

Supporting Information

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SI Text

Verification of Transferred DNA (T-DNA) Integration by Genomic DNA Analysis. The genomic DNA from transformed hairy roots was isolated (Qiagen Dneasy kit) and then subjected to PCR amplification using T-DNA specific primers with STR primers serving as a positive control (Fig. S1). Specifically, primers for PCR amplification were designed to amplify the complete STR gene (STR_{for}: CCATGGCAAACCTTTCTGAATCTAAATCC and STR_{rev}: GGTCACCCTAGCTAGAAACATAA-GAATTTTC), a 500-bp region of the CaMV 35S promoter (CaMV 35S_{for}: TAGAGGACCTAACAGAAC and CaMV 35S_{rev}: CCGTGTCTCTCCAAATG), an 800-bp region of the antibiotic resistance NPTII gene (NPTII_{for}: atgcaattacctatcgc and NPTII_{rev}: tcagaagaactcgaagaag) and a 550-bp region of the PDK intron (PDK_{int}_{for}: aatagtaattctagctggttg and PDK_{int}_{rev}: tcttgtacaagtggtctag).

Primers for real-time RT-PCR of transformed hairy roots for tryptophan decarboxylase (TDC_{for}: TACTTGGATGGAATC-GAACG and TDC_{rev}: ACAAATGTGGTTGCTTGACC, amplicon size 106 bp) anthranilate synthase, alpha subunit (AS α _f: GAACGTTTGCCTTCTCTTC and AS α _{for}_{rev}: CAGCG-GACTTGATAAGACGA, amplicon size 105 bp), strictosidine synthase (STR_{for}: GTCCAAGATGGCCGAGTTAT and STR_{rev}: TATGTCCTCCACACAATGG, amplicon size 140 bp), strictosidine glucosidase (SGD_{for}: ATATTGAT-GCTCGGGAAAGG and SGD_{rev}: AGACGGCTTCCTA-CAAGAGC, amplicon size 109 bp) and Orca3 (ORCA3_{for}: ATCCAGGATTTGGTTGGGTA and ORCA3_{rev}: CTCTA-ACGGGTCCGGAAATA, amplicon size 143 bp). (See Fig. S1.)

Assessment of Alkaloid Production Rescue by Addition of Tryptamine. Ten root tips from hairy roots transformed with pTDCi were subcultured in 50 mL of Gamborg's B5 liquid media with

tryptamine as described in *Materials and Methods*. Samples were ionized by ESI with a Micromass LCT Premier TOF Mass Spectrometer. The LC was performed on Acquity Ultra Performance BEH C18, 1.7 μ m, 2.1 \times 100 mm column on a gradient of 10–60% acetonitrile/water (0.1% TFA) over 13 min at a flow rate of 0.6 mL/min. The capillary and sample cone voltages were 1,300 and 60 V, respectively. The desolvation and source temperature were 300 and 100 $^{\circ}$ C. The cone and desolvation gas flow rates were 60 and 800 L/hour. (See Figs. S2 and Fig. S3.)

Assessment of Alkaloid Mutasynthesis. See Figs. S4–S7 and Table S1.

Assessment of the Stability of Alkaloid Production Suppression in Subsequent Subcultures. Ten root tips from hairy roots transformed with pTDCi were subcultured every 2–3 weeks in 50 mL of Gamborg's B5 liquid media and grown at 26 $^{\circ}$ C in the dark at 125 rpm. Eighteen-day-old hairy roots were processed as described in *Materials and Methods*. (See Fig. S8.)

Morphology of 2-Week-Old TDCi and Wild-Type Hairy Roots. See Fig. S9 *a* and *b*.

Expression Levels of Secologanin Biosynthetic Genes SLS and G10H. Primers for real-time RT-PCR of transformed hairy roots for secologanin synthase (SLS) (SLS_{for}: GGATTGGGCATG-GTTTACTC and SLS_{rev}: CCATGGGTTTAGACAAGGCT, amplicon size 140 bp) and geraniol-10-hydroxylase (G10H) (G10H_{for}: TGCTTGACCTGTTTGTAGC and G10H_{rev}: TCCTCTGCCGATTACTTGTG, amplicon size 132 bp). (See Fig. S10.)

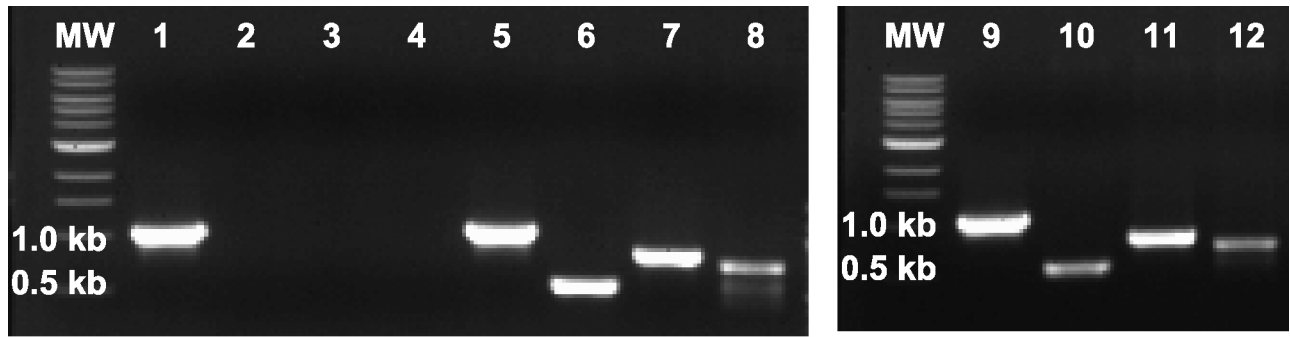


Fig. S1. 1% agarose gel of PCR amplification of TDCi and wild-type hairy root genomic DNA. Lane 1: template, wild type; primers, STR. Lane 2: template, wild type; primers, CaMV35S. Lane 3: template, wild type; primers, NPTII. Lane 4: template, wild type; primers, PDK intron. Lane 5: template, TDCi cell line 3; primers, STR. Lane 6: template, TDCi cell line 3; primers, CaMV35S. Lane 7: template, TDCi cell line 3; primers, NPTII. Lane 8: template, TDCi cell line 3; primers, PDK intron. Lane 9: template, TDCi cell line 15; primers, STR. Lane 10: template, TDCi cell line 15; primers, CaMV35S. Lane 11: template, TDCi cell line 15; primers, NPTII. Lane 12: template, TDCi cell line 15; primers, PDK intron

