Figure S1. Morphological features of the plant material (leaf, stem and bud) used for TfELN preparation. (A) Leaves and flower buds attached to stems. (B) Magnified view of the bud area in panel A. (C) Close-up of a stem. (D) Close-up of a flower bud. (E) Close-up of a leaf (adaxial surface). (F) Close-up of a leaf (abaxial surface). TfELN, *Talinum fruticosum*-derived exosome-like nanoparticle.

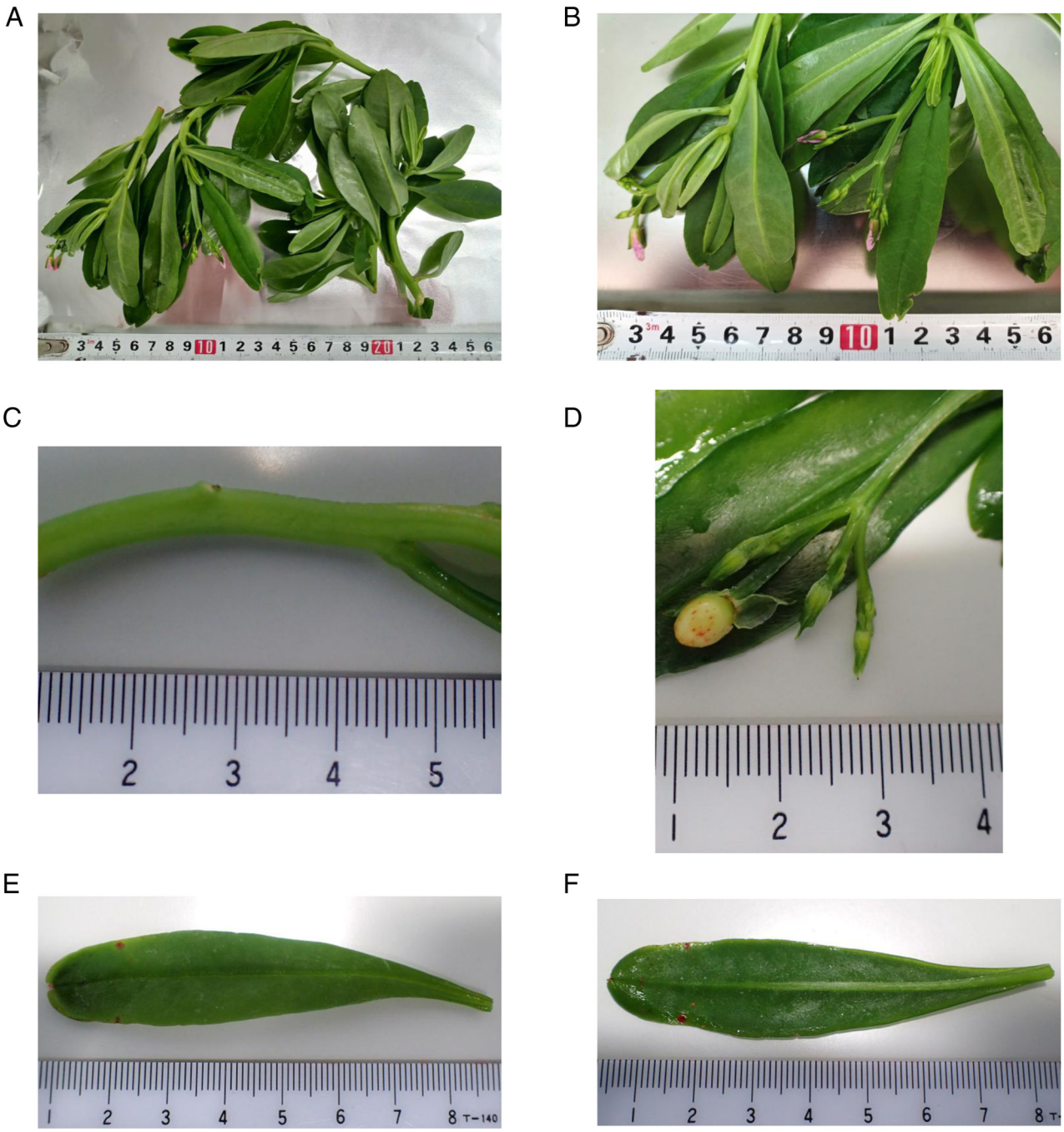


Figure S2. Morphological features of the plant material (flower) used for TfELN preparation. (A) A nearly blooming flower. White arrowheads indicate the characteristic longitudinal ridges of the rachis. (B) Close-up of a nearly blooming flower with separated sepals. (C) Close-up of the inner structure of a nearly blooming flower. TfELN, *Talinum fruticosum*-derived exosome-like nanoparticle.

