Microsatellite markers, sequence information, repeat motifs, and allele size used for the genetic diversity analysis in tomato.

Locus	Orig. Acc.	Size	Motif	Primer pairs
TSR1	AF220603	306	TA26	F[1]ATCGTGGCGATAATTTG
				R TCCTTGATTTCTTTCATC
TSR 2	AQ367308	229	AT15	F TCAAGTGAGTTTATCTGCCCAC
				R GCTCATCCTACACATTCATGCTC
TSR 5	AQ367719	180	AG11	F CTTCGACGGGGTTTAGAGTTTTTC
				R GGACAGGTGAATGGGTCAAAGAC
TSR 6	AQ367720	314	ATT18	F ACGACCCACTATTAGTTTC
				R TTGGACACAGAGAAAAAAC
TSR 10	BH014932	197	TA8 CA13	F GGTTGTCGGTTAGATAATCTCCCAC
				R TTTTGGCTCTGCTAACAAAGC
TSR 14	BH015910