-sensitive (Am, Amsterdam) and copper-tolerant plants (Im, Imsbach), unexposed (0) or exposed to 50 μM CuSO₄ for 24 and 48 h (respectively, 24 and 48). A, Ethidium bromide-stained agarose gel of the quantitative RT-PCR products. Also included is the internal control, *GAPDH*. B, Northern-blot analysis. Each lane was loaded with 8 μg of total RNA. Radioactively labeled *SvMT2b* was used as a probe.
expression was largely unaffected by copper treatment (Fig. 3) and the level of SvMT2b expression was higher in leaves than in roots (data not shown).

Southern-blot analysis showed considerable differences in band intensities between the populations (Fig. 4B), whereas DNA loading was similar for all the samples (Fig. 4A). Digestion of leaf DNA with MboI and hybridization with SvMT2b probe generated a faint band at 1.43 kb for Amsterdam and a very intense band at 1.37 kb for Imsbach and Marsberg. Two smaller faint bands were also detected for Imsbach DNA.

**SvMT2b mRNA Expression Analysis in Interecotypic Crosses**

Two pair crosses were made between plants from the highly copper-tolerant population Imsbach (EC_{100} > 400 μM) and the copper-sensitive population Amsterdam (EC_{100} < 12 μM). Thirty F1 plants were pair-crossed to produce F2 seed. These seeds were pooled and approximately 500 F2 seedlings were screened for copper tolerance (see “Materials and Methods”), using the lowest copper concentration that completely stopped root growth as a tolerance measure (Schat and Ten Bookum, 1992b). Eighteen seedlings with the sensitive Amsterdam phenotype (EC_{100} ≤ 12 μM) and 12 copper-tolerant seedlings (EC_{100} ≥ 100 μM) were selected and pair-crossed (sensitive × sensitive and tolerant × tolerant) to produce nine sensitive and nine tolerant F3 families. Twenty-four plants of each of these families were screened for tolerance. The copper-sensitive F3 families appeared to be devoid of any copper-tolerant individuals. The tolerant F3 families showed a degree of segregation (EC_{100} values between 50 and 400 μM CuSO4) but were devoid of any copper-sensitive individuals. The average tolerance levels in these families (EC_{100} between 100 and 200 μM) were consistently lower than that of the tolerant parent population Imsbach (EC_{100} approximately 500 μM).

The expression levels of the SvMT2b gene in copper-sensitive and copper-tolerant F3 plants were determined to investigate the role of this gene in copper tolerance in *Silene vulgaris*. It seemed that the copper-sensitive F3 plants (1–9) varied discretely in SvMT2b expression (Fig. 5A). The plants from the families 3, 4, and 8 had a low expression level comparable with that of Amsterdam plants. The copper tolerant F3 plants (10–18) showed the same variation in SvMT2b mRNA levels. The plants from the families 10 and 17 showed low expression.
There was a perfect correlation between high SvMt2b expression, as established with quantitative RT-PCR, and the presence of at least one Imsbach allele, as established by allele-specific PCR. Imsbach allele-specific primers did not produce clear bands for the plants of the families with low SvMt2b expression, i.e. 3, 4, 8, 10, and 17, showing that these were homozygous for the Amsterdam allele (Fig. 5B). Only plants from the tolerant families 12 and 16 were homozygous for the Imsbach allele (Fig. 5C).

Enhanced SvMt2b expression was more or less evenly distributed over the sensitive and the tolerant F3 selection lines, implying that this gene does not act as a primary determinant in copper tolerance. The possibility remains that it would act as a hypostatic enhancer of the level of tolerance in tolerant plants, however. This was investigated by genotyping less tolerant (EC100 < 100 μM CuSO4) and more tolerant (EC100 > 150 μM CuSO4) plants selected from tolerant F3 families that segregated for SvMt2b expression. The F3 families were produced by paircrossing eight tolerant F2 plants with different genotypes for SvMt2b (four crosses between a heterozygote and an Amsterdam-type homozygote, and one heterozygote × heterozygote cross) but equal levels of tolerance. The result was that five F4 families were screened for tolerance (25 plants per family) and the five least tolerant, as well as the five most tolerant plants of each of the families were genotyped for SvMt2b (see below). High-level tolerance appeared to be significantly positively associated with the possession of the highly expressed Imsbach allele (G-test with Yates’ correction: G = 21.7; P < 0.001). Plants lacking the Imsbach allele were over-represented among the less tolerant plants (expected 43%, observed 90% [n = 20]), whereas plants possessing the Imsbach allele were over-represented among the more tolerant ones (expected 57%, observed 85% [n = 20]) (Fig. 6).

