

Supplementary file

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Figure S1. A multiple alignments of amplified AHBA synthase gene obtained from leaves stems, and roots of *G. heterophylla* originated from South Africa from 2017 and 2018 collections using global alignment from Clone Manager 9 Professional edition. The green highlighted indicates non-matching nucleotides, while the dot indicates the identical nucleotide. Am = *Actinosynnema mirum* (DMS 43827), the microbial reference. QH = *G. heterophylla* cultivating in our laboratory. SeL17 = leaves of *G. heterophylla* from 2017 collection. SeS17 = stems of *G. heterophylla* from 2017 collection. SeR17 = roots of *G. heterophylla* from 2017 collection. SeL18 = leaves of *G. heterophylla* from 2018 collection. SeS18 = stems of *G. heterophylla* from 2018 collection. SeR18 = roots of *G. heterophylla* from 2018 collection.



Figure S2. Multiple amino acid alignments of the translated AHBA synthase gene obtained from leaves stems, and roots of *G. heterophylla* originated from South Africa and the reference AHBA synthase enzyme encoded by the rifK gene from *Amycolatopsis mediterranei*. The highlighted amino acids in red and boxes indicate conserved active residues of the AHBA synthase enzyme from *A. mediterranei*.

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rcbl_GH      1 CAGAGACTAAAGCGAGTGTGGATTCAAGGCTGGCGTTAAAGATTATAAATTGACTTATTATCTCTGACTATGAAACCAAGATACTGATATCTTGGCAGCATTCCGAGTAACCTCAACCTGGAGTTCGGCTGAA
rcbl_SeL17   1 .....
rcbl_SeL18   1 .....
rcbl_SeR17   1 .....
rcbl_SeR18   1 .....
rcbl_SeS17   1 .....
rcbl_SeS18   1 .....

rcbl_GH      141 GAAGCAGGGGCGCGGTAGCTGCTGAATCTTCTACTGTTACATGGACAACCTGTGTGGACCGATGGGCTTACCAGTCTTGATCGTTACAAAGGACGATGCTACCCATCGAGCCCGTGTGTGGAGAAGAAATCAATTAT
rcbl_SeL17   141 .....
rcbl_SeL18   141 .....
rcbl_SeR17   141 .....
rcbl_SeR18   141 .....
rcbl_SeS17   141 .....
rcbl_SeS18   141 .....

rcbl_GH      281 TGCTTATGTAGCTTATCCTTTAGACCTTTTCGAAGAAGGTTCTGTACTACATGTTTACTTCCATTGTGGGTAATGTCCTTTGGGTTCAAAGCCCTGGCGCTCTACGCTCTGGAGGATTGGGAATCCCCCTGCTTAT
rcbl_SeL17   281 .....
rcbl_SeL18   281 .....
rcbl_SeR17   281 .....
rcbl_SeR18   281 .....
rcbl_SeS17   281 .....
rcbl_SeS18   281 .....

rcbl_GH      421 CTAAAACTTTCCAAAGGCCGCGCATGTTATCCAAGTTGAGAGAGATAAATTGAACAAGTATGGACGCCCTCTATTGGGGTGACTATTAAACCTAAATTGGGATTATCCGCTAAGAATTATGTTAGAGCAGTTTATGAA
rcbl_SeL17   421 .....
rcbl_SeL18   421 .....
rcbl_SeR17   421 .....
rcbl_SeR18   421 .....
rcbl_SeS17   421 .....
rcbl_SeS18   421 .....

rcbl_GH      561 TGTCCTCG
rcbl_SeL17   561 .....
rcbl_SeL18   561 .....
rcbl_SeR17   561 .....
rcbl_SeR18   561 .....
rcbl_SeS17   561 .....
rcbl_SeS18   561 .....