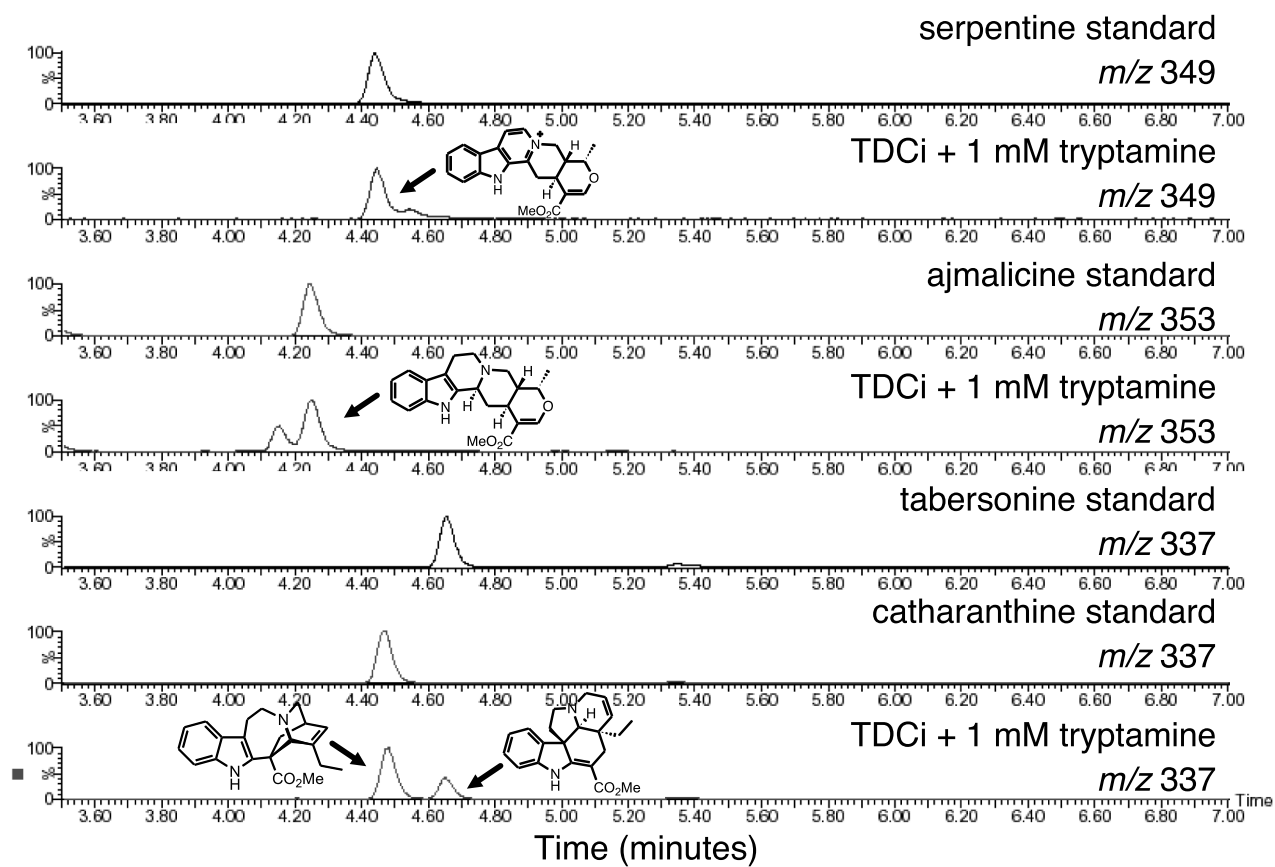


Fig. S2. Extracted LC-MS chromatograms showing the presence of ajmalicine, serpentine, catharanthine and tabersonine. These compounds are only present when tryptamine is added to the culture media. Results using a concentration of 1.0 mM tryptamine are shown. Authentic standards of ajmalicine **3**, serpentine **4**, catharanthine **5**, and tabersonine **6** are used to validate the structural assignments of these compounds.

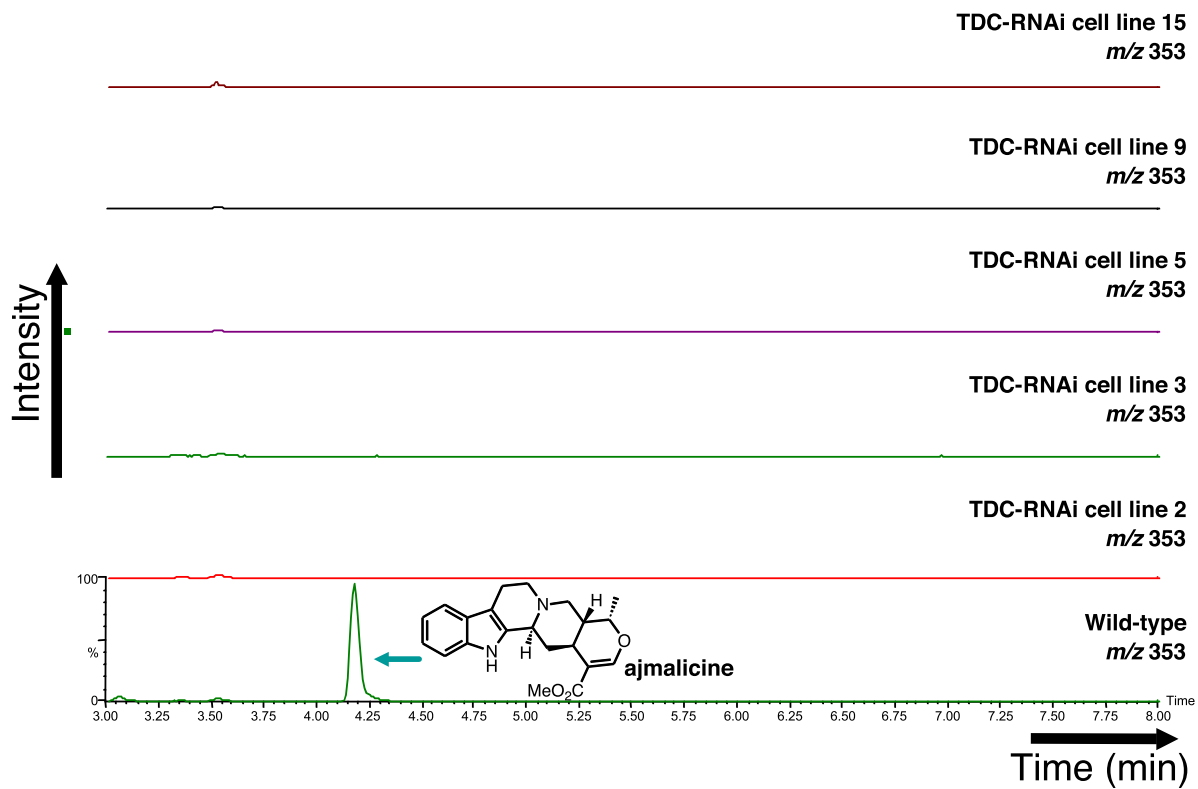


Fig. S3. Extracted LC-MS chromatograms showing the absence of A. ajmalicine, B. serpentine, C. catharanthine and tabersonine in five silenced lines. Wild-type lines are shown for comparison. Note that wild-type lines do not produce catharanthine 5 at *m/z* 337; only tabersonine is observed in wild-type lines at this mass. (D) Total ion counts for five silenced lines.