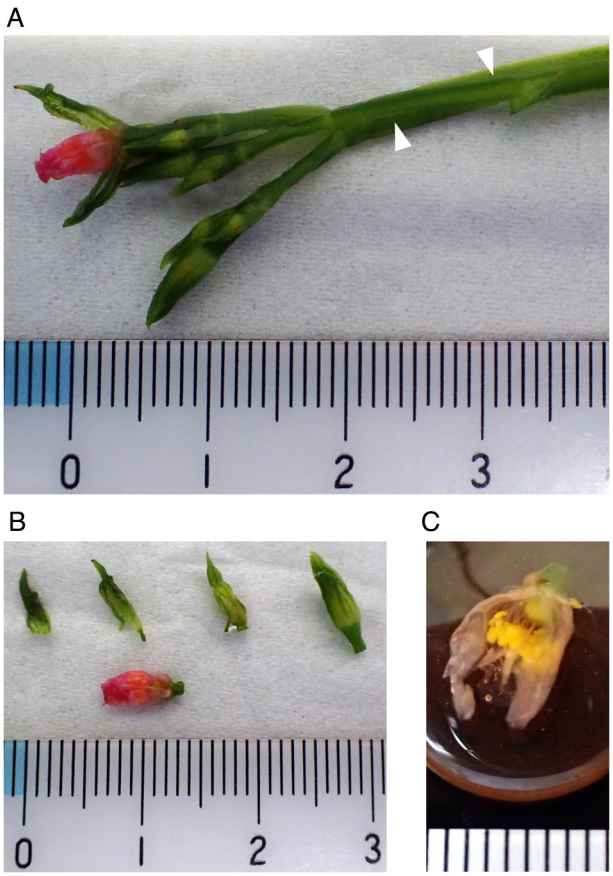
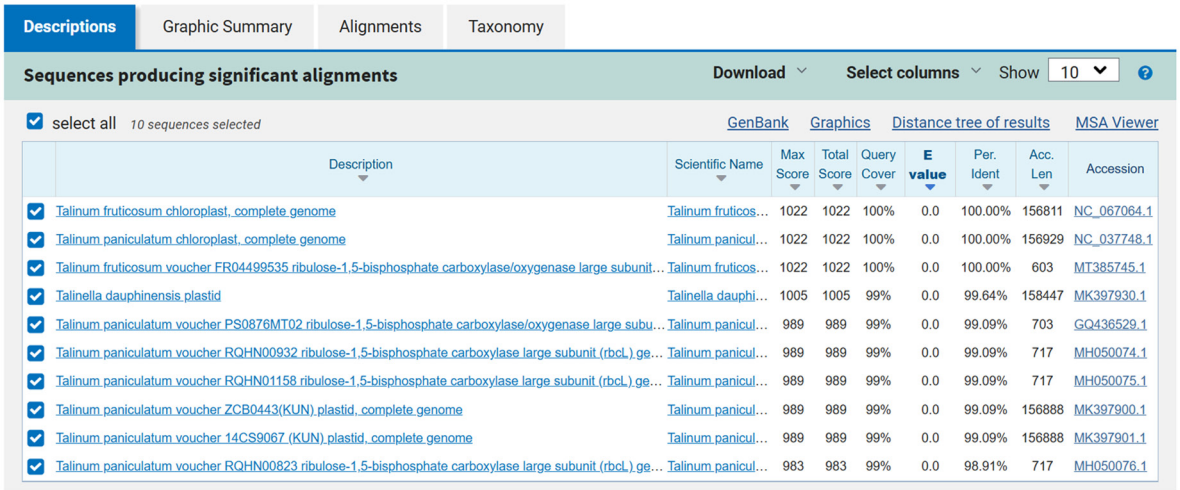


Figure S3. DNA barcoding of the *rbcL* locus (553 bp). (A) Screenshot of the top 10 BLASTN hits (Descriptions table) for the *rbcL* sequence, shown in the default BLASTN order (sorted by E-value) against the NCBI nucleotide database. (B) Screenshot of a representative pairwise alignment between the query *rbcL* sequence and a reference *Talinum fruticosum* sequence (top *T. fruticosum* hit), illustrating the sequence similarity across the aligned region. Note: The *rbcL* barcode region can be highly conserved among closely related *Talinum* species; therefore, *rbcL* barcoding is presented as supportive molecular evidence together with the *matK* results (Fig. S4) and diagnostic morphological characteristics (Figs. S1 and S2) for species identification. *rbcL*, ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit gene; bp, base pairs; BLASTN, Basic Local Alignment Search Tool for nucleotides; NCBI, National Center for Biotechnology Information; *matK*, maturase K gene.

