Silencing of germacrene A synthase genes reduces guaianolide oxalate content in Cichorium intybus L.

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ABSTRACT
Chicory (Cichorium intybus L.) is a medicinal and industrial plant from the Asteraceae family that produces a variety of sesquiterpene lactones (STLs), most importantly bitter guaianolides: lactucin, lactucopicrin and 8-deoxylactucin as well as their modified forms such as oxalates. These compounds have medicinal properties; however, they also hamper the extraction of inulin – a very important food industry product from chicory roots. The first step in guaianolide biosynthesis is catalyzed by germacrene A synthase (GAS) which in chicory exists in two isoforms – GAS long (encoded by CiGASlo) and GAS short (encoded by CiGASsh). AmiRNA silencing was used to obtain plants with reduced GAS gene expression and level of downstream metabolites, guaianolide-15-oxalates, as the major STLs in chicory. This approach could be beneficial for engineering new chicory varieties with varying STL content, and especially varieties with reduced bitter compounds more suitable for inulin production.

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Introduction
Chicory (Cichorium intybus L.) is a widely used medicinal and industrial plant from the Asteraceae family. Numerous chicory varieties are cultivated for different purposes. The upper parts of the plant are used as salad and vegetable (chicons), both slightly bitter. The underground taproot is an important source of inulin, a fructose polymer commonly used in the food industry. Its traditional uses include animal feed, a cheap coffee replacement, and many medicinal applications. Lately, chicory is viewed by the industry as functional food – nutritious with benefits for human health, and its importance is increasing, especially in developing countries, due to relative ease of cultivation and low agricultural input.

Chicory’s pest resistance, as well as its bitter flavor, is due to the presence of secondary metabolites, namely sesquiterpene lactones (STLs), accumulating largely in the latex of the plant. STLs are responsible for some of the medicinal properties of chicory, including antifungal, antimalarial, anti-inflammatory, anti-tumor, and cytotoxic activity. However, they can also act as allergens and irritants. Bitter compounds in chicory are of economic importance as well. Since some varieties are used for human consumption, and consumers prefer different bitterness levels depending on the market and traditional uses, having a wider selection of less bitter varieties could push chicory use to new markets. Chicory roots are also a major source of inulin, used in the food industry as prebiotic, sweetener, fat-replacing and texturizing agent. The extraction of inulin is hindered by the co-extraction of STLs, raising the cost of inulin production. Thus, having varieties with lowered STL production would be highly beneficial.

The most diversified and abundant group of STLs in chicory are the guaianolides, all derived from a common precursor – germacrene A. Present both in leaves and roots of the plant, the most common guaianolides in chicory are lactucin, lactucopicrin, and 8-deoxylactucin, as well as...
their modified forms – oxalates, sulfates and glycosides, with oxalates being the most abundant form.\textsuperscript{3} These compounds are mainly responsible for the bitter taste of chicory and lettuce.\textsuperscript{6} The first step in guaianolide biosynthesis is the conversion of farnesyl diphosphate (FPP) to germacrene A (Figure 1), catalyzed by germacrene A synthase (GAS).\textsuperscript{12} This enzyme is encoded in chicory by two genes, whose cDNAs – CiGASlo (long isoform) and CiGASsh (short isoform) – have been isolated previously.\textsuperscript{19} The two isozymes have 72\% similarity at the amino acid level, and both convert FPP to germacrene A, as confirmed by heterologous expression.\textsuperscript{19} CiGASlo transcript is encoded by a single gene mapped on a locus on LG9, and CiGASsh is mapped on one locus on LG3 with at least three gene copies, two the result of a recent duplication.\textsuperscript{13} However, not much is known about the function of the two isoforms \textit{in planta}. Elucidating the function of these genes would be beneficial for the production of new chicory varieties with different STL content, which has been slow using traditional methods since the species is self-incompatible with high heterozygosity level.\textsuperscript{20}

Gene silencing is one of the methods used to study gene function in plants and bioengineer plant varieties. Unlike the conventional approach by producing mutant lines, RNA interference (RNAi) offers a quicker and cheaper alternative to obtain mutant phenotype with benefits of high specificity, dominant phenotype regardless of gene copy number and production of lines with varying degree of silencing.\textsuperscript{21} RNAi has the potential in plant metabolic engineering to increase or decrease the production of the desired compounds\textsuperscript{22} or to suppress their degradation.\textsuperscript{23} In this study, RNAi was used to produce chicory lines with decreased production of STLs using amiRNA approach, which was shown to be more specific and efficient than using longer hairpin constructs.\textsuperscript{21,24,25}