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Figure S3. A multiple alignments of amplified rcbL gene obtained from leaves stems, and roots of *G. heterophylla* originated from South Africa from 2017 and 2018 collections using global alignment from Clone Manager 9 Professional edition. The dot indicates the identical nucleotide. QH = *G. heterophylla* cultivating in our laboratory, the authentic material. SeL17 = leaves of *G. heterophylla* from 2017 collection. SeS17 = stems of *G. heterophylla* from 2017 collection. SeR17 = roots of *G. heterophylla* from 2017 collection. SeL18 = leaves of *G. heterophylla* from 2018 collection. SeS18 = stems of *G. heterophylla* from 2018 collection. SeR18 = roots of *G. heterophylla* from 2018 collection.

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MatK_GH      1 AGATGTTTCTTTGCAITTTATTACGATTTGTTCTCCATGAGTATTGAGCTTGGAAATAGTCTTCTTACTCCAAAGAAATCCATTACATTTTTCACAAAGTAAATCCAGATTTTCTTGTCTCTATATAATCTTATG
MatK_SeL17   1 .....
MatK_SeL18   1 .....
MatK_SeR17   1 .....
MatK_SeR18   1 .....
MatK_SeS17   1 .....
MatK_SeS18   1 .....

MatK_GH      141 TGTGGATACGAATCTATCTTTCTTTCTACGTAACACAGATTCCTCAITTAGCGTCAACATCCCTCTCGGGTCTCTTGTAGCGAATCCATTCTATGGAATAATAGAACATCTTCAGAGTCTTCTCTAATTATTTT
MatK_SeL17   141 .....
MatK_SeL18   141 .....
MatK_SeR17   141 .....
MatK_SeR18   141 .....
MatK_SeS17   141 .....
MatK_SeS18   141 .....

MatK_GH      281 CAGGTTATCCTTTGGTTGTGAAGGATCCTTGACACATTATGTTAGATATCAAGGAAATTCATTCTGGCTTCAAAAGATATGCCATTTCTGATGAATAAATGGAAATTTTACCTTGTTAATTATGTCATGTCATTT
MatK_SeL17   281 .....
MatK_SeL18   281 .....
MatK_SeR17   281 .....
MatK_SeR18   281 .....
MatK_SeS17   281 .....
MatK_SeS18   281 .....

MatK_GH      421 TTTTGGGGGTATCAACCGGAAGGATCTATATAACCAATTATCCAGCATTCCTCGACTTTTATGGCTATCTTCAAGTGTGGGACTAAATCTTCAGTGGTACGGGATCAATGGTGGCAATGCATTTCTAATAG
MatK_SeL17   421 .....
MatK_SeL18   421 .....
MatK_SeR17   421 .....
MatK_SeR18   421 .....
MatK_SeS17   421 .....
MatK_SeS18   421 .....

MatK_GH      561 ATACGCTATGAGAACTCGATACAGAGTTCACCTTATTTCTTTGATTGGATTATTGGCAAAAGCGAGATTTGTAACTATTAGGACATCCATTAGTAAACGACCCGGGCTGATTCATCGGATTCGGATATTATC
MatK_SeL17   561 .....
MatK_SeL18   561 .....
MatK_SeR17   561 .....
MatK_SeR18   561 .....
MatK_SeS17   561 .....
MatK_SeS18   561 .....

MatK_GH      701 GACCGATTGTGCGTATATGCACAAATCTTTCTCATTATTACAGTGGATCCTCAAAAAAAGAGTTTGTATCGAATAAATATGTAC
MatK_SeL17   701 .....
MatK_SeL18   701 .....
MatK_SeR17   701 .....
MatK_SeR18   701 .....
MatK_SeS17   701 .....
MatK_SeS18   701 .....

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Figure S4. A multiple alignments of amplified matK gene obtained from leaves stems, and roots of *G. heterophylla* originated from South Africa from 2017 and 2018 collections using global alignment from Clone Manager 9 Professional edition. The dot indicates the identical nucleotide. QH = *G. heterophylla* cultivating in our laboratory, the authentic material. SeL17 = leaves of *G. heterophylla* from 2017 collection. SeS17 = stems of *G. heterophylla* from 2017 collection. SeR17 = roots of *G. heterophylla* from 2017 collection. SeL18 = leaves of *G. heterophylla* from 2018 collection. SeS18 = stems of *G. heterophylla* from 2018 collection. SeR18 = roots of *G. heterophylla* from 2018 collection.

