

doi: [10.22058/JPMB.2024.2046808.1320](https://doi.org/10.22058/JPMB.2024.2046808.1320)**Supplementary Materials****Supplementary Table 1.** Responses of SSR markers to genetic diversity indexes across entire populations.

Population	Locus	N	Na	Ne	I	Ho	He	uHe	F
Pop_1	Locus_1	3	2	1.8	0.637	0	0.444	0.533	1
	Locus_2	3	3	3	1.099	0	0.667	0.8	1
	Locus_3	3	3	3	1.099	0	0.667	0.8	1
	Locus_4	3	1	1	0	0	0	0	0
	Locus_5	3	3	2.571	1.011	0.333	0.611	0.733	0.455
	Locus_6	3	3	2.571	1.011	0.667	0.611	0.733	-0.091
Pop_2	Locus_1	5	3	2.778	1.055	0	0.64	0.711	1
	Locus_2	5	4	3.571	1.332	0	0.72	0.8	1
	Locus_3	5	5	5	1.609	0	0.8	0.889	1
	Locus_4	5	1	1	0	0	0	0	0
	Locus_5	5	4	3.571	1.332	0	0.72	0.8	1
	Locus_6	5	4	3.571	1.332	0	0.72	0.8	1
Pop_3	Locus_1	12	4	3.429	1.286	0	0.708	0.739	1
	Locus_2	12	7	5.647	1.817	0.083	0.823	0.859	0.899
	Locus_3	12	7	6	1.864	0	0.833	0.87	1
	Locus_4	12	2	1.18	0.287	0	0.153	0.159	1
	Locus_5	12	7	5.538	1.82	0	0.819	0.855	1
	Locus_6	12	7	4.721	1.755	0.167	0.788	0.822	0.789
Std. Dev.			1.94	1.523	0.568	0.167	0.262	0.284	0.386

Pop_1/2/3 = Individual population; Locus_1/2/3/4/5/6 = DN239472, DN240063, Ma513026332, Ma513019043, Ma513036168, and Ma513035997 respectively; N = Number of individuals per population; Na = Number of different alleles; Ne = Number of effective alleles; I = Shannon's information index; Ho = Observed heterozygosity; He = Expected heterozygosity; uHe = Unbiased expected heterozygosity; F = Fixation index (inbreeding coefficient); Std. Dev. = Standard deviation.

doi: [10.22058/JPMB.2024.2046808.1320](https://doi.org/10.22058/JPMB.2024.2046808.1320)**Supplementary Table 2.** AMOVA based on SSR markers for 20 accessions of *Musa* spp.

Source of variation	Degrees of freedom	Sum of squares	Mean squares	Estimated variance	% Variation
Among Population	2	11.775	5.888	0.141	6%
Among Individual	17	73.500	4.324	2.087	88%
Within Individual	20	3.000	0.150	0.150	6%
Total	39	88.275	-	2.378	100%

Supplementary Table 3. Pairwise population matrix F_{ST} values (below the diagonal) and Nei genetic distance (above the diagonal)

	Pop_3	Pop_2	Pop_1
Pop_1	0.857	0.862	0.000
Pop_2	0.398	0.000	0.193
Pop_3	0.000	0.076	0.150

Pop_1/2/3: All Populations