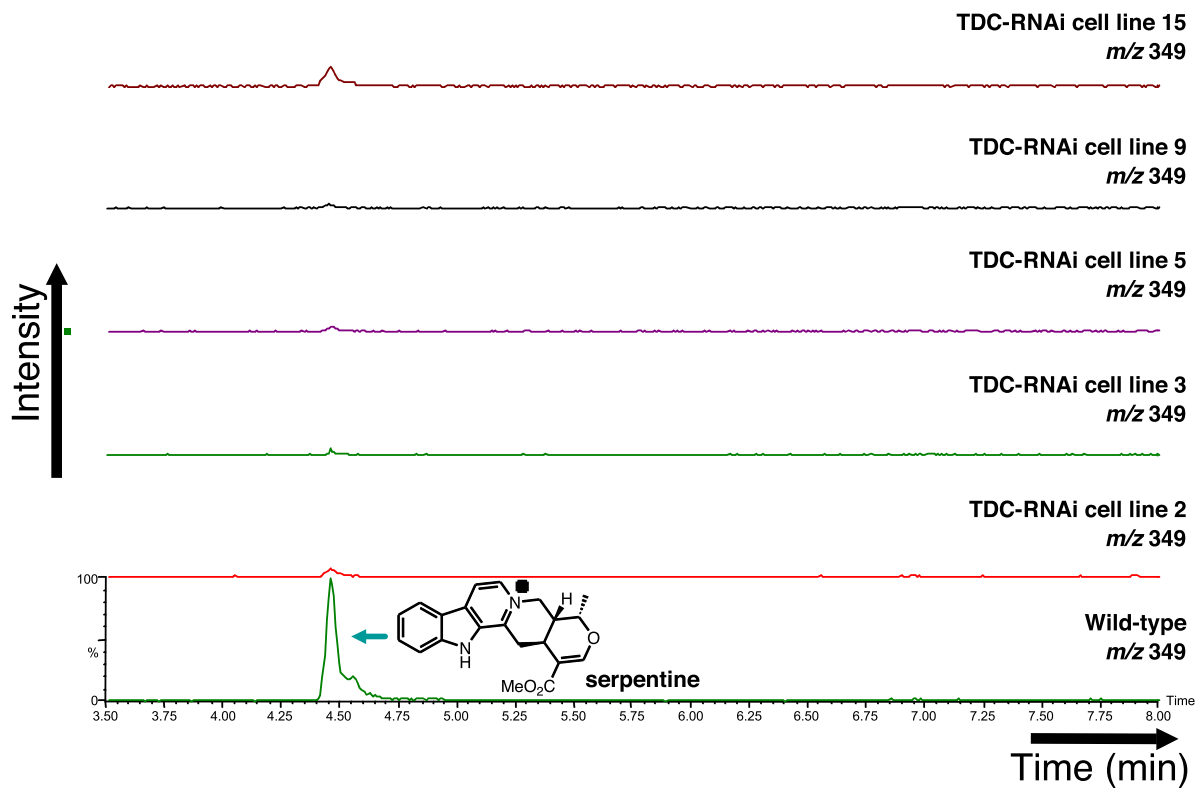


Fig. S3 (continued).

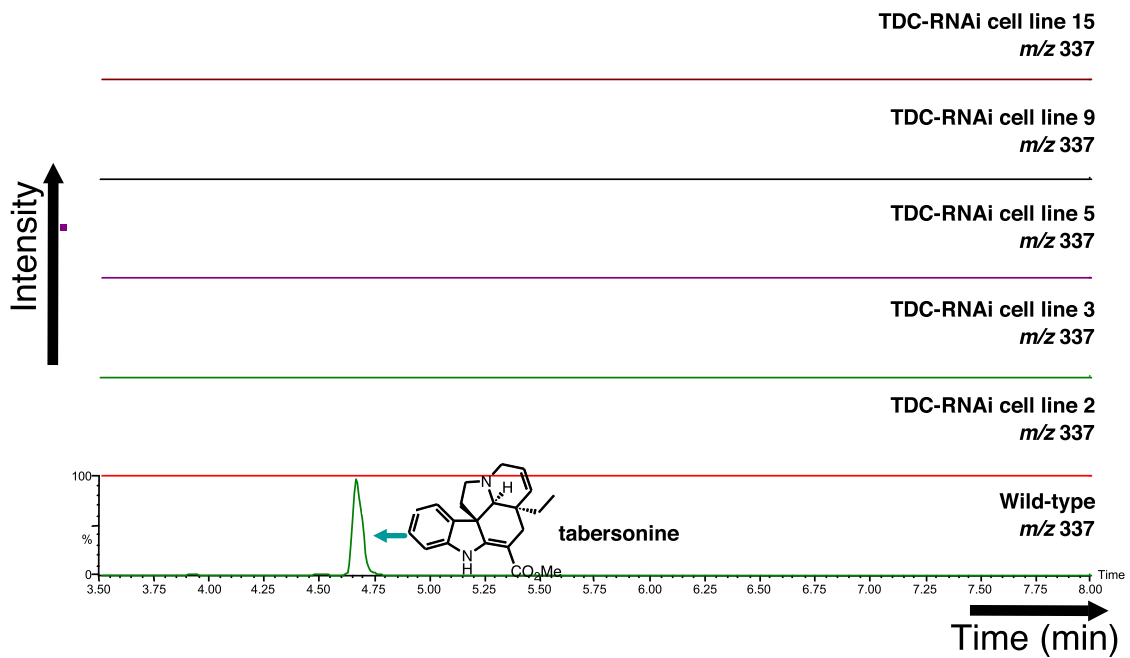


Fig. S3 (continued).

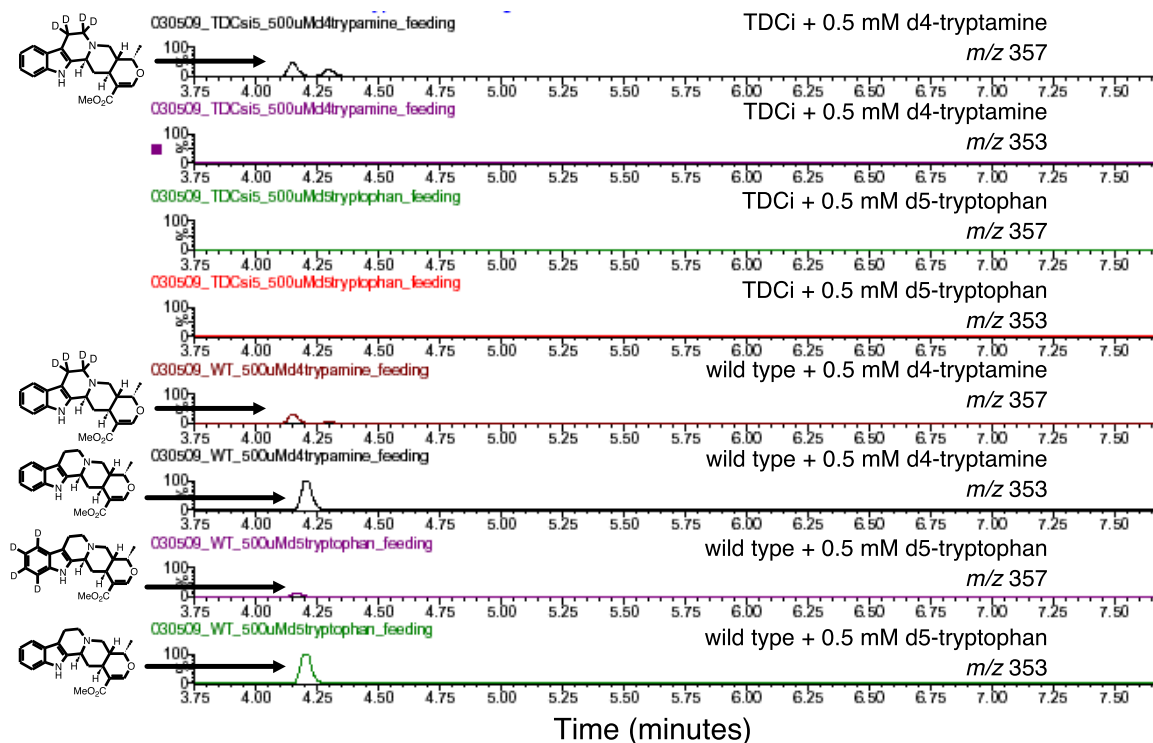


Fig. S4. Extracted LC-MS chromatograms showing the presence of deuterated ajmalicine (A), serpentine (B), and catharanthine and tabersonine (C). In the tryptophan decarboxylase suppressed line, these compounds are only present when $\alpha,\alpha,\beta,\beta$ -d4-tryptamine (CDN Isotopes) is added to the culture media. In the wild-type line, deuterated alkaloids are present when either $\alpha,\alpha,\beta,\beta$ -d4-tryptamine (CDN Isotopes) or 2',4',5',6',7'-d5-tryptophan (CDN isotope) is added to the culture media. Results using a concentration of 0.5 mM d4-tryptamine or 0.5 mM d5-tryptophan are shown.