**Material and Methods**

**Vector Construction**

Silencing constructs were designed according to CiGASlo (GenBank: AF497999) and CiGASsh (GenBank: AF498000) mRNA sequences. The cloning procedure is given in Supplementary figure 1. AmiRNAs were amplified from pRS300 vector (Addgene, USA) by replacing a sequence of Arabidopsis micro RNA (miR319a) with a desired sequence through a series of overlapping PCR reactions.\textsuperscript{26} The reactions were performed with Phusion High-Fidelity polymerase (New England Biolabs Inc., USA) according to the manufacturer’s protocol (Supplementary tables 1 and 2). The mixture contained 200 ng pRS300 DNA and 0.4 µM primers from Supplementary table 3. Primers were designed according to Schwab et al.\textsuperscript{26} AmiRNA sequences specific for either CiGASlo (amiGASlo, TATCTAAGAT-)

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**Figure 1.** STL biosynthesis in chicory and the most abundant guaianolide compounds, modified from Bogdanović et al.\textsuperscript{13} GAS – germacrene A synthase,\textsuperscript{12} GAOs – germacrene A oxidases,\textsuperscript{14,15} COS – costunolide synthase,\textsuperscript{16,17} KLS – kauniolide synthase.\textsuperscript{18} Silencing target – GAS is marked by the red arrow. Dashed lines mark several consecutive steps in biosynthesis.
ATCTTCACCGT) or CiGASsh gene (amiGASsh, TA-
ATAGTTTGTCAAGCTGCGC), were chosen based
on good hybridization with the target (−35 to −40 kcal
mol⁻¹) and very low off-target binding. Amplified
amiRNAs were first cloned into pDONR207
(Invitrogen, USA) using Gateway® BP Clonase®
Enzyme Mix (Invitrogen, USA) and recombinant
colonies were selected on LB plates supplemented
with gentamicin. The presence of the insert was con-
firmed by colony PCR and the cloned fragment was
sequenced using DYEnamic ET Terminator Cycle
Sequencing Kit (GE Healthcare, UK) with primers
given in Supplementary table 3. Selected clones were
transferred by three-way Gateway reaction into
pKGW-RR-MGW for expression in plants using
Gateway® LR Clonase® II Enzyme mix (Invitrogen,
USA), under the control of 35S promoter and termi-
nator. The vector also contains a streptomycin/specti-
nomycin bacterial resistance gene, a kanamycin plant
resistance gene and DsRED as a fluorescent marker for
transformation under the control of AtUBQ10
promoter. Successful cloning of amiRNA fragment
was confirmed by colony PCR for the insert and vec-
tor-insert borders (Supplementary table 3). The plas-
mids were named pKGW-amiGASlo and pKGW-
amiGASsh.

Establishment of Chicory in Vitro Culture and
Regeneration of Transformed Plants

*Cichorium intybus* L. Blue (Samen Mauser,
Switzerland) was used for all experiments, and its
*in vitro* culture was maintained as described earlier. Agrobacterium rhizogenes A4M70GUS
contained pRiA4 plasmid with integrated GUS
cassette in the TL region. Expression vectors
were inserted by electroporation. Transformation
with A4M70GUS strains carrying amiRNA con-
structs was conducted as described before for the
empty A4M70GUS strain. Regenerated shoots
forming spontaneously on root cultures were
excised and grown separately.