Pair crosses were also made between highly copper-tolerant plants from the population Imsbach and the moderately copper-tolerant plants from the population Marsberg. Three F1 plants derived from different crosses were selfed, and the F2 families were screened for tolerance. Six of the least tolerant (EC100: 50–100 μM CuSO4) and six of the most tolerant (EC100 > 250 μM CuSO4) F2 seedlings of each F2 family were genotyped for SvMt2b. There was no significant cosegregation of allele origin with copper tolerance in these crosses. Sixteen of 18 plants tested, both from the low-tolerance and high-tolerance selected lines, possessed one or two Imsbach alleles, which strongly suggests that the differential tolerance of Imsbach and Marsberg plants is unrelated to the difference in the primary structure of the predicted SvMt2b proteins.

DISCUSSION

The SvMt2b gene was classified as type 2 within the MT-II class due to the presence of Cys-Cys and Cys-X-Cys motifs in the N-terminal domain (Robinson et al., 1993). Already 27 genes of this type have been referred to by Rauser (1999). Transcripts of MT-IIs occur in various of plant organs such as roots, leaves, stems, flowers, and seeds, either constitutively, or induced by different environmental conditions (Rauser, 1999). S. vulgaris MT2b is highly homologous with MT genes found in M. crystallinum and in Oryza sativa (OsMT-2; Hsieh et al., 1996). Responses of MT expression to copper treatment are different between these species despite the high homology. In Arabidopsis the MT2b mRNAs were abundant in leaves and to a lesser extent in roots from mature plants and exposure of seedlings to copper resulted in only a slight increase (Zhou and Goldsbrough, 1995). This pattern is comparable with the results found in the present study. Mineta et al. (2000) found that MT2a promoter activity in copper-treated Arabidopsis was highest in and around the vascular tissue, whereas copper accumulated mainly in the cortex. Also, MT2b promoter activity was found to be highest in the stele (Bundithya and Goldsbrough, unpublished data; mentioned in Cobbett and Goldsbrough [2000]). These results suggest that copper itself is not directly involved in MT2 transcription.

The Southern blot showed big differences in band intensities between Amsterdam, Marsberg, and Imsbach (Fig. 3b). Recent results have revealed that SvMt2b is composed of two exons and a long intron, inserted after bp 69 of the coding sequence (A. Ter-©ahtauta, unpublished data). The SvMt2b coding sequence contains one MboI restriction site located in exon I. The probe that we used was specific to exon II, implying that the number of SvMt2b containing restriction fragments should be equal to the number of copies of this gene in the genome. The probe, which completely matched exon II from Imsbach...

Figure 6. Cosegregation of SvMt2b allele origin and copper tolerance in F4 lines derived from crosses between copper-tolerant F1 plants. PCR products of SvMt2b using Imsbach allele-specific primers and leaf DNA from plants of the S. vulgaris populations Amsterdam and Imsbach, and from 12 plants of different F3 lines (C1, C2, and C3). Low-tolerance plants and high-tolerance plants were selected from crosses between tolerant low-expression homozygotes and tolerant high-expression heterozygotes. M, Marker (250-bp DNA mass ladder, MRC Holland); Am, Amsterdam; Im, Imsbach.
plants, contained 5- and 4-bp mismatches with exon II from Amsterdam and Marsberg plants, respectively, which is far from sufficient to produce the band intensity differences under the stringency conditions applied. Thus, it seems that the intense bands in Imbsch and Marsberg must have resulted from the presence of a number of identical SvMT2b containing repeats. The size of these repeats is unknown, but may be longer than 1.37 kb, because the intron, which has not been completely sequenced, contains at least two MboI sites (A. Tervahauta, unpublished data). Further analysis of the repeat structure by long PCR and reverse PCR has been unsuccessful thus far. Tandem repeat of SvMT2b seems to be likely however, and might account for the overexpression in the tolerant plants. To our knowledge, no other plant MT tandem repeat has been described so far. However, a tandem repeat of the yeast MT gene, CUP1, has been found in cadmium-resistant (Tohoyama et al., 1996) and copper-resistant strains (Fogel et al., 1983; Tohoyama et al., 1992).