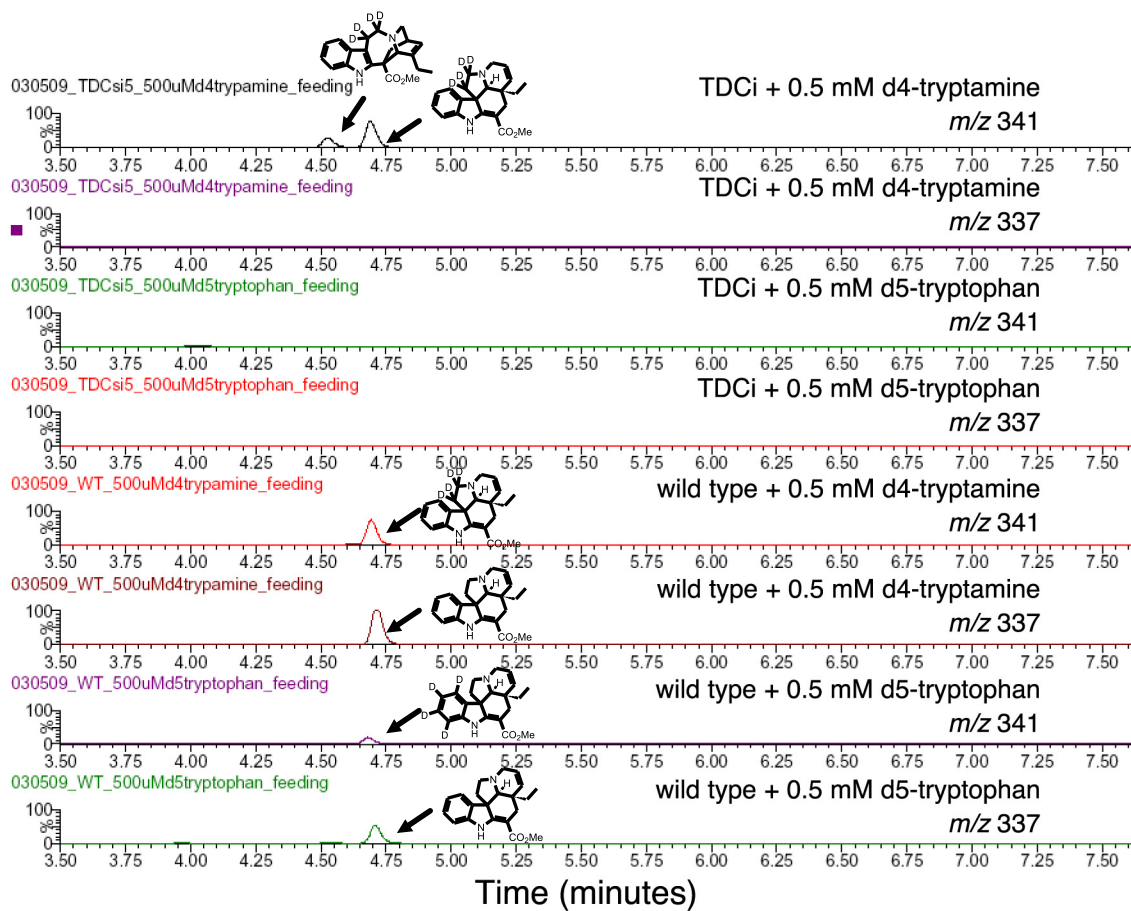


Fig. S4 (continued).

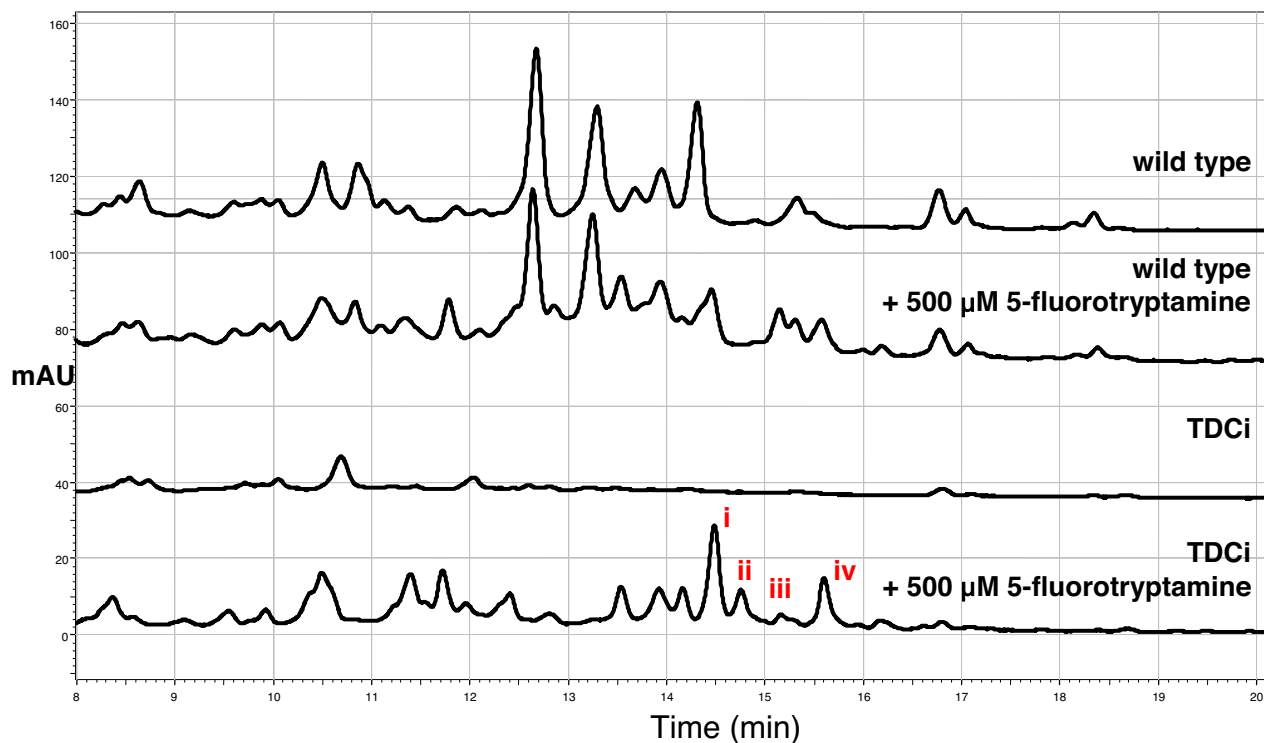


Fig. S5. Metabolite production in wild-type and TDCi line as evidenced by high performance liquid chromatography analysis of *C. roseus* hairy root extracts. The alkaloid extracts were run on a Hibar RT 250–4 prepacked reverse phase column using a gradient of 10–60% acetonitrile/water (0.1% TFA) over 25 min at 1 mL/min. Alkaloids were monitored at 280 nm. (i) Fluoro-ajmalicine 3. (ii) Fluoro-catharanthine 5. (iii) Fluoro-tabersonine 6. (iv) Fluoro-serpentine 4.