Genomic DNA of suspected transformants was
extracted from leaves of 1-month-old plantlets
using a mini-prep CTAB method and treated
with RNase A (Fermentas, USA) using the manufac-
turer’s protocol. The PCR mixtures consisted of 100
ng of genomic DNA, 1 µM specific primers
(Supplementary table 3) and standard components
according to Fermentas protocol for Taq recombi-
nant polymerase, in a 25 µl volume. The primers
specific for DsRED were used to confirm the pre-

cence of pKGW-amiRNA plasmids, while virD1-
specific primers were used to exclude bacterial con-
tamination. Transgenic plants originating from dif-
ferent HR clones were grown as rosettes for 10 weeks
before being used for gene expression and guaiano-
lide oxalate content analyses. Clone lines were pro-
gagged as hairy-root cultures. Stable transgene
expression in clone lines was further confirmed by
observing DsRED fluorescence detected macroscopi-
cally using a green LED light (515–530 nm) with
a red long-pass 600 nm emission filter, and by con-

focal microscopy using Leica TCS SP5 II with 543
nm excitation line, 500–530 nm detection and
a HCX PL APO CS 20.0 × 0.70 DRY UV objective.

Quantification of GAS Gene Expression by
qRT-PCR

RNA was isolated from chicory roots and shoots
using the CTAB method. Total RNA was treated
with DNase I (Fermentas, USA) according to the
manufacturer’s protocol and reverse transcribed
using RevertAid First Strand cDNA Synthesis Kit
(Fermentas, USA). Quantification of CiGASlo and
CiGASsh gene expression in untransformed controls
(eight genotypes of parent plants used for transfor-
mation) and plants expressing pKGW-amiGASlo
and pKGW-amiGASsh silencing constructs (19
clones originating from these eight genotypes) was
performed by qRT-PCR. The reactions were set with
Maxima SYBR Green mix (Fermentas, USA), with
cDNA corresponding to 100 ng RNA and 0.3 µM
primers (Supplementary table 3). The amplification
and the preparation of standards for absolute quan-
tification were carried out as described previously.
Constitutive expression of 18S rRNA gene was con-
firmed in parallel using universal plant 18S rRNA
primers. qPCR results were analyzed using 7000
System SDS Software.

Quantification of Guaianolide Oxalates by
HPLC-HESI-MS/MS

Sesquiterpene lactone oxalate (lactucin-15-oxalate,
8-deoxylactucin-15-oxalate and lactucopicrin-15-
oxalate) content was quantified in untransformed
plants and plants expressing pKGW-amiGASlo and pKGW-amiGASsh silencing constructs. The same material was used for qRT-PCR and metabolite analyses.

Chicory root and shoot (100 mg and 400 mg, respectively) were frozen and powdered in liquid nitrogen. Extraction was performed using 0.133% formic acid in methanol. Samples were sonicated for 10 min and then centrifuged for 5 min at 21000 g at room temperature. Extraction was repeated twice, and the two supernatants were combined and diluted with deionized water in a 1:1 ratio. The extracts were then filtered with Minisart® RC15 (Sartorius, Germany) filters.

Chicory extracts were analyzed with a Dionex Ultimate 3000 UPLC system (Thermo Fisher Scientific, Bremen, Germany) coupled to a TSQ Quantum Access MAX triple-quadrupole mass spectrometer with HESI source (Thermo Fisher Scientific). The chromatographic separation was achieved using a 50 × 2.1 mm Hypersil gold C18 column (Thermo Fisher Scientific), with 1.9 µm particle diameter. Mobile phases were: A – 0.1% Formic acid and B – acetonitrile. The elution gradient was as follows: 0 – 3 min 5–20% B; 3–5 min 20–40% B; 5–7.5 min 40–50% B, 7.5–8.5 min 50–60% B; 8.5–10 min 60–95% B, 10–13.5 min 95% B, 13.5–14 min 95–5% B, followed by re-equilibration till 18 min with 5% B at a constant flow of 0.4 ml min−1 and temperature of 30 °C. The vaporizer temperature was set to 100 °C, voltage –3500 V, capillary temperature 275 °C, sheath gas pressure 30 AU, ion sweep gas pressure 0 AU, auxiliary gas flow 7 AU, capillary offset –35 V, tube lens offset –65 V. For qualitative analyses full scan, product ion scan, and parent ion scan were utilized, while for quantification multiple reaction monitoring (MRM) was used. For MRM detection the following mass transitions were used: 8-deoxylactucin-15-oxalate m/z 331 [M-H]− -> m/z 259, collision energy (CE) 10 eV and m/z 331 -> m/z 215, CE 15 eV; lactucin-15-oxalate m/z 347 [M-H]− -> m/z 275, CE 15 eV and m/z 347 -> m/z 213, CE 15 eV, lactucopicrine-15-oxalate m/z 481 [M-H]− -> m/z 242, CE 15 eV and m/z 481 -> m/z 213, CE 20 eV. For all fragmentation experiments, the collision gas pressure was held at 1.5 mTorr. Due to lack of authentic standards, relative quantification was performed by normalizing the peak intensity of each analyte in each sample to the maximal measured peak intensity of the corresponding analyte.