High SvMT2b mRNA accumulation in plants from the Amsterdam × Imbsch F2 crosses was strictly dependent on the presence of at least one Imbsch allele. Low-expression F3 plants were all homozygous for the Amsterdam allele. This implies that high expression could be conferred by a dominant cis-acting regulatory component or, possibly, a closely linked trans-acting component. Enhanced SvMT2b expression as such is not sufficient to produce increased copper tolerance, relative to the sensitive parent population, as indicated by the presence of high-expression plants among the non-segregating copper-sensitive F3 families. However, a strict cosegregation between high-level copper tolerance and SvMT2b overexpression did occur in tolerant F2 families (Fig. 5). Thus, overexpression of SvMT2b can confer additional copper tolerance, although only in combination with components of the genetic background of a copper tolerant plant, suggesting that SvMT2b acts as a hypostatic enhancer, rather than as a primary tolerance gene. An important role for hypostatic enhancers in copper tolerance has also been demonstrated in Mimulus guttatus (Macnair, 1983; Smith and Macnair, 1998).

There are differences in the predicted amino acid sequences of the SvMT2b protein between the S. vulgaris populations. This could result in a change in the three dimensional structure of the protein (Keeton et al., 1993). It is difficult to assess whether such changes have any influence on the stability or the physiological role of the protein in the plant. At any rate, the differences in SvMT2b amino acid sequences between Imbsch and Marsberg had no effect on the copper tolerance as shown by the lack of cosegregation with tolerance in the F2 families derived from Imbsch × Marsberg crosses.

Overexpression of SvMT2b restored cadmium and copper tolerance in hypersensitive yeast, suggesting that the SvMT2b protein increased the cellular sequestration capacity, probably through binding the metals. We were unable to assess the cellular SvMT2b protein levels in S. vulgaris, probably because of their sensitivity to oxidation. However, the highly significant cosegregation of enhanced SvMT2b expression with high tolerance in tolerant F4 families indicates that the mRNAs were indeed translated into functional proteins. It is very difficult to detect this type of MT proteins, therefore not much is known about post-transcriptional processing of MTs. However, Murphy et al. (1997) succeeded in detecting MT proteins in Arabidopsis, and they found no major discrepancies between the patterns of mRNA expression and the corresponding protein levels.

SvMT2b overexpression in both the Imbsch and Marsberg populations must have resulted from independent evolution. Gene flow between these populations is very unlikely (Schat et al., 1996). Moreover, the Marsberg SvMT2b sequence is much more similar to the Amsterdam sequence than to the Imbsch one. Thus, MT2b amplification might be a common phenomenon. Unequal crossing-over constitutes a plausible mechanism for such gene amplifications. The absence of high SvMT2b expression in the populations Amsterdam, Wijlre, and Gaschurn suggests that there may be selection against it on non-metalliferous soil.

In conclusion, the copper-tolerant populations showed a constitutively higher SvMT2b expression, which could result from gene amplification. This overexpression does not produce copper tolerance by itself but merely increases the level of tolerance produced by one or more epistatic primary tolerance genes. Further studies of copper tolerance genes and their interactions are necessary to get a better understanding of the different mechanisms involved in copper tolerance in S. vulgaris.

MATERIALS AND METHODS

Plant Materials

Seeds of Silene vulgaris plants were collected from the copper mines near Imbsch and Marsberg (Germany) and from the botanical garden of the Vrije Universiteit of Amsterdam (The Netherlands). Characteristics of these sites and of the local S. vulgaris populations have been given in Schat and Ten Boekum (1992a). In addition, seeds were also collected from non-metallicolous populations growing in limestone grassland at Wijlre (The Netherlands) and a subalpine meadow near Gaschurn (Austria).