Table S1. Overview of the halogenase gene received from *A. mirum* (our reference) and presented in the roots of *G. heterophylla* collected from South Africa.

Name of the samples	Sequence length (bp)	Accession number	Microorganism	GenBank ID	Sequence ID	% homology
<u>Reference</u>						
Am_Halogenase	454	OL944594	<i>Actinosynnema mirum</i> DSM 43827	ACU37095.1	CP001630.1	100%
<u>2017 collection</u>						
2017-SeR-Halogenase-1	449	OK754597	<i>Catenulispora acidiphila</i> DSM 44928	ACU69473.1	CP001700.1	78%
2017-SeR-Halogenase-2	512	OK649330	<i>Amycolatopsis</i> sp. WAC1375	AGE12641.1	JX576190.1	85%
2017-SeR-Halogenase-3	462	OK649333	<i>Variovorax</i> sp. PAMC28562	QNK76028.1	CP060296.1	80%
2017-SeR-Halogenase-4	476	OK754598	<i>Amycolatopsis</i> sp. YIM 10	QFU88391.1	CP045480.1	81%
2017-SeR-Halogenase-5	494	OK649331	<i>Streptomyces chartreusis</i> ATCC 14922	QEV72535.1	CP023689.1	78%
<u>2018 collection</u>						
2018-SeR-Halogenase-1	456	OK754599	<i>Urbifossiella limnaea</i> ETA A1	QDU18131.1	CP036273.1	80%
2018-SeR-Halogenase-2	474	OK649332	<i>Amycolatopsis</i> sp. WAC1375	AGE12641.1	JX576190.1	86%
2018-SeR-Halogenase-3	457	OK649335	<i>Catenulispora acidiphila</i> DSM 44928	ACU69473.1	CP001700.1	78%
2018-SeR-Halogenase-4	443	OK649334	<i>Variovorax</i> sp. PAMC28562	QNK76028.1	CP060296.1	80%
2018-SeR-Halogenase-5	456	OK649336	<i>Catenulispora acidiphila</i> DSM 44928	ACU69473.1	CP001700.1	78%
2018-SeR-Halogenase-6	458	OK754600	<i>Amycolatopsis</i> sp. YIM 10	QFU88391.1	CP045480.1	82%

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa.

Name of the samples	Sequence length (bp)	Accession number	Sequences
Reference			
Am_Halogenase	454	OL944594	GTGCGGGAGGGCGCGCAGGTCGTCGGGCTGCTGGAGGAGGGCGGCCGGG TGGTGGGCGTGCGCTACCGCGAGGGCGGGGTCGAGCGCGAGGAGCGGGC CCGGTACGTGGTGGACGCCACCGGCCGGGCAGGCGTGGTCGCCAACCGGT TCGGGCTGCGGCGGATGATCGAGGACCTGCGCATGGTGGCGGTGTTCCAC CACCGCGACGGGCTGGACGAGGCGCACAAACCCGGCCACGAGGGCGACA TCCAGGTCGGCAGTCACGCGGACGGGTGGATCTGGGCGATCCCGCTGTCTG GCGGACCGGATCAGCGTGGGCACGGTGATGCACCGCGACCGGCTGCGCG GTCGCACCCCCGCCGAGGCGTTCGCCGAGCACGTCGAGCGGGTGCCAGG ATCAACCAGCGGCTCACCGGCACACGGCGACCTCGGACTTCTGGGTGGA GACCzGACA
2017 collection			
2017_SeR_Halogenase_1	449	OK754597	TCCTCGACCTGTTGGGCGCCCGCGAAACGGTGGCGAATCACGGCTTCGTG CGCAAGGACGGCGCGTACTTCGAATGGGGCCCGGAGAACTGGGACCTCG ACTTCAACCACCTGACCGGCGCCAACGGCTACAGCTACCAGGTGATCCGC TCCGAGTTCGACCACCTGTTACTCAAACGGGCCGCGGACAACGGCGTCGA TGTCGCGAGGGGGTCAGGGTCGTGGAGCTGACCTTCGACGATGAGCGGC CGGTCGCCGCGCGCTGGGTGGCTACCGGTGACCGGGAAACCGGCGGTACG ATCGAGTTCGACTTCCTGGTCGACGCCTCTGGCCGGGCGGCGTGATGGCC ACCAAGTACCTGCGCAACCGCACCTACCTGGAGGCGTTCAGGAACGTCGG CGTCTGGTCGTACTGGCGGGGGTTACCCCGCTCGACCGCGGTCCGAAG