Data Analysis

Statistical analysis of silencing effect on GAS gene expression and guaianolide oxalate content was performed using R Software and MASS package for R. Comparison of organ dependent CiGASlo and CiGASsh expression as well as guaianolide oxalates in control plants was evaluated using Wilcoxon signed-rank test. The effects of transformation with silencing constructs on the reduction of CiGASlo and CiGASsh expression as well as the downstream metabolite content in control plants was evaluated using Box-Cox power transformation was used to stabilize the dependent variable variances (in order to remove heteroscedasticity) prior to ANOVA, and normality and homoscedasticity of transformed data were confirmed by Levene’s test and by checking the residual and quantile-quantile plots. Statistically significant differences were estimated using Tukey’s post hoc test. The effect of CiGASlo and CiGASsh expression (continuous explanatory variable) on the relative content of the three guaianolide oxalates (response variable) in shoots and roots was tested using multiple linear regression.

Results and Discussion

Chicory Transformation with Silencing Constructs

Chicory was transformed with silencing constructs designed to be specific for either CiGASlo (pKGW-amiGASlo) or CiGASsh (pKGW-amiGASsh), using
A. rhizogenes rather than A. tumefaciens. The advantage of A. rhizogenes transformation is that no plant hormones are required; hairy root (HR) morphology facilitated the selection and regeneration of transformed plants, which occurred spontaneously and rapidly. Initial selection of root clones was performed based on the HR phenotype (Figure 2(a)), rather than kanamycin resistance (due to nptII, present on the binary vector), since kanamycin is less efficient in co-transformation events, as it does not discriminate against chimeric roots. Selected root clones spontaneously regenerated shoots (Figure 2(b)) which were grown separately and displayed normal plant morphology (apart from better developed and branched roots), as expected from previous results. The obtained chicory plants were tested by genomic PCR (Figure 2(c)) to select transgenic plants carrying the amiRNA constructs. T-DNA from the silencing vectors was present in 118 out of 183 tested plants (64.48%) (Table 1). A similar co-transformation efficiency was achieved using the MSU440 A. rhizogenes strain in Lotus japonicus. Interestingly, not all regenerated chicory plants originating from the same HR clone were transformed, suggesting the chimeric nature of hairy-roots as reported by Limpens et al. Roots of most confirmed plants were reliably expressing the DsRED marker over several months in culture (Figure 2(d,e)), with variable intensity. Only two transgenic plants that did carry a silencing construct had no observable fluorescence in the roots at any time point, while four plants had transient expression present only in the first subculture. Transgene expression from binary plasmids can vary depending on integration site, gene silencing, and other factors, and is usually present in 20–50% of HR clones obtained from A. rhizogenes-transformed plants.

**GAS Gene Expression Is Reduced in Transformed Clones**

QRT-PCR analysis revealed that both CiGASlo and CiGASsh were expressed in in vitro regenerated untransformed plantlets, with CiGASsh transcripts being on average 12.3 times more abundant in roots and 6.24 times more abundant in shoots in comparison to CiGASlo (Figure 3). In a previous study, Bouwmeester et al. showed, using semi-quantitative Northern analysis, that CiGASlo had higher expression in all tested tissues than CiGASsh, except in taproot inner tissue, where CiGASsh was predominantly expressed, and in whole green seedlings where the expression of the two genes was comparable. Similar results