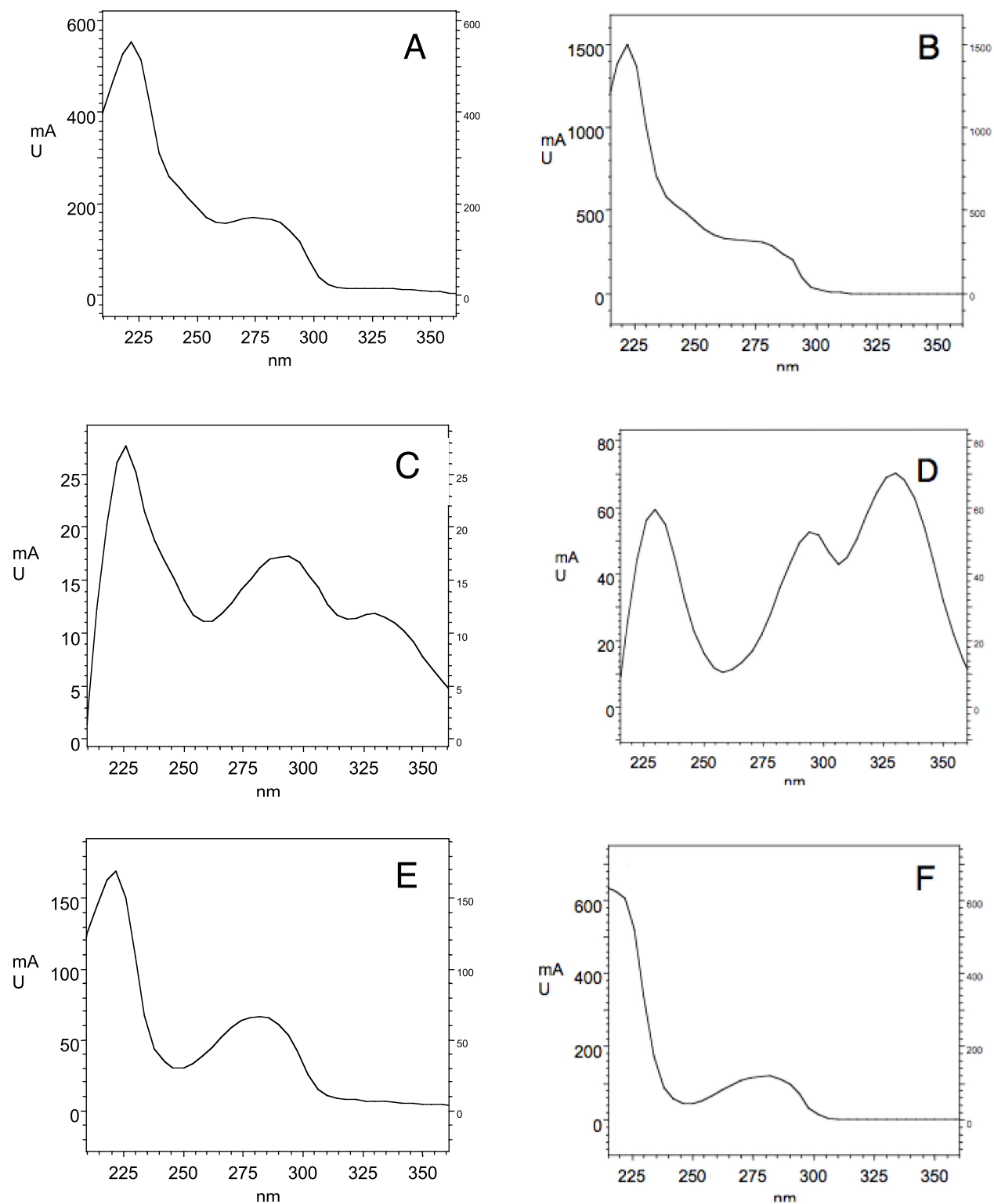


Fig. S6. UV spectra of alkaloid standards and selected unnatural alkaloids from TDCi hairy root fed with 5-fluorotryptamine (0.5 mM). (A) 5-fluoroajmalicine (fraction *i* in Fig. S4). (B) Ajmalicine standard. (C) 5-fluorotabersonine (fraction *iii* in Fig. S4). (D) Tabersonine standard. (E) 5-fluorocatharanthine (fraction *ii* in Fig. S4). (F) Catharanthine standard. (G) 5-fluoroserpentine (fraction *iv* in Fig. S4). (H) serpentine standard.

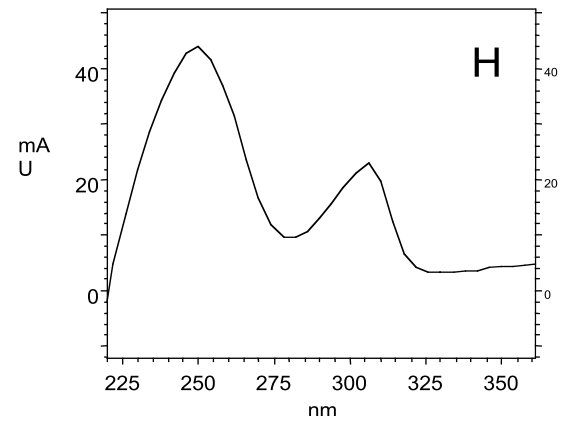
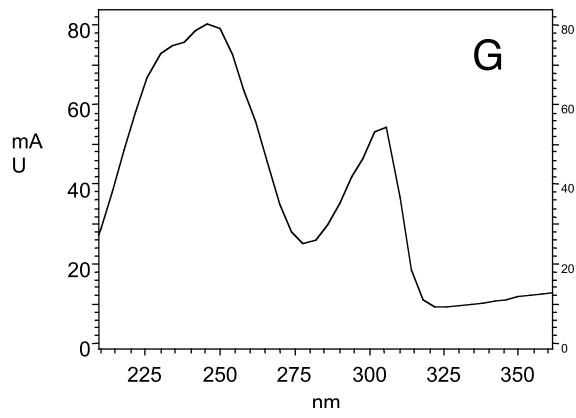


Fig. S6 (continued).