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa. (continue)

Name of the samples	Sequence length (bp)	Accession number	Sequences
2017 collection (continue)			
2017_SeR_Halogenase_2	512	OK649330	GCTTTCCCGCGGTACCAGATCGGGGAGTCGTTGCTGCCGTCGACGGTCCAT GGCGTGTGCCGCATGCTCGGCGCCGCGGACGAACTGGCGGAGGCGGGTTT CCCGGTGAAGCGGGGCGGCACGTTCCGCTGGGGCGCTCGTCCGGAGCCGT GGACGTTCTCCTTCTCTGTCTCCCCGAGGATCACGGGTCCGTCGTCTCGC CTATCAGGTGGAACGGGCGCGGTTTCGACCAGATCTTGCTGAACAACGCCA AGCGCAAGGGTGTGGTGGTGCGGGAGGGGAGCACGGTCACCGGTGCGCT GGAGGAGGGTGAGCGTGTTACGGGTTTGCGTTACGCCGATCCCGACGGTA ACCAGCACGAGGTGTCCGCGACTTTCGTGATCGACGCGTCGGGCAACAAG AGTCGTCTGTACTCCAATGTCGGTGGCTCGCGGAACTATTCGGAGTTCTTC CGCAGCTTGGCGCTGTTTCGGCTACTTCGAGGGCGGCAAGCGGCTGGCCGC TCCGTACTC
2017_SeR_Halogenase_3	462	OK649333	GTCGCGCTGTTTCGACAGGCTCGGCGTACGCGACCAGATCGAGCGCATCGG CATGCCCAAGTTTGGCGTCGAATTCGTGTCGCCGGATCACGATCGCGCCGC TTTCGTGCAATTCGCCGAGGCCTGGGACAAGTCGATGCCCTATGCCTGGCA GGTGCGACGCTCCGAAATGGACGAGATCCTCTTTCGCAACGCCGCGGCGC GGGGCGCGGAGGCCATCGAAGGCTGCCGGGTGCGCGAAGTCAGCTTCGA CGCCGATGGTGCCACGTGCAGGCGGTGCTCGACGATGGAACCCGGCGTC AATGGCGGGCGCGCTTCGTACTCGATGCCTCCGGCCGCGACACCTTCCTGT CGAACAAGCTCAAGGCCAAGCTGAAGAACCCGCGCCACAACAGCTCTGC GCTGTTTCGGCCATTTTCGTGAACGCCGAGCGACTGCCCGGCAAGCTCGAAG GCAACATCACG

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa. (continue)