Tolerance Testing

Seed germination, hydroponic preculture, nutrient and test solution compositions, and growth chamber conditions were exactly as in Schat et al. (1996). Tolerance testing was performed using a sequential exposure method described in Schat and Ten Boekum (1992b). In short, plants were
exposed to a sequence of linearly increasing concentrations of copper in the test solution (2-d exposure to each concentration). Prior to exposure to the first concentration, the roots were stained black by dipping them in a stirred suspension of finely powdered active carbon (Schat and Ten Bookum, 1992b). At each transfer to a higher concentration the plants were checked for root growth and subsequently retained. The lowest copper concentration that completely stopped root growth (lowest 100%-effect-concentration [EC100]) was taken as a tolerance measure. Consequently the plants were checked for root growth and subsequently stained. The lowest copper concentration that subsequently restained. The lowest copper concentration that completely stopped root growth (lowest 100%-effect-concentration [EC100]) was taken as a tolerance measure. The sensitive parent population (Amsterdam) was screened using 25-µM (Marsberg), and 100-µM (Imbsbach) concentration steps, respectively. To select sensitive and tolerant plants from the Amsterdam × Imbsbach F2 crosses, 250 seedlings were tested using 4-µM concentration steps and another 250 using 50-µM steps. Supposedly sensitive and tolerant F2 lines derived from crosses among sensitive (EC100 < 12 µM) and tolerant (EC100 > 100 µM) F2 plants were screened using 4-µM and 50-µM intervals, respectively. Moderately tolerant and highly tolerant plants from Marsberg × Imbsbach F2 crosses were selected using 25- and 50-µM concentration steps, respectively. Tolerant F2 families segregating for MT2b expression were screened with 50-µM intervals.

**cDNA Library Construction and Screening**

A λgt11 cDNA library was prepared from leaves of untreated copper-tolerant plants (population Imbsbach). Total RNA was isolated according to the guanidine hydrochloride method (Logemann et al., 1987). Poly-A+ mRNA was isolated using an Oligotex mRNA kit (Qiagen USA, Valencia, CA). cDNA was prepared with a cDNA Synthesis Kit (Pharmacia Biotech, Piscataway, NJ), size-selected with a SizeSep 300 Spin Column (Pharmacia Biotech), and ligated with EcoRI-adaptors and finally with EcoRI-precut λgt11-arms. The library was packaged using a Gigapack III Gold Packaging Extract (Stratagene, La Jolla, CA), titrated (approximately 1 × 1011 pfu/mL). The amplified library was plated (approximately 6,000 plaques on a plate of 9 cm in diameter) and lifted on Nylon membranes (Boehringer Mannheim/Roche, Basel). DIG-labeled DNA probes were produced using specific primers for Arabidopsis MT1a, MT2a, MT2b, and MT3 (MTh, 5'-GAATTCCGCGACGGAAAGA-3' and 5'-AGTTGTGCTGACCTCCTTTGGTG-3'; MT2a, 5'-CCGAAATTCCTCGAGAAAATGTCCTGGC-3' and 5'-GTGCAATTGCCTCGAGTCAAA-3'; MT2b, 5'-GATGCTTTCGTCTCTGGAA-3' and 5'-ATGTCGCGGCTGGTCAAA-3'). The plants were grown hydroponically for 2 weeks before DNA and/or RNA extraction. Some of the plants were exposed to 50 µM CuSO4 for 24 or 48 h before harvest. At harvest, roots were shortly rinsed with distilled water and the whole root system or/and a mature leaf was cut off, immediately frozen in liquid nitrogen, and stored at −80°C until extraction.

**Characterization of 5oMT2b Expression Patterns**

**Plant Culture**

The plants were grown hydroponically for 2 weeks before DNA and/or RNA extraction. Some of the plants were exposed to 50 µM CuSO4 for 24 or 48 h before harvest. At harvest, roots were shortly rinsed with distilled water and the whole root system or/and a mature leaf was cut off, immediately frozen in liquid nitrogen, and stored at −80°C until extraction.

**DNA/RNA Isolation**

DNA isolation was performed according Doyle and Doyle (1990). Total RNA was isolated using the RNeasy Plant Mini Kit (Qiagen).

**cDNA Preparation**

Single-stranded cDNA was prepared from 2 µg of RNA, 20 pmol of RACE dT primer, 0.25 mM deoxynucleoside triphosphates (Life Technologies/Gibco-BRL, Cleveland), 200 units of M-MLV reverse transcriptase (Life Technologies/Gibco-BRL), and 1 × RT first strand buffer (Life Technologies/Gibco-BRL), in a total volume of 20 µL.