<table>
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<th>Construct</th>
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<th>pKGW-amiGASsh</th>
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<td>Initial number of HR clones</td>
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<td>97</td>
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<tr>
<td>Number of regenerated plants tested positive for DsRED</td>
<td>46</td>
<td>72</td>
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Figure 2. Chicory transformation with A. rhizogenes strains carrying silencing constructs. (a) Hairy-roots developing on inoculated leaves 17 days after transformation. (b) Spontaneously regenerated shoots of one HR clone. (c) DsRED gene presence or absence in genomic DNA of tested plants 1–5 (amplicon length: 349 bp), bacterial vector DNA (+), no template control (-). (d) DsRED fluorescence of one transformed HR clone (DsRED+), compared to non-transformed root (WT). (e) Confocal micrograph of DsRED fluorescence in epidermal root cells of an HR clone.
were obtained by our group using plants grown in the greenhouse. It is well known that the gene expression commonly differs between *in vitro* and *ex vitro* cultured plants. Promoter activity analysis using promoter-eGFP fusions confirmed that the two isoforms had different promoter activity, with the *CiGASlo* promoter being active in both roots and shoots, while the *CiGASsh* promoter was predominantly active in roots.

The expression of *CiGASsh* and *CiGASlo* was significantly higher in roots as compared to shoots for both control and transformed clones, as revealed by ANOVA (with *p*-values *p* < .001 and *p* < .01, respectively). This was confirmed for control plants by nonparametric Wilcoxon signed-rank test (*p* < .05 for both gene expression). These results are in accordance with previous results on chicory from greenhouse obtained by Bouwmeester et al. and Bogdanović et al. In *Lactuca sativa*, where STLs also accumulate in latex, two germacrene A synthases – *LTC1* and *LTC2* – were found to be expressed constitutively in roots, but only *LTC2* was highly expressed in leaves. In species where terpenes accumulate mainly in leaf trichomes, GAS genes are more active in young leaves than in roots, as in *Artemisia annua*, *Tanacetum parthenium*, and sunflower. In *Achillea millefolium*, where volatile terpenoids constitute the most important fraction, the highest expression of GAS gene was detected in flowers and leaves, and much less in rhizome, root and stem tissues.

In order to reduce the guaianolide production in chicory, two GAS genes that convert FPP to germacrene A (Figure 1) were selected as silencing targets. Since amiRNAs, which imitate natural miRNAs, are more specific and more reliable for predicting possible off-target effects as compared to long hpRNA constructs, this approach was chosen for silencing. Comparison of *CiGASlo* and *CiGASsh* expression in control (untransformed) plants and selected pKGW-amiGASlo and pKGW-amiGASsh transformants (showing DsRED fluorescence) confirmed that silencing was successful (Figure 3). The silencing of two GAS genes was significant, with transcript levels reduced up to 30.8 times for *CiGASlo* and up to 70.7 times for *CiGASsh* as compared to parent plants (Table 2). Variable level of silencing in different transgenic lines (Figure 3) is probably due to a positional effect of amiRNA integration and can be useful to select lines with adequate silencing levels to help characterize gene function or to produce varieties with differing STL levels. ANOVA

![Figure 3](image-url)

*Figure 3.* *CiGASlo* (a) and *CiGASsh* (b) expression (transcript copy number per cDNA corresponding to 100 ng RNA, determined by absolute quantification) in roots and shoots of controls and plants transformed with pKGW-amiGASlo and pKGW-amiGASsh constructs. To stabilize the expression data variance log transformation was used prior to visualization and statistical analyses. Statistically significant differences within roots or shoots, obtained by Tukey’s *post hoc* test at *p* < .05 are marked with different letters.
analysis indicated that there are no significant differences in the strengths of \textit{CiGASlo} and \textit{CiGASsh} silencing in shoots and roots; in other words, either gene was silenced in both shoots and roots by a similar degree.

Surprisingly, silencing constructs were not specific toward either of the two genes. Since these two genes have a similar coding sequence – 72% identity on the deduced amino acid level and 75% identity over 83% query cover at the mRNA level (Supplementary figure 2), amiRNAs could be directly affecting the nonspecific transcript, a problem usually present when the two transcripts have five or fewer mismatches in amiRNA target region. In our system, amiGASlo has nine mismatches compared to \textit{CiGASsh}, and amiGASsh has six mismatches to \textit{CiGASlo} (Supplementary figure 2), not counting the last nucleotide in the target region, which is always modified to A in amiRNA. Non-target silencing can also be a consequence of feedback regulation, when the two genes participate in the same signal transduction chain, as in the case of MADS box genes in Arabidopsis. MiRNAs can also be involved in transitive RNAi – spreading of the silencing outside of the initial target sequence. The proposed mechanism for this action is second-strand synthesis and trans-acting siRNA (small interfering RNA) production, mediated by RNA-dependent RNA polymerases, which in turn target other mRNAs for miRNA-like cleavage. Even though amiRNAs are designed having in mind rule sets to reduce nonspecific targeting and transitive RNAi, amplification of the silencing signal can be dependent on other factors which are harder to control, like structural characteristics of the primary transcript and amiRNA construct.