Name of the samples	Sequence length (bp)	Accession number	Sequences
2017 collection (continue)			
2017_SeR_Halogenase_4	476	OK754598	GCACGGGATCTGCGCCATGCTCGGCGTCCGGGACGAGGTCGAGCGGGCCG GGTTCGTCCGGAACGGGGCGGCACCTTCAAATGGGGGTCTGAACCCGGAC CCGTGGACGTTTCGCGTTCGCCGCGTCGGAGCGGATGGCGGGGCCGACGTC CTACGCCTACCAGGTCGAGCGCACCCGCTTCGACGCCCTGCTGCTCGACA ACGCCGTGCGGTGCGGCGCCGACGTCCGGCAGGGGCATCGCGTGCTCGGC ACGCTGCGCGACGAGGACGGCCGGATCGCCGGTGCCCGCTACCTCGACGA CGCGGGGCGGGAGGGGCACGCCACCGCGCGGTTTCGTCTGTTGACGCGTCG GGCAACGGCAGCACGCTGCACAACGACATCGGCGGCGCCCGCGAGTACT CACCGCATTCGCGCAACCTGGCGCTGTTTCGGCTACTTCGCGGGCGGCCGCC GGGCACCGGAACCCAACGCGGGCAACA
2017_SeR_Halogenase_5	494	OK649331	CACGGCCTGTGCCGGCTGCTCGGCGTGGCCGACGAGGTGGCCGGCGCCGG GTTACCCCTCAAACGCGGCGGCACGTTCCGCTGGGGCCGTAGCGCAGAGC CCTGGCAGTTCAGCTTCGCCATGTCGCCCCGGGTGCCGGAGCCGATGTCCA CCGCGTTCCAGGTCGAGCGGTCCCGGTTTCGACGAGATCCTGCTGCGCAAC GCCGCCGACAACGGCGTGGTCTCGAGAGGGCAACCGGGTGCGCGCGG TCACCCGGGACGGCACCGGCCGGGTTCGACGGGGTCGAGTACACCGGCCG GGACGGCGTGCGCACACCGTGCGCGCCCGCTACGTGGTGGACGCGTCGG GCAACACCAGCAGGATCCACGGTCAGGTTCGGCGCCAGGGTGCGGTCCGA CTTCTTCGCGACCTCGCGGTGTTTCGGCTACTTCGCCGGCGGTGCCCGGCT GCCGCGACCGCACAGCGGCAACATCTTCTGCGCCACCTTCGACGC

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa. (continue)

Name of the samples	Sequence length (bp)	Accession number	Sequences
2018 collection			
2018_SeR_Halogenase_1	456	OK754599	AGCGGCTCGGCATGCTCGACAAGATGAAGGGGAGCCACTTCGTCAAGAA GTACAGCGTCCAGTTCGTCAACCAGCACGGCAGGCTGTCCGAGCCGTTCT ATTTCCTCGACCACCGGCCGCACGAGTCGTGCGAGACGTGGCAGGTCAAG CGCGAGGAGCTTGACGTGGCGCTGCTCGACAACGCCCCGCGAGCACGGCGC CGAGGTGCATGAAGGCGTGCGCGTCCTGAACGTGCTGTTTCGAGGGGGACC GGGCCGTGCGCGTCCGCATCCAGGACGAGGCGGGGGCCGAGCGGGAGGT GCGGGCGAAGGTCATCGTGGACGCGAGCGGGCAGGGGTCGTGATCATG AGCCGGCTCGGCCTGCGCGAGTGGGACCCGGTCCTCAAGAAGGCCGCCCT GTGGACGTACTGGGAGGGCGCCTACCGCGACACCGGCAAGGACGAGGGG GCGACGCTCG
2018_SeR_Halogenase_2	474	OK649332	CATGGCGTGTGCCGCATGCTCGGCGCCGCGGACGAACTGGCGGAGGCGGG TTTCCCGGTGAAGCGGGGCGGCACGTTCCGCTGGGGCGCTCGTCCGGAGC CGTGGACGTTCTCCTTCTGTCTCCCCGAGGATCACGGGTCCGTGCTCGTT CGCCTATCAGGTGGAACGGGCGCGGTTTCGACCAGATCTTGCTGAACAACG CCAAGCGCAAGGGTGTGGTGGTGCGGGAGGGGAGCACGGTACCCGGTGC GCTGGAGGAGGGTGAGCGTGTTACGGGTTTTCGTTACGCCGATCCCGACG GTAACCAGCACGAGGTGTCCGCGACTTTCGTGATCGACGCGTCGGGCAAC AAGAGTCGTCTGTACTCCAATGTTCGGTGGCTCGCGGAACTATTTCGGAGTTC TTCCGCAGCTTGGCGCTGTTTCGGCTACTTCGAGGGGCGGCAAGCGGCTGGCC GCTCCGTACTCGGGGAACATC

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa. (continue)