A



Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments — Download — Select columns — Show 10

select all *10 sequences selected* — GenBank | Graphics | Distance tree of results | MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Talinum fruticosum chloroplast, complete genome	Talinum fruticos...	1022	1022	100%	0.0	100.00%	156811	NC_067064.1
Talinum paniculatum chloroplast, complete genome	Talinum panicul...	1022	1022	100%	0.0	100.00%	156929	NC_037748.1
Talinum fruticosum voucher FR04499535 ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit...	Talinum fruticos...	1022	1022	100%	0.0	100.00%	603	MT385745.1
Talinella dauphinensis plastid	Talinella dauphi...	1005	1005	99%	0.0	99.64%	158447	MK397930.1
Talinum paniculatum voucher PS0876MT02 ribulose-1,5-bisphosphate carboxylase/oxygenase large subu...	Talinum panicul...	989	989	99%	0.0	99.09%	703	GQ436529.1
Talinum paniculatum voucher RQHN00932 ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) ge...	Talinum panicul...	989	989	99%	0.0	99.09%	717	MH050074.1
Talinum paniculatum voucher RQHN01158 ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) ge...	Talinum panicul...	989	989	99%	0.0	99.09%	717	MH050075.1
Talinum paniculatum voucher ZCB0443(KUN) plastid, complete genome	Talinum panicul...	989	989	99%	0.0	99.09%	156888	MK397900.1
Talinum paniculatum voucher 14CS9067 (KUN) plastid, complete genome	Talinum panicul...	989	989	99%	0.0	99.09%	156888	MK397901.1
Talinum paniculatum voucher RQHN00823 ribulose-1,5-bisphosphate carboxylase large subunit (rbcL) ge...	Talinum panicul...	983	983	99%	0.0	98.91%	717	MH050076.1

B

Query: rbcL, rbcLa-F/rbcLa-R, 553-bp

Subject: Talinum fruticosum chloroplast, complete genome (NC_067064.1)

Score	Expect	Identities	Gaps	Strand
1022 bits(553)	0.0	553/553(100%)	0/553(0%)	Plus/Plus

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Query  1      TTTTGTTGGATTTAAAGCAGGTGTTAAAGATTACAAATTGACTTATTATACTCCTCAATA  60
Sbjct  56992  TTTTGTTGGATTTAAAGCAGGTGTTAAAGATTACAAATTGACTTATTATACTCCTCAATA  57051

Query  61     TCAACCCCTGGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCC  120
Sbjct  57052  TCAACCCCTGGATACTGATATCTTGGCAGCATTCCGAGTAACTCCTCAACCTGGAGTTCC  57111

Query  121    GTCAGAAGAAGCAGGAGCTGCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGT  180
Sbjct  57112  GTCAGAAGAAGCAGGAGCTGCAGTAGCTGCCGAATCTTCTACTGGTACATGGACAACTGT  57171

Query  181    ATGGACCGACGGACTTACCAGTCTTGATCGTTACAAAGGGCGATGCTACCACATTGATGC  240
Sbjct  57172  ATGGACCGACGGACTTACCAGTCTTGATCGTTACAAAGGGCGATGCTACCACATTGATGC  57231

Query  241    CGTTCCTGGAGAAGACAATCAATATATTTGTTATGTAGCTTACCCCTTAGACCTTTTTGA  300
Sbjct  57232  CGTTCCTGGAGAAGACAATCAATATATTTGTTATGTAGCTTACCCCTTAGACCTTTTTGA  57291

Query  301    AGAAGGTTCTGTTACTAATATGTTTACTTCCATTGTGGGTAATGTATTTGGGTTCAAAGC  360
Sbjct  57292  AGAAGGTTCTGTTACTAATATGTTTACTTCCATTGTGGGTAATGTATTTGGGTTCAAAGC  57351