### Table 2

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**GAS Gene Silencing Reduces Guaianolide Oxalate Content**

To evaluate the impact of silencing of the GAS genes on guaianolide production, the concentration of three downstream metabolites, 8-deoxylactucin-15-oxalate, lactucin-15-oxalate, and lactucopicrin-15-oxalate was analyzed by HPLC-HESI-QqQ. The three compounds were selected since they were present in high amounts in untransformed plants and could reliably be identified by comparing MS/MS fragmentation patterns (Supplementary figure 3) with literature data. Guaianolide oxalates constitute the main fraction of STLs in chicory and are more abundant than free guaianolides, so we expected their quantity to reflect the effects of silencing. Guaianolide oxalates were indeed detected in both roots and shoots of chicory plants (Figure 4). Our findings corroborated the results obtained by Sessa et al. who identified guainolide-15-oxalates as major STLs in both lettuce and chicory plants.

The relative abundance of lactucin-15-oxalate and 8-deoxylactucin-15-oxalate was significantly higher in the shoots than in the roots of control plants (\( p < .01 \), Wilcoxon signed-rank test), with a shoot-to-root ratio in individual plants varying from 2.44 to 7.89 for lactucin-15-oxalate and 1.50 to 6.54 for 8-deoxylactucin-15-oxalate. The content of lactucopicrin-15-oxalate did not differ significantly in shoots and roots (\( p < .01 \), Wilcoxon signed-rank test), with shoot-to-root ratio in individual plants varying from 0.48 to 3.64. To our best knowledge, there are no data on organ distribution of guaianolide-15-oxalates in chicory, while data for related species are limited. In chicory at the rosette stage, free guaianolides are usually more abundant...
in the root than in the shoot, but their content may change during development and particularly upon flowering.

Prior to discussing the effects of silencing on guaianolide oxalates content, it should be noted that the transformation with A. rhizogenes per se, e.g. its Rol genes, can boost the production of secondary metabolites in a variety of species. However, chicory plants transformed with the same (but empty) A. rhizogenes strain, A4M70GUS had more free guaianolides only at the flowering stage, while at the rosette stage (used in the current setup) guaianolide content was comparable in transformed and control plants.

Introduction of the GAS-silencing constructs resulted in a significant reduction of the guaianolide oxalate content (Figure 4): up to 185.2 times for lactucin-15-oxalate, up to 166.4 times for 8-deoxy-lactucin-15-oxalate and up to 8.7 times for lactucopicrin-15-oxalate in some of the clone lines, as compared to the levels in parent plants (Table 2).

To elucidate whether the levels of guaianolide-15-oxalates in different parental and transgenic clones depend on the level of GAS gene expression, the relationships between relative abundance of guaianolide-15-oxalates and the expression of CiGASlo and CiGASsh in roots and shoots of tested clones are presented as scatter plots (Figure 5) and as Person’s correlation heatmaps (Figure 6). The obtained data suggest that lactucin-15-oxalate and 8-deoxy-lactucin-15-oxalate accumulate significantly less with decreasing expression of GAS genes in the shoots (Figure 5) whereas in roots this correlation is less clear. Also, the correlation between CiGASsh and CiGASlo expression and compound content is higher and more significant in shoots (Figure 6). The correlation between CiGAS gene expression and guaianolide oxalate content in roots depends on the compound, with lactucin-15-oxalate having the highest significant correlation and lactucopicrin-15-oxalate having no significant correlation (Figure 6). These results suggest that the accumulation of guaianolide oxalates can be altered by manipulation of GAS expression in the shoots, probably reflecting natural means of regulation of their synthesis. On the other hand, regardless of higher CiGAS gene expression in roots (Figure 4), it seems that other mechanisms or enzymatic reactions (e.g. any of the steps from germacrene A oxidation to conjugation with oxalic acid, see Figure 1) may control the accumulation of guaianolide oxalates in roots. Also, their (in)stability and turnover may be different in different organs, while their polar nature may provide a higher
degree of mobility within the tissues and laticifer network in comparison to nonpolar STLs.