Name of the samples	Sequence length (bp)	Accession number	Sequences
2018 collection (continue)			
2018_SeR_Halogenase_3	457	OK649335	CCTCGACCTGTTGGGCACCCGCGAAACGGTGGCGAATCACGGCTTCGTGC GCAAGGACGGCGCGTACTTCGAATGGGGCCCGGAGAACTGGGACCTCGA CTTCAACCACCTGACCGGCGCCAACGGCTACAGCTACCAGGTGATCCGCT CCGAGTTCGACCACCTGTTACTCAAACAGGCCGCGGACAACGGCGTCGAT GTCCGCGAGGGGGTCAGGGTCGTGGAGCTGACCTTCGACGATGAGCGGCC GGTCGCCGCGCGCTGGGTGACTACCGGTGACCGGGAAACCGGCGGTACGA TCGAGTTCGACTTCCTGGTCGACGCCTCTGGCCGGGCGGCGTGATGGCCA CCAAGTACCTGCGCAACCGCACCTACCTGGAGGCGTTCAGGAACGTCGGC GTCTGGTCGTACTGGCGGGGGGTTACCCCGCTCGACCGCGGTCCGAAGGG CGCCATC
2018_SeR_Halogenase_4	443	OK649334	GTTCGACAGGCTCGGCGTACGCGACCAGATCGAGCGCATCGGCATGCCCA AGTTCGGCGTCGAATTCGTGTCGCCGGATCACGATCACGCCGCTTTCGTCTG AATTCGCCGAGGCCTGGGACAAGTCGATGCCCTATGCCTGGCAGGTGCGA CGCTCCGAAATGGATGAGATCCTTTTTTCGCAACGCCGCGGCGCGGGGCGC GGAGGCCATCGAAGGCTGCCGGGTGCGCGAAGTCAGCTTCGACGCCGACG GTGCCCACGTGCAGGCGGTGCTCGACGATGGAACCCGGCGTCAATGGCGG GCGCGCTTCGTACTCGATGCCCCCGGCCGCGACACCTTCCTGTCTGAACAAG CTCAAGGCCAAGCTGAAGAACCCGCGCCACAACAGCTCTGCGCTGTTTCGG CCATTCGTGAACGCCGAGCGACTGCCCCGCAAGCTCGAAG

Table S2. Obtained halogenase gene sequences from *A. mirum* (our reference) and the roots of *G. heterophylla* collected from South Africa. (continue)

Name of the samples	Sequence length (bp)	Accession number	Sequences
2018 collection (continue)			
2018_SeR_Halogenase_5	456	OK649336	ATCCTCGACCTGTTGGGCGCCCGCGAAACGGTGGCGAATCACGGCTTCGT GCGCAAGGACGGCGCGTACTTCGAATGGGGCCCGGAGAACTGGGACCTC GACTTCAACCACCTGACCGGCGCCAACGGCTACAGCTACCAGGTGATCCG CTCCGAGTTCGACCACCTGTTACTCAAACAGGCCGCGGACAACGGCGTCG ATGTCCGCGAGGGGGTCTGGGTCTGTGGAGCTGACCTTCGACGATGAGCGG CCGGTCGCCGCGCGCTGGGTGGCTACCGGTGACCGGGAAACCGGCGGTAC GATCGAGTTCGACTTCCTGGTCGACGCCTCTGGCCGGGGCCGGCGTGATGGC CACCAAGTACCTGCGCAACCGCACCTACCTGGAGGCGTTCAGGAACGTCTG GCGTCTGGTCGTACTGGCGGGGGGTACCCTGCTCGACCGCGGTCCGAAG GGCGCC
2018_SeR_Halogenase_6	458	OK754600	GCACGGGATCTGCGCCATGCTCGGCGTCCGGGACGAGGTCGAGCGGGCCG GGTTCGTCCGGAACGGGGCGGCACCTTCAAATGGGGGTCTGAACCCGGAC CCGTGGACGTTTCGCGTTCGCCGCGTCGGAGCGGATGGCGGGGCGGACGTC CTACGCCTACCAGGTCGAGCGCACCCGCTTCGACGCCCTGCTGCTCGACA ACGCCGTGCGGTGCGGCGCCGACGTCCGGCAGGGGCATCGCGTGCTCGGC ACGCTGCGCGACGAGGACGGCCGGATCGCCGGTGCCCGCTACCTCGACGA CGCGGGGCGGGAGGGGCACGCCACCGCGCGGTTCGTCTGTGGACGCGTCG GGCAACGGCAGCACGCTGCACAACGACATCGGCGGCGCCCGCGAGTACT CACCGCATTCCCGCAACCTGGCGCTGTTTCGGCTACTTCGCGGGCGGCGCCG GGCACCGG