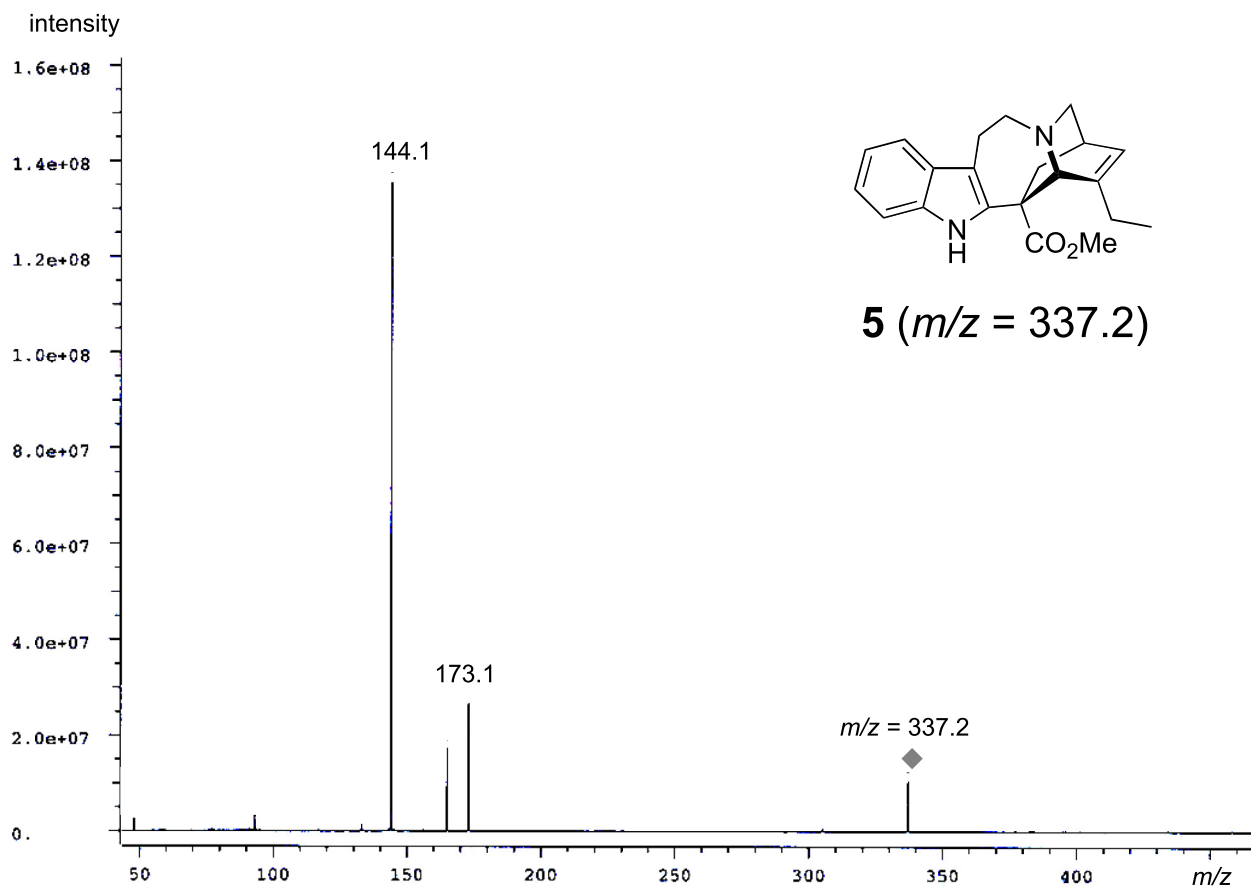


Fig. S7. MS/MS analysis for catharanthine **5** standard (A), fluorinated catharanthine **5a** (B), tabersonine **6** standard (C), and fluorinated tabersonine (D). (A) Catharanthine is identified as the $m/z = 337.2$ ion showing the fragments $m/z = 173.1$ and 144.1 . (B) Fluorinated catharanthine is identified as the $m/z = 355.2$ ($337.2 + 18$) ion showing the fragments $m/z = 191.1$ ($173.1 + 18$) and 162.1 ($144.1 + 18$). (C) Tabersonine is identified as the $m/z = 337.2$ ion showing the fragments $m/z = 305.2$, 277.2 , 249.1 , 228.1 , 196.1 and 168.1 . (D) Fluorinated tabersonine is identified as the $m/z = 355.2$ ($337.2 + 18$) ion showing the fragments $m/z = 323.2$ ($305.2 + 18$), 295.2 ($277.2 + 18$), 267.1 ($249.1 + 18$), 246.1 ($228.1 + 18$), 214.1 ($196.1 + 18$), and 186.1 ($168.1 + 18$).

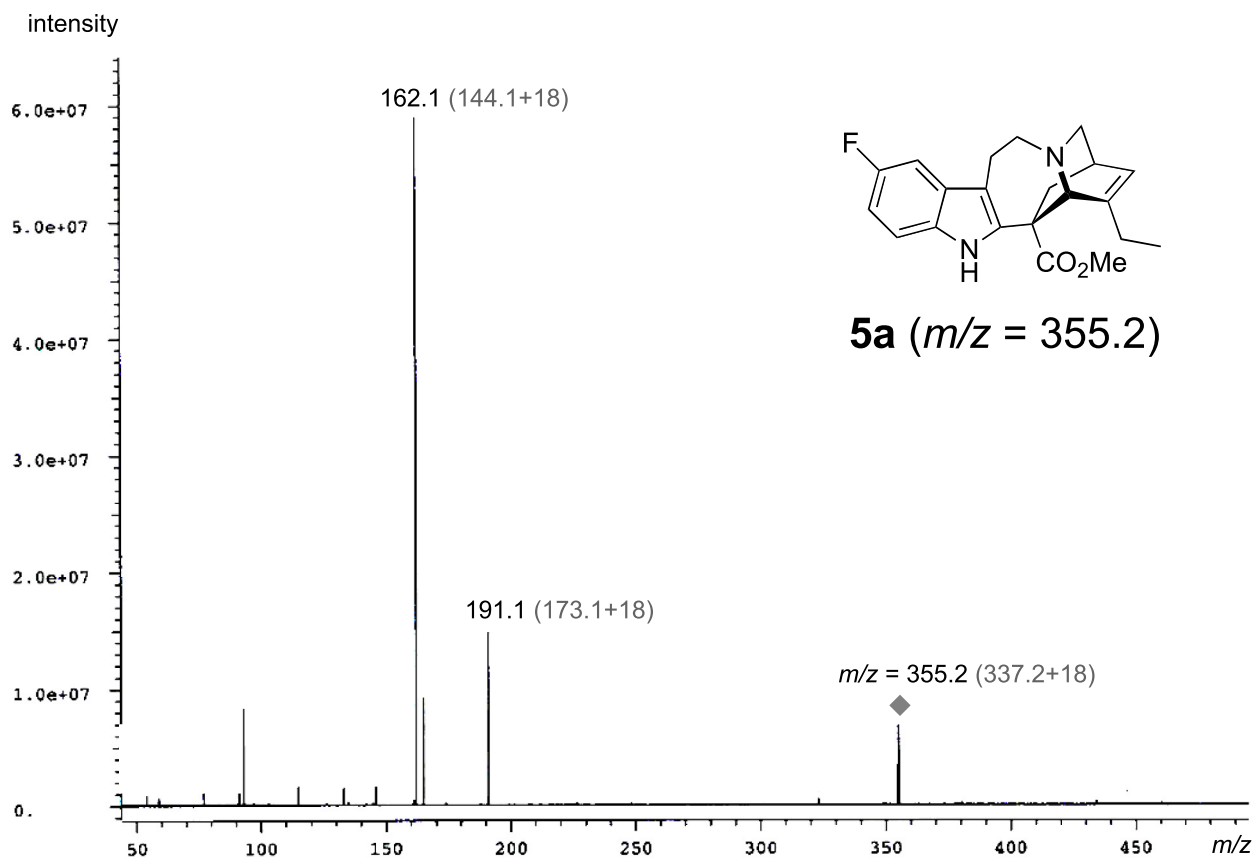


Fig. S7 (continued).