Query  361    CCTTCGTGCTCTACGTTTGGAGGATTTGCGAATCCCTGTTGCTTATATCAAAACTTTCCA  420
Sbjct  57352  CCTTCGTGCTCTACGTTTGGAGGATTTGCGAATCCCTGTTGCTTATATCAAAACTTTCCA  57411

Query  421    AGGCCCGCCTCACGGTATCCAGGTTGAGAGAGATAAATTGAACAAGTATGGCCGTCCTCT  480
Sbjct  57412  AGGCCCGCCTCACGGTATCCAGGTTGAGAGAGATAAATTGAACAAGTATGGCCGTCCTCT  57471

Query  481    ATTGGGATGCACTATTAAGCCGAAATTGGGGTTATCTGCTAAAAACTATGGTCGAGCAGT  540
Sbjct  57472  ATTGGGATGCACTATTAAGCCGAAATTGGGGTTATCTGCTAAAAACTATGGTCGAGCAGT  57531

Query  541    TTATGAATGTCTT  553
Sbjct  57532  TTATGAATGTCTT  57544
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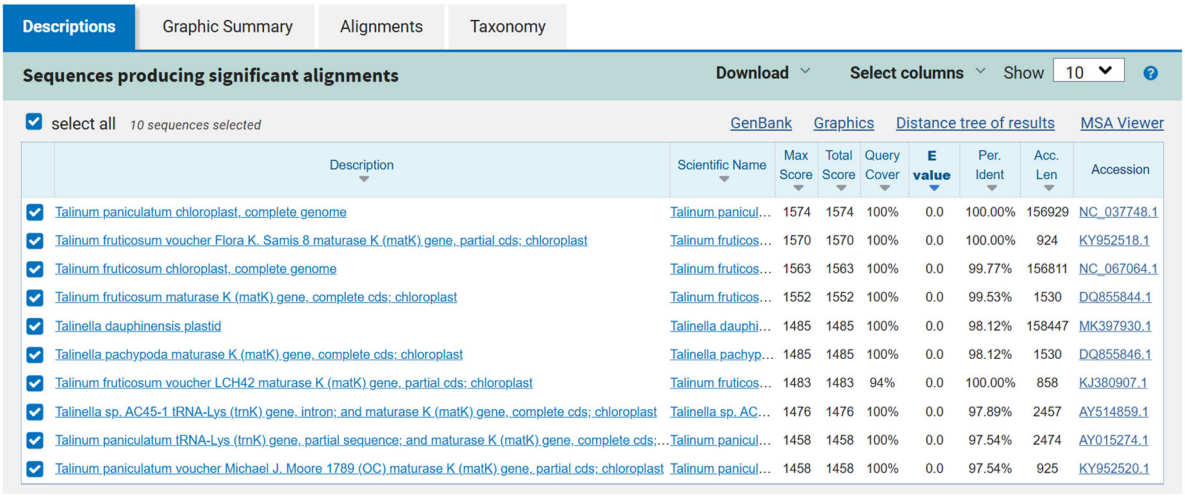
Figure S4. DNA barcoding of the *matK* locus (852 bp). (A) Screenshot of the top 10 BLASTN hits (Descriptions table) for the *matK* sequence, shown in the default BLASTN order (sorted by E-value) against the NCBI nucleotide database. (B) Screenshot of a representative pairwise alignment between the query *matK* sequence and a reference *Talinum fruticosum* sequence (top *T. fruticosum* hit), illustrating the sequence similarity across the aligned region. Note: A hit showing 100% identity with 94% query coverage reflects complete identity within the aligned region, with the remaining region not covered by the query sequence (i.e., no overlapping bases available for comparison). Species identification was determined based on the combined evidence from DNA barcoding (Figs. S3 and S4) and morphological characteristics (Figs. S1 and S2). *matK*, maturase K gene; bp, base pairs; BLASTN, Basic Local Alignment Search Tool for nucleotides; NCBI, National Center for Biotechnology Information.

