



**Figure S1.** Pearson correlation coefficient ( $r$ ) matrix and heatmap for the 19 considered quantitative morphological traits.

**Table S1.** Number of alleles detected for each SSR locus.

SSR name	GenBank accession	Detected alleles (n)
Aang01	AY865575	7.00
Aang03	AY865577	2.00
Aang07	AY865579	1.00*
Aang12	AY865581	1.00*
Aang14	AY865583	1.00*
Aang18	AY865586	1.00*
Aang21	AY865587	1.00*
Aang22	AY865588	1.00*
Aang24	AY865590	2.00
Aang27	AY865591	1.00*
Aang28	AY865592	2.00
Aang35	AY865594	3.00
Aang37	AY865596	1.00*
Aang45	AY865601	2.00
Aang46	AY865602	5.00
Aang47	AY865603	2.00
Ag20	AJ749964	4.00
Ag45	AJ749966	3.00
Ag56	AJ749967	3.00
Ag62	AJ749968	2.00
Ara11382	JN896697	2.00
Ara11384	JN896698	3.00
Ara2027	JN896693	7.00
Ara20681	JN896699	3.00
Ara5179	JN896694	1.00*
Ara5182	JN896695	2.00
Ara5595	JN896696	2.00
CRCAC2	AF522867	2.00

\* Monomorphic SSR markers discarded for statistical analyses.

**Table S2.** Pairwise  $F_{ST}$  among each population (p-value<0.001).

	NLU	ARG	UNK	ESU	ITM	ITV
NLU	0.000					
ARG	0.465	0.000				
UNK	0.383	0.343	0.000			
ESU	0.419	0.497	0.400	0.000		
ITM	0.403	0.408	0.380	0.460	0.000	
ITV	0.377	0.349	0.285	0.387	0.003	0.000