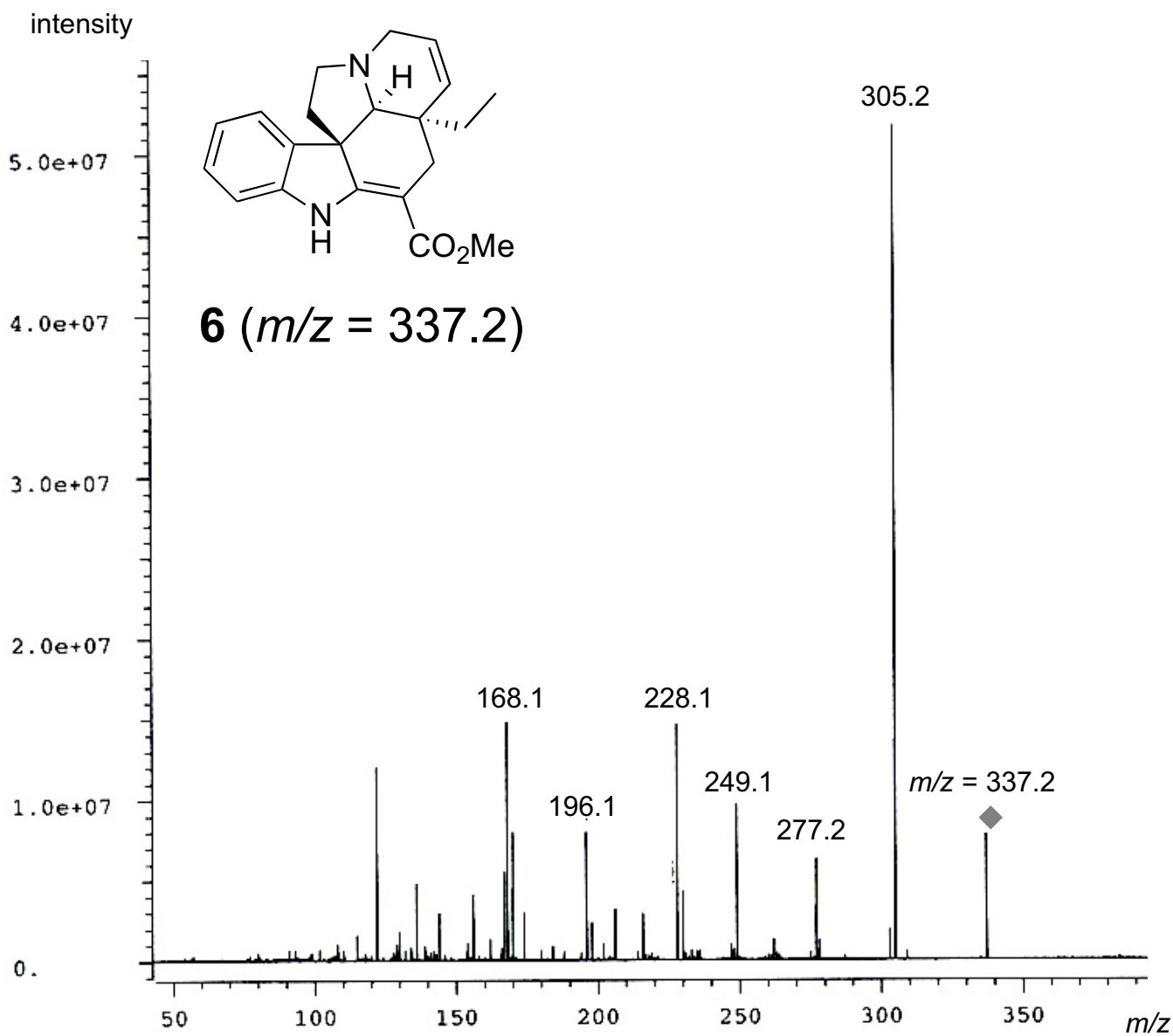


Fig. S7 (continued).

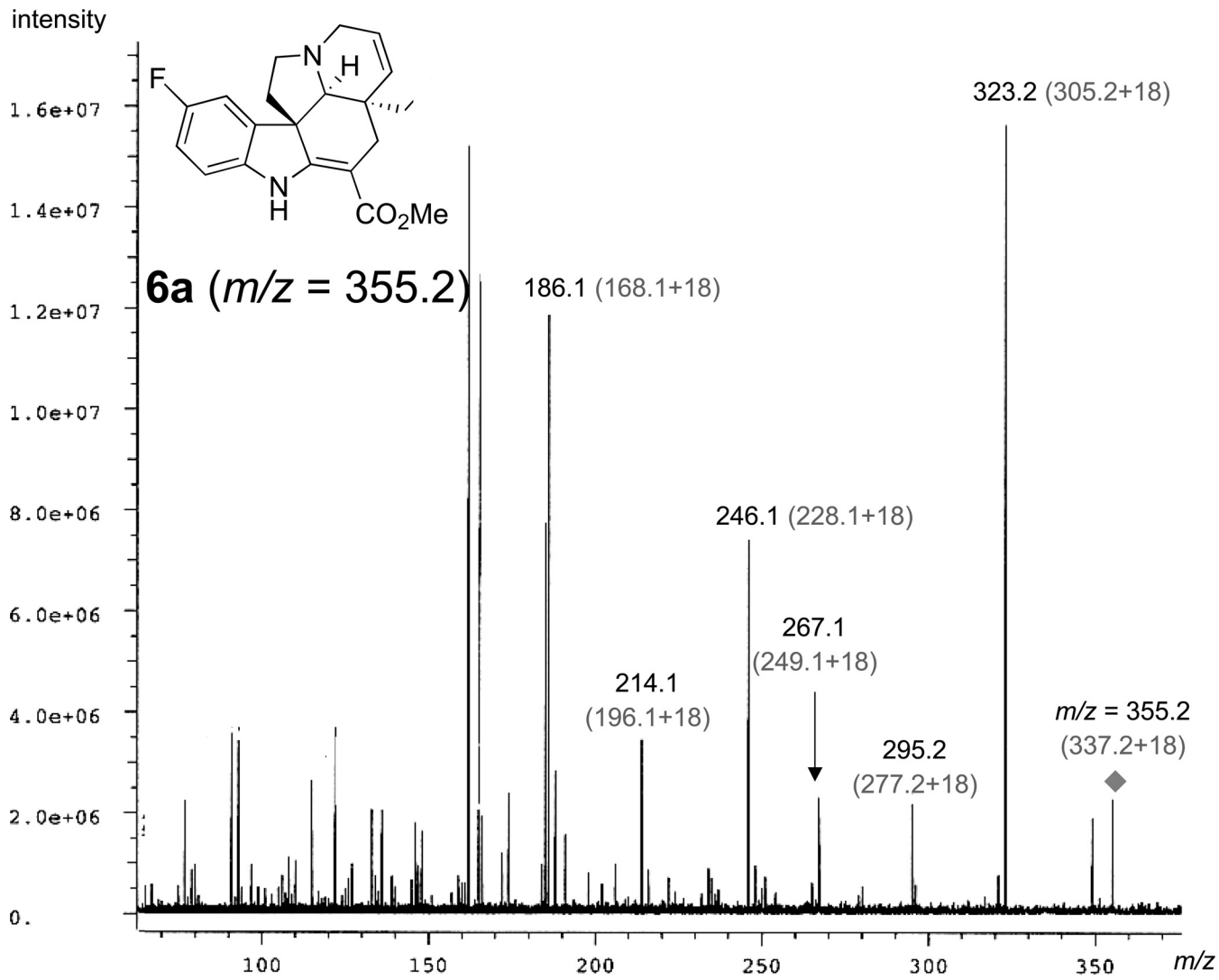


Fig. S7 (continued).