A



Descriptions | Graphic Summary | Alignments | Taxonomy

Sequences producing significant alignments Download Select columns Show 10

select all *10 sequences selected* GenBank Graphics Distance tree of results MSA Viewer

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
Talinum paniculatum chloroplast, complete genome	Talinum panicul…	1574	1574	100%	0.0	100.00%	156929	NC_037748.1
Talinum fruticosum voucher Flora K. Samis 8 maturase K (matK) gene, partial cds; chloroplast	Talinum fruticos…	1570	1570	100%	0.0	100.00%	924	KY952518.1
Talinum fruticosum chloroplast, complete genome	Talinum fruticos…	1563	1563	100%	0.0	99.77%	156811	NC_067064.1
Talinum fruticosum maturase K (matK) gene, complete cds; chloroplast	Talinum fruticos…	1552	1552	100%	0.0	99.53%	1530	DQ855844.1
Talinella dauphinensis plastid	Talinella dauphi…	1485	1485	100%	0.0	98.12%	158447	MK397930.1
Talinella pachypoda maturase K (matK) gene, complete cds; chloroplast	Talinella pachyp…	1485	1485	100%	0.0	98.12%	1530	DQ855846.1
Talinum fruticosum voucher LCH42 maturase K (matK) gene, partial cds; chloroplast	Talinum fruticos…	1483	1483	94%	0.0	100.00%	858	KJ380907.1
Talinella sp. AC45-1 tRNA-Lys (trnK) gene, intron; and maturase K (matK) gene, complete cds; chloroplast	Talinella sp. AC…	1476	1476	100%	0.0	97.89%	2457	AY514859.1
Talinum paniculatum tRNA-Lys (trnK) gene, partial sequence; and maturase K (matK) gene, complete cds;…	Talinum panicul…	1458	1458	100%	0.0	97.54%	2474	AY015274.1
Talinum paniculatum voucher Michael J. Moore 1789 (OC) maturase K (matK) gene, partial cds; chloroplast	Talinum panicul…	1458	1458	100%	0.0	97.54%	925	KY952520.1

B

Query: matK, 390F/1326R,852-bp

Subject: Talinum fruticosum voucher Flora K. Samis 8 maturase K (matK) gene, partial cds; chloroplast (KY952518.1)

Score	Expect	Identities	Gaps	Strand
1570 bits(850)	0.0	850/850(100%)	0/850(0%)	Plus/Minus

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Query  3    CTTTTTTCTTGAAGAGCCACTATAATAATGAGAAAGATTTCTGCATATACGCCCAAACCG  62
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Query  63   ATCAAGAATATCCGAATCTAATAAATCTGTCCAGACCGACTTACTAATGGGATGTCCTAA  122
Sbjct  864  ATCAAGAATATCCGAATCTAATAAATCTGTCCAGACCGACTTACTAATGGGATGTCCTAA  805
Query  123  TACGTTACAAAATTTCGCTTTAGCCAACGACCCAACCAGAGGAATAATTCGAACTATGGT  182
Sbjct  804  TACGTTACAAAATTTCGCTTTAGCCAACGACCCAACCAGAGGAATAATTCGAACTATGGT  745
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Query  243  CACTGAAGAATTGAGTCGAACACTTGaaaaaaaCCCCATAAAATCGAGGGAATGTTTTGA  302
Sbjct  684  CACTGAAGAATTGAGTCGAACACTTGAAAAAAACCCCATAAAATCGAGGGAATGTTTTGA  625
Query  303  TAATAGATTGATATCGATTCTTCTTGGTTGAGACCACAGGGAAAAATGACATTGCCAAAA  362
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Query  423  TGATTTTCCTCGATACCTAACATAATGTGGGAAAGGGTCTTTGAAAAGCCATAAGATAAC  482
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Sbjct  444  GCGAAAATCCTTAGTAAAAGTTTTGACTTTTACTAGATATTCTAGTTTTCCGTAAAAATA  385
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Sbjct  324  AAAAACGAAAATGGATTCGTATTCACATACATGGAAATTATATAGGAACAGGAATAATCG  265
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Sbjct  264  TTGATTCCTTTTTGAAAAAATAGAAATGGATTTTTGGGGAGTAATAAGACTATTCCAATT  205
Query  723  ACGATACTCATAAAGAAAGAATCGTAATAAATGCAAAGAAGAAACATCTTTCACCCAATA  782
Sbjct  204  ACGATACTCATAAAGAAAGAATCGTAATAAATGCAAAGAAGAAACATCTTTCACCCAATA  145
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Sbjct  144  ACGAAGAGTTTGAACCAAGATTTCGAGATGGATAGGGTAAGGTATTAATATTTCTAACAC  85
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Sbjct  84   ATAATTTAAA  75
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