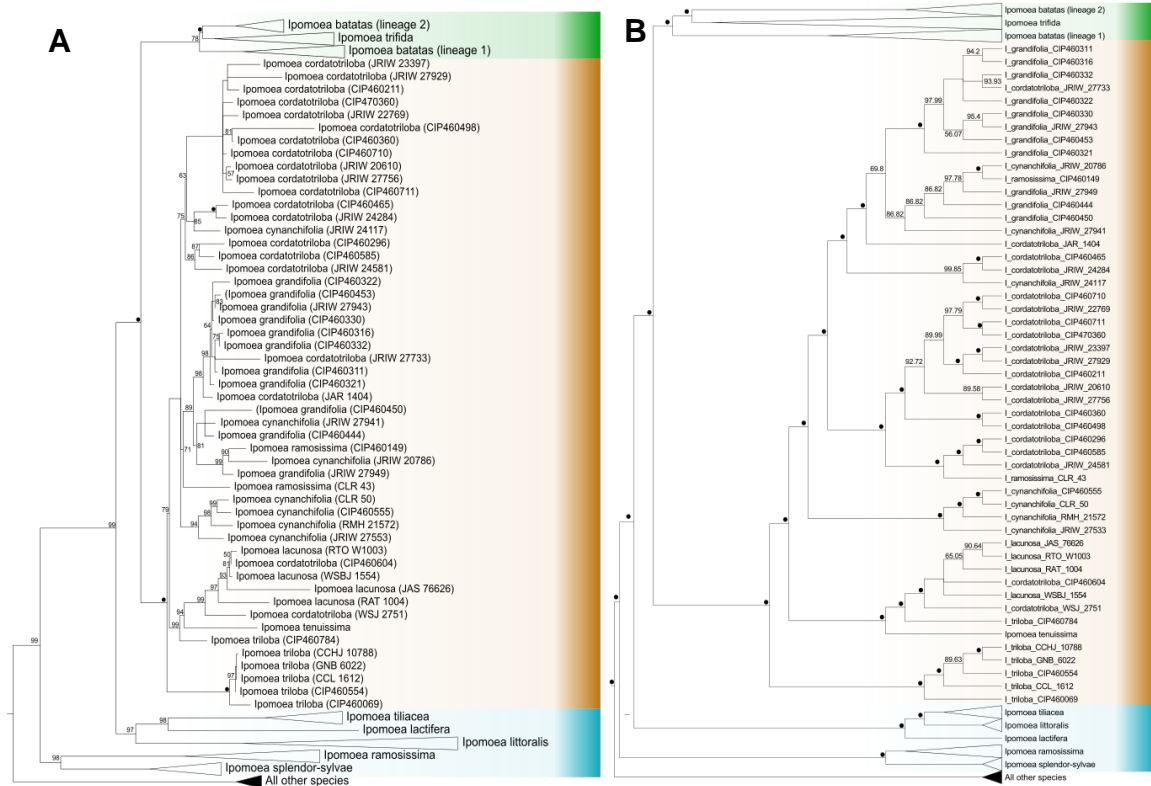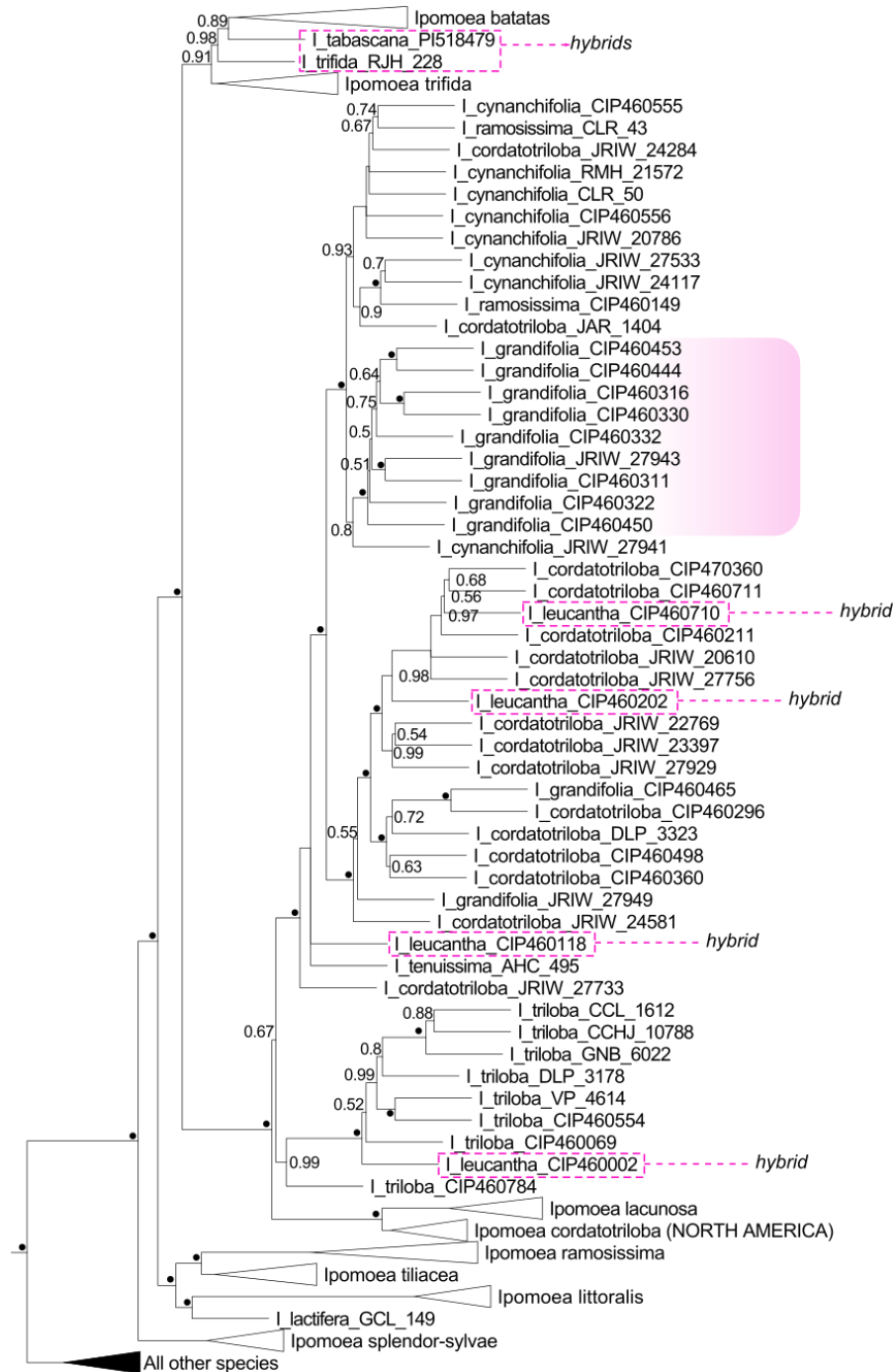**Figure S1. Nuclear phylogenies of sweet potato and its CWRs, Related to Figures 2 and 3.**

