

Table S2. List of the 30 publicly available *Ipomoea* cp genomes in the NCBI repository.

Genbank Accession	Specimen	Size	Taxon	Accession/ Cultivar	Source
KF242497	<i>I. cordatotriloba</i>	161,046	Batatas	REM 317	1
KF242492	<i>I. setosa</i>	161,035	Batatas	REM 68	1
KF242493	<i>I. splendor-sylvae</i>	161,925	Batatas	REM 763	1
KF242496	<i>I. trifida</i>	161,033	Batatas	REM 753	1
KF242476	<i>I. trifida</i>	161,300	Batatas	PI 618966	1
KP212149	<i>I. batatas</i>	161,303	Batatas	Xushu 18	2
KF242473	<i>I. batatas</i>	161,193	Batatas	PI 508520	1
KF242474	<i>I. batatas</i>	161,871	Batatas	PI 518474	1
KF242475	<i>I. batatas</i>	161,466	Batatas	PI 561258	1
KF242480	<i>I. cairica</i>	161,203	Cairica	REM 184	1
KF242481	<i>I. diamantinensis</i>	161,266	Cairica	REM 37	1
KF242486	<i>I. murucoides</i>	160,072	Murucoides	REM 351	1
KF242491	<i>I. polpha</i>	161,205	Murucoides	REM 85	1
KF242499	<i>I. obscura</i>	161,250	Obscura	REM 271	1
KF242489	<i>I. pedicellaris</i>	160,657	Obscura	REM 403	1
KF242478	<i>I. amnicola</i>	161,172	Pes-caprae	REM 36	1
KF242479	<i>I. argillicola</i>	161,119	Pes-caprae	REM 38	1
KF242490	<i>I. pes-caprae</i>	160,168	Pes-caprae	REM 767	1
KF242483	<i>I. eriocarpa</i>	160,976	Pes-tigridis	REM 190	1
KF242485	<i>I. involucrata</i>	160,531	Pes-tigridis	REM 851	1
KF242500	<i>I. pes-tigridis</i>	162,140	Pes-tigridis	REM 854	1
EU118126	<i>I. purpurea</i>	162,046	Quamoclit	Grandpa Ott's	3
KF242482	<i>I. dumetorum</i>	161,191	Quamoclit	REM 218	1
KF242484	<i>I. hederifolia</i>	161,383	Quamoclit	REM 476	1
KF242498	<i>I. minutiflora</i>	161,190	Quamoclit	REM 535	1
KF242488	<i>I. orizabensis</i>	160,940	Quamoclit	REM 178	1
KF242494	<i>I. ternifolia</i>	161,409	Quamoclit	REM 452	1
KF242495	<i>I. tricolor</i>	160,776	Quamoclit	REM 448	1
KF242487	<i>I. nil</i>	161,548	Quamoclit	REM 459	1
AP017304	<i>I. nil</i>	161,897	Quamoclit	TKS	4

References

1. Eserman, L. A., Tiley, G. P., Jarret, R. L., Leebens-Mack, J. H. & Miller, R. E. Phylogenetics and diversification of morning glories (tribe ipomoeae, convolvulaceae) based on whole plastome sequences. *American journal of botany* **101**, 92–103 (2014).
2. Yan, L. *et al.* Analyses of the complete genome and gene expression of chloroplast of sweet potato [*ipomoea batata*]. *PLoS One* **10**, e0124083 (2015).
3. McNeal, J. R., Kuehl, J. V., Boore, J. L. & de Pamphilis, C. W. Complete plastid genome sequences suggest strong selection for retention of photosynthetic genes in the parasitic plant genus *cuscuta*. *BMC Plant Biology* **7**, 57 (2007).
4. Hoshino, A. *et al.* Genome sequence and analysis of the japanese morning glory *ipomoea nil*. *Nature communications* **7** (2016).