To the best of our knowledge, this is the first successful report on reducing the concentration of bitter guaianolide compounds by gene silencing in plants. There are reports describing silencing effects and reduction of other terpenoid groups, like volatile terpenoids in tobacco and cotton, and monoterpene alkaloids in Catharanthus roseus, with gene expression reduced between 4 and 6.67 times, and compounds of interest reduced between 1.43 and 10 times. In a transient silencing assay by agroinfiltration in tobacco, two RNAi constructs were able to silence 5-epi-aristolochene synthase, an enzyme involved in sesquiterpenoid biosynthesis, 3.4 and 6.2 times compared to the control expression value, with 5-epi-aristolochene emission consequently reduced 8.4 and 2.8 times compared to the control emission level,

Figure 5. Scatter plots of the relationship between the relative compound abundance of guaianolide oxalates (8-deoxylactucin-15-oxalate, lactucin-15-oxalate, and lactucopicrin-15-oxalate) and expression (copy number) of CiGASlo and CiGASsh genes in roots and shoots of clone lines (control plants – ○, plants transformed with pKGW-amiGASlo – □ and with pKGW-amiGASsh – △). The statistical significance of the interaction of plant part (root and shoot) and gene expression on compound content was estimated using multiple linear regression, $p < .05$ is marked with *, $p < .01$ is marked with ** while $p < .001$ is marked with ***.

Figure 6. Pearson’s correlation heatmap between relative compound abundance of guaianolide oxalates (8-deoxylactucin-15-oxalate, lactucin-15-oxalate, and lactucopicrin-15-oxalate) and expression (copy number) of CiGASlo and CiGASsh genes in roots and shoots. Significance of correlation is marked with * for $p < .05$, ** for $p < .01$ and *** for $p < .001$. 


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respectively. Silencing of squalene synthase, producing the substrate for triterpene and sterol biosynthesis, was also reported to be 2.7 and 4.2 times reduced compared to control expression levels. The gene for this enzyme was also silenced in apple by virus-induced gene silencing by 1.72 fold. Recently, silencing of amorpha-4,11-diene synthase, which encodes the first step in artemisinin biosynthesis, was achieved in Artemisia annua. The authors report a stable Agrobacterium transformation of A. annua using hpRNA constructs and selecting several lines with substantial gene silencing – 25 times reduction of gene expression compared to untransformed control plants. When assessing the content of artemisinin, a cadinanolide STL (a compound synthetized several steps downstream from the silenced gene, which is comparable to our system), the authors also found a substantial reduction of 20-fold in selected clone lines. However, when measuring amorpha-4,11-diene, a direct product of the silenced gene, no reduction could be observed, but there was a significant increase of this compound in young leaves of silenced lines compared to controls and a comparable level in mature or dry leaves of clones to controls. These results suggest that the effect of silencing genes from the diverse group of terpenoid synthases can be difficult to predict and interpret. In our system, some lines displayed a reduction of gene expression and STL oxalate content of several orders of magnitude (Table 2), suggesting that gene silencing with amiRNAs could be a good method for the production of low-bitterness chicory clones.

Conclusions

In conclusion, amiRNA constructs proved to be a powerful, though not isoform-specific, tool for silencing of two GAS genes in chicory. The silencing success was clearly demonstrated not only at the level of expression of CiGASlo and CiGASsh, but more importantly at the level of downstream metabolites, guainolide-15-oxalates, the major STLs in chicory. This approach and the obtained clones may have practical application in engineering varieties with reduced guaianolide content, facilitating inulin extraction and obtaining products of superior quality.

Abbreviations

amiRNA artificial micro RNA  
CiGASlo Chicory germacrene A synthase, long isoform  
CiGASsh Chicory germacrene A synthase, short isoform  
GAS germacrene A synthase  
hpRNA hair-pin RNA  
HR hairy roots  
mRNA micro RNA  
MS Murashige and Skoog basal medium  
RNAi RNA interference  
STL sesquiterpene lactone  
WT wild type

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Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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