Phylogeny of *Ipomoea* series *Batatas* (excluding hybrid species *I. leucantha* and *I. tabascana*) inferred from 307 nuclear regions that do not show recombination. Blue, perennial species; orange, annual species; green, sweet potato and *Ipomoea trifida*. Black dots indicate 100% support. Triangles represent monophyletic species with 100% support. (A) Inferred using Astral-II. Values at the nodes indicate bootstrap support for a partition (100 replicates from gene trees). (B) Inferred using Approximate Maximum Likelihood with all regions concatenated. Values at the nodes indicate local support values with the Shimodaira-Hasegawa test (1,000 resamples).

Figure S2. Chloroplast phylogenies of sweet potato and its CWRs, Related to Figures 2 and 3.

Phylogeny of *Ipomoea* series *Batatas* (excluding hybrid species *I. leucantha* and *I. tabascana*) inferred from whole chloroplast sequences. Blue, perennial species; orange, annual species; green, sweet potato and *I. trifida*. Triangles represent monophyletic species with 100% support.
(A) Maximum Likelihood (RAxML, 1,000 bootstrap replicates). Values at the nodes indicate bootstrap support. Black dots indicate 100% support.
(B) Maximum parsimony analysis using indels only, Majority Rule consensus. Values at the nodes indicate bootstrap support.