**SEQUENCING OF 5oMT2b ALLELES**

The primers 5'-TTCAGTAATTTAACCCCTTGAG-3' and 5'-GCTTTGTTTTTACCCCTTGAG-3', based on the non-coding regions of a MT2b-like cDNA (5oMT2b) found in the library (see above), were used to amplify and sequence the coding regions of the corresponding cDNAs of plants from the populations Amsterdam and Marsberg. PCR was performed using 2 µL of cDNA, 20 pmol of each primer, 1 mM deoxynucleoside triphosphates (0.25 mM each) (Life Technologies/Gibco-BRL), 1 unit of Taq polymerase (MRC Holland), and 1 × Taq buffer (MRC Holland), adjusted to a total volume of 25 µL with sterilized water. An annealing temperature of 55°C and 34 cycles were used. PCR products of the expected lengths were sequenced. Sequencing was performed using the Terminator Cycle Sequencing Core Kit (Perkin-Elmer Applied Biosystems, Foster City, CA).

**Allele-Specific PCR**

The primers used for the allele-specific PCR were 5'-GAAAATGTCGTGCTGTAATGGA-3' and 5'-GTTCATTGGCAATGCGAGG-3' for the Imbsbach allele and 5'-GAAAATGTCGTGCTGTAATGGT-3' and 5'-GCTGGAGTATGAGCGCTT-3' for the Amsterdam allele, giving
Quantitative PCR

The primers used for the quantitative RT-PCR were 5'-GAAAATGTCGTGCTGTAATGG-3' and 5'-AAGGGTTGC-ACTGCGAGTTG-3', based on a part of the *SvMT2b* cDNA that was identical in plants from Amsterdam, Marsberg, and Imsbach. A house-keeping gene GAPDH (glyceraldehyde-3-phosphate dehydrogenase) was used as a positive internal control. The primers 5'-TTGGATCTCTACTGACAAGGA-CAAGGCT-3' and 5'-TGAATCCCCCATTGGTTGCT-TACC-3', designed on the basis of published sequences of *S. vulgaris* GAPDH, were used for the quantitative RT-PCR, using cDNA of plants from Imsbach as a template, was confirmed with PCR and sequencing using vector specific "Sensitive Yeast Mutants" complementation of copper-sensitive and cadmium-sensitive yeast mutants.

Four micrograms of total DNA isolated from leaves of plants from the populations Amsterdam, Marsberg, and Imsbach, was digested overnight at 37°C with the restriction enzyme *MboI* and electrophoresed overnight on a 0.7% agarose gel in 0.5x SSC/0.1% (w/v) SDS at 65°C for 15 min and two times more in 0.2x SSC/0.1% (w/v) SDS at 68°C for 15 min. The blots were exposed to a chemiluminescence film (Hyperfilm ECL, Amersham Life Science). DNA loading was checked by ethidium bromide staining.

Complementation of Copper-Sensitive and Cadmium-Sensitive Yeast Mutants

*SoMT2b* was amplified with PCR from a *ucl1* clone lysate using primers 5'-GCGGAATTCGTGCTGCTGTAATGGAA-3' and 5'-CGGCTCGAGCTCATTTGCAAGGTTG-3' containing EcoRI and *XhoI* restriction sites for cloning into the pAJ401 *Escherichia coli* (yeast shuttle vector). pAJ401 was derived from pFL60 (Minet and Lacroute, 1990) by interchanging *EcoRI* and *XhoI* cloning sites. Recombinants were first introduced into *E. coli*, selected by ampicillin resistance, and the presence of *SoMT2b* gene was confirmed with PCR and sequencing using vector specific primer 5'-CATCAAGGAAATTTACTGCTCATTTGCAAG-3'. Plasmid DNA miniprep was made and introduced into cadmium-sensitive (JWY53, *Δcyf1*, Wemmie et al., 1994) and copper-sensitive yeasts (DBY746, a common laboratory yeast strain; DM771-6C, *Δcup1*). First transformant selection in yeast was made by uracil auxotrophy.

ACKNOWLEDGMENTS

The plasmid pAJ401 was kindly provided by Dr. Anu Saloheimo (Biotechnology and Food Research, VTT, Finland). The JWY53 yeast strain was supplied by Professor W. Scott More-Rowley (The University of Iowa College of Medicine), Professor Peter Goldsbrough (Purdue University) provided the Arabidopsis MT-plasmids. The authors would also like to thank Gregory Koningstein (Department of Molecular Microbiology, Faculty Biology, Vrije Univers-
siteit, Amsterdam) for assisting with the sequencing of the SoMT2b cDNAs.

Received December 22, 2000; returned for revision February 14, 2001; accepted April 19, 2001.

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