Table S3. Statistic analysis of the AHBA synthase gene expression of *G. heterophylla* collected from South Africa in 2017 and 2018 and cultivated at our laboratory in Germany.

		2017-SeL	2017-SeS	2017-SeR	2018-SeL	2018-SeS	2018-SeR	GH-Lab
2017-SeL	Mean difference	—	-0.0278	0.0102	0.01313	0.01437	0.00537	-0.02963
	<i>p</i> -value	—	0.083	0.004	0.004	0.002	0.867	0.131
2017-SeS	Mean difference		—	0.0380	0.04093	0.04217	0.03317	-0.00183
	<i>p</i> -value		—	0.044	0.041	0.038	0.041	1.000
2017-SeR	Mean difference			—	0.00293	0.00417	-0.00483	-0.03983
	<i>p</i> -value			—	0.194	0.080	0.904	0.074
2018-SeL	Mean difference				—	0.00123	-0.00777	-0.04277
	<i>p</i> -value				—	0.333	0.674	0.068
2018-SeS	Mean difference					—	-0.00900	-0.04400
	<i>p</i> -value					—	0.583	0.064
2018-SeR	Mean difference						—	-0.03500
	<i>p</i> -value						—	0.062
GH-Lab	Mean difference							—
	<i>p</i> -value							—

One-way ANOVA analysis with Games-Howell Post-Hoc test. GH-Lab indicated *G. heterophylla* cultivated in our laboratory. 2017-SeL, 2017-SeS, and 2017-SeR indicate the leaves, stems, and roots parts of the 2017 collection of *G. heterophylla* originated from Seweweekspoort, South Africa, while 2018-SeL, 2018-SeS, and 2018-SeR indicate the counterpart from the 2018 collection

Table S4. Statistic analysis of the FRS gene expression of *G. heterophylla* collected from South Africa in 2017 and 2018 and cultivated at our laboratory in Germany.

		2017-SeL	2017-SeS	2017-SeR	2018-SeL	2018-SeS	2018-SeR	GH-Lab
2017-SeL	Mean difference	—	0.105	0.00440	0.10897	0.1513	-0.0632	-0.00240
	<i>p</i> -value	—	0.005	1.000	0.002	< .001	0.247	0.999
2017-SeS	Mean difference		—	-0.10033	0.00423	0.0466	-0.1680	-0.10713
	<i>p</i> -value		—	0.042	0.992	0.011	0.041	< .001
2017-SeR	Mean difference			—	0.10457	0.1469	-0.0676	-0.00680
	<i>p</i> -value			—	0.017	0.012	0.215	0.989
2018-SeL	Mean difference				—	0.0424	-0.1722	-0.11137
	<i>p</i> -value				—	0.065	0.024	0.014
2018-SeS	Mean difference					—	-0.2146	-0.15373
	<i>p</i> -value					—	0.021	< .001
2018-SeR	Mean difference						—	0.06083
	<i>p</i> -value						—	0.276
GH-Lab	Mean difference							—
	<i>p</i> -value							—

One-way ANOVA analysis with Games-Howell Post-Hoc test. GH-Lab indicated *G. heterophylla* cultivated in our laboratory. 2017-SeL, 2017-SeS, and 2017-SeR indicate the leaves, stems, and roots parts of the 2017 collection of *G. heterophylla* originated from Seweweekspoort, South Africa, while 2018-SeL, 2018-SeS, and 2018-SeR indicate the counterpart from the 2018 collection