Figure S3. Nuclear phylogeny of sweet potato and its CWRs including hybrids, Related to Figure 2.

Approximate Maximum Likelihood phylogeny of *Ipomoea* series *Batatas* inferred from 307 nuclear regions that do not show recombination, showing the position of the hybrid species. Triangles represent monophyletic species with 100% support. Values at the nodes indicate bootstrap support (100 replicates from gene trees) for a partition. Black dots indicate 100% support. Purple dashes indicate putative hybrid specimens: *I. tabascana*, tetraploid *I. trifida* and *I. leucantha*, and purple shading area indicates most *I. grandifolia* specimens.
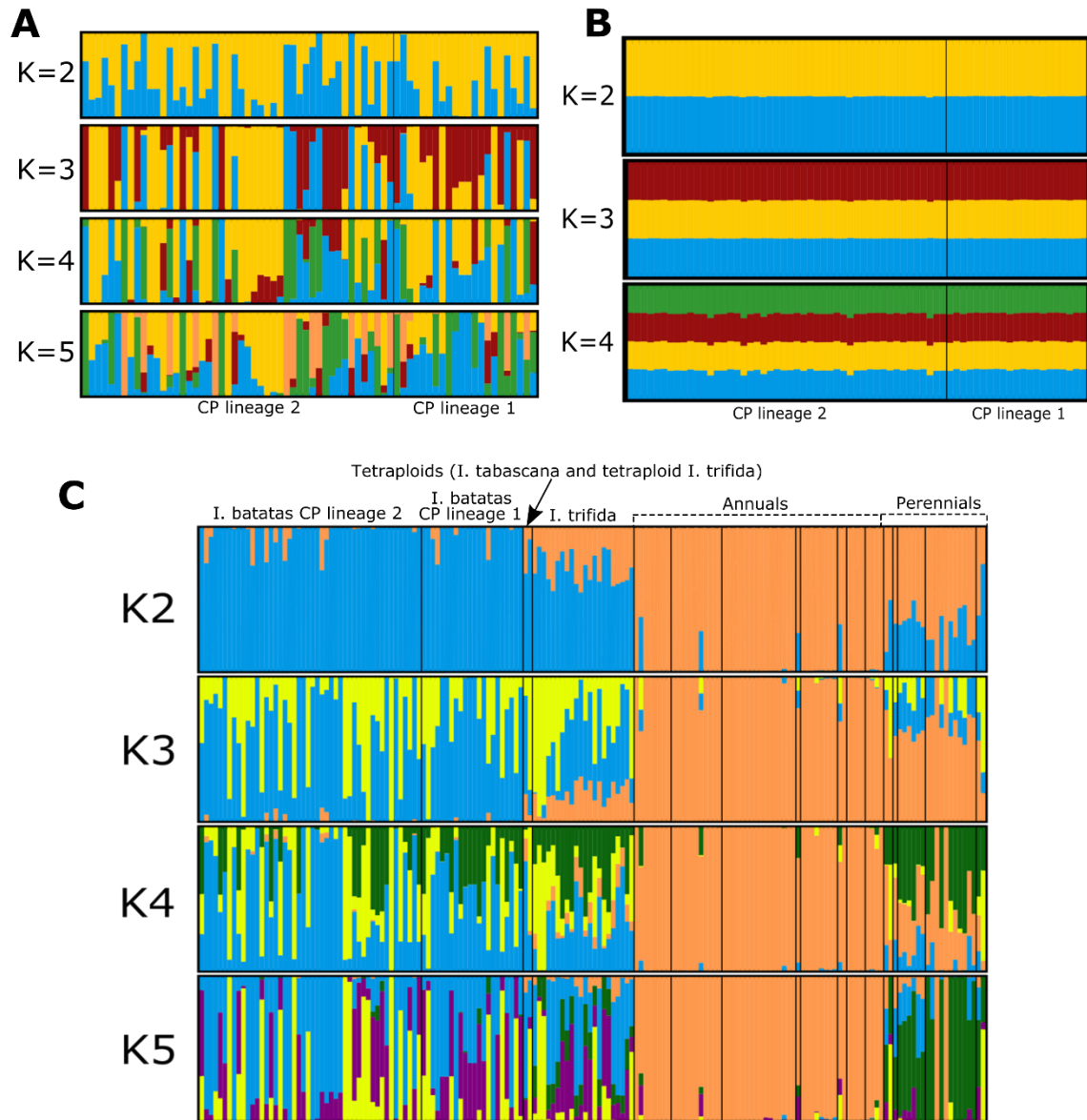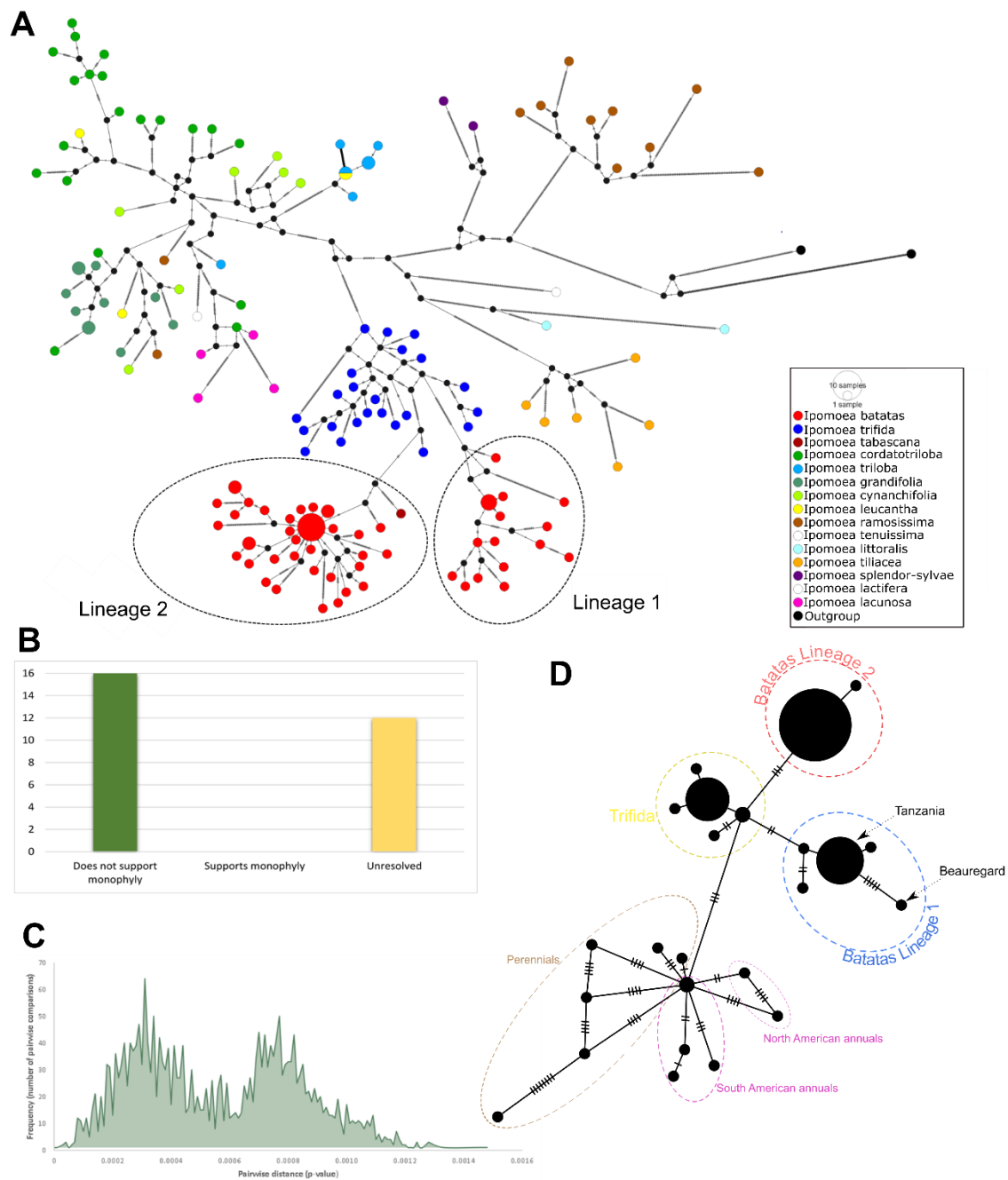
Figure S4. Additional population structure analyses, Related to Figures 2 and 3.