Stability of Alkaloid Production Suppression in TDCi Hairy Roots

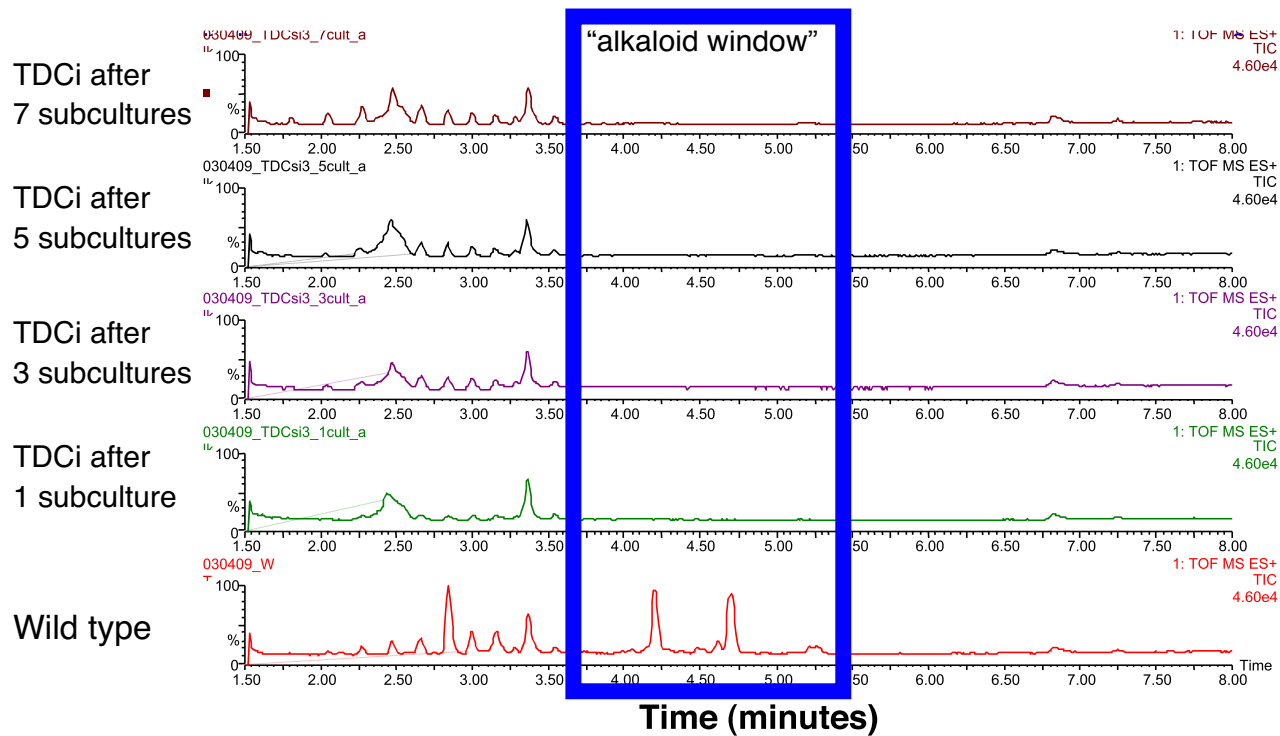


Fig. S8. Metabolite production in TDCi hairy roots after 1, 3, 5 and 7 subcultures as evidenced by LC-MS analysis of *C. roseus* extracts. "Alkaloid window" represents the range of retention time that natural *C. roseus* alkaloids usually elute.



Fig. 59. (a) Two-week-old wild-type hairy roots in solid Gamborg's B5 media.



Fig. S9 (continued). (b) Two-week-old TDCi hairy roots in solid Gamborg's B5 media.

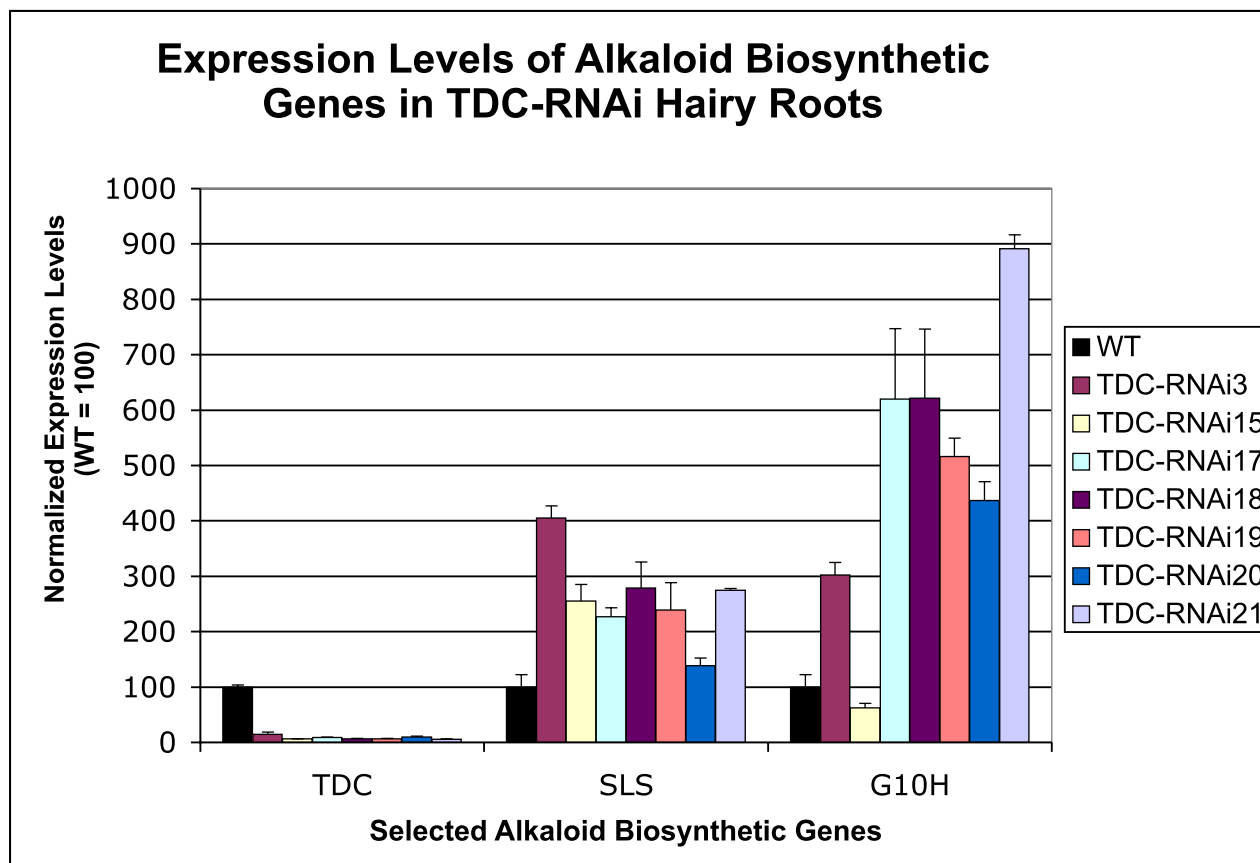


Fig. S10. Expression levels of SLS and G10H in 7 different TDCi lines measured by RT PCR. Expression levels of the silenced lines are normalized to the expression levels in the wild-type hairy root line. TDC (tryptophan decarboxylase) expression levels are shown for comparison. SLS (secologanin synthase), G10H (geraniol-10-hydroxylase).

Other Supporting Information Files

[Table S1](#)