K is the number of assumed ancestral populations.
(A) Sweet potato only using nuclear coding regions.
(B) Sweet potato only using the nuclear ribosomal non-coding *ITS* DNA region.
(C) *Ipomoea* series *Batatas* using nuclear coding regions.

**Figure S5. Additional analyses of chloroplast data, Related to Figure 3.**

(A) Integer Neighbor-Joining chloroplast network of all species in *Ipomoea* series *Batatas*.
(B) None of the 28 most variable regions in the chloroplast genome supports monophyletic sweet potato.
(C) Pairwise distance between all sweet potato chloroplast genomes.
(D) Median-Joining *rpl32-trnL* network of all species in *Ipomoea* series *Batatas*, showing the position of the two commercial sweet potato varieties Beauregard and Tanzania.
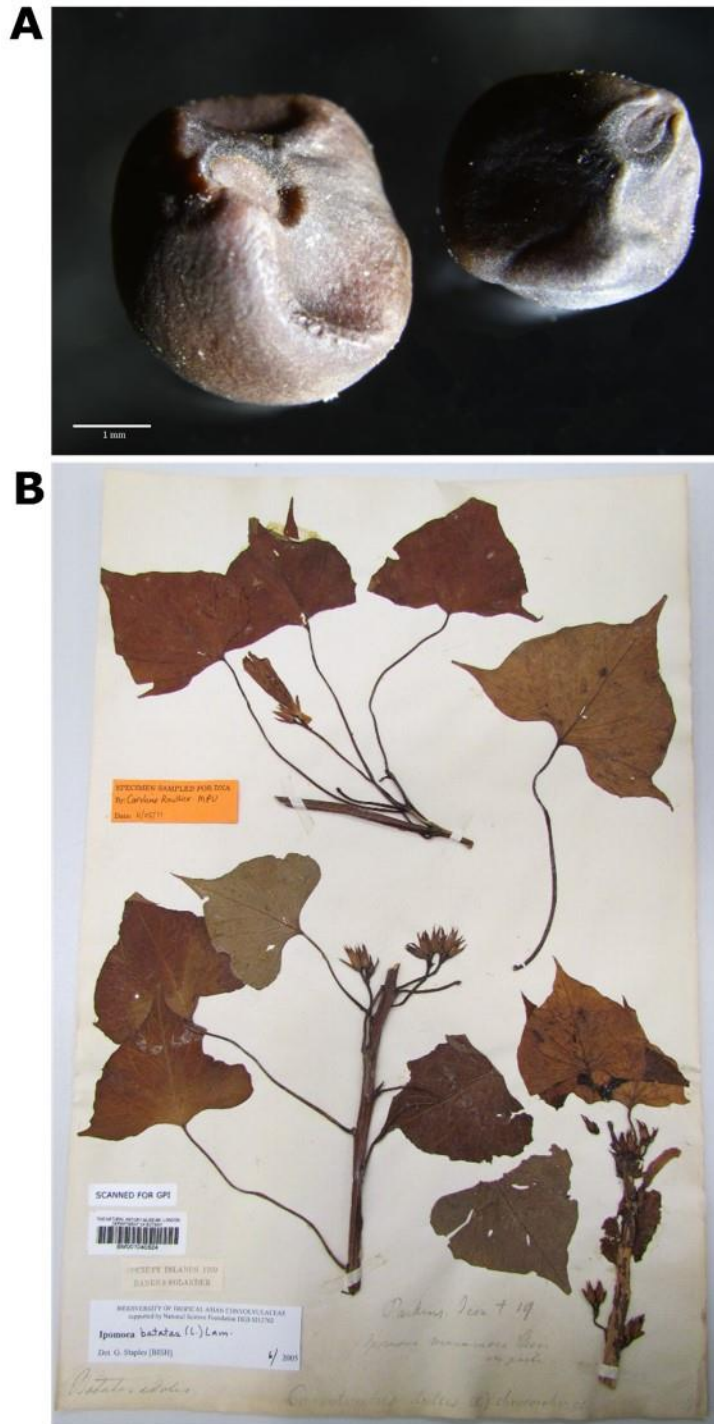
Figure S6. Pictures of *Ipomoea seeds* and a historic specimen, Related to Figure 7.

(A) Seeds of *Ipomoea littoralis* (left; *L.J. Brass 13940* [BM]) and *Ipomoea batatas* (right; *S9 55* [USDA]).
(B) *Ipomoea batatas* specimen collected in 1769 by Banks and Solander in the Society Islands.
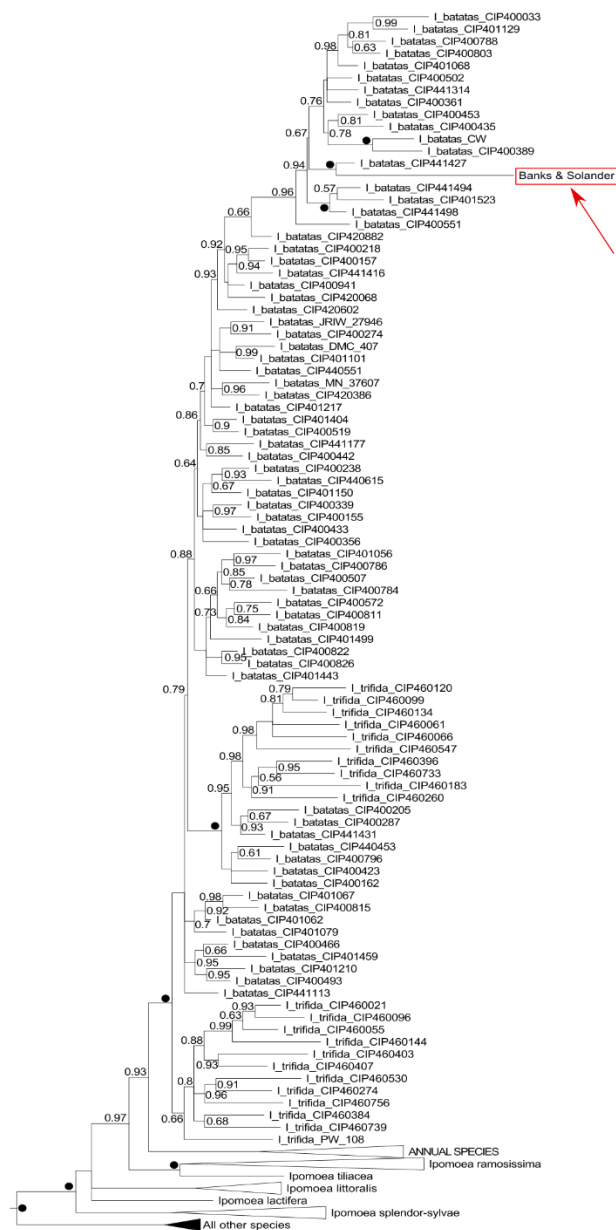
Figure S7. Nuclear phylogeny including Banks and Solander specimen, Related to Figure 7.

Position of the sweet potato specimen collected by Banks and Solander in a phylogenetic tree based on 12,905 nuclear variable positions, inferred using FastTree 2. Values at the nodes indicate local support values with the Shimodaira-Hasegawa test (1,000 resamples). Black dots indicate 100% support.

Table S1. Relative population sizes for *Ipomoea batatas* and *I. trifida* inferred from our plastome dataset, Related to Figure 5.

Population	Ne*	Minimum age (years)
TB_1B_2	0.07	~500,000
TB_2	0.06	~250,000
T	0.28	Extant population
B_1	0.27	Extant population
B_2	1	Extant population

T = *I. trifida* lineage; B_1 = *I. batatas* CL1; B_2 = *I. batatas* CL. TB_1B_2 = lineage ancestral to all three lineages. *TB2* = lineage ancestral to *T* and B_2. *Effective population sizes (Ne) are expressed as a proportion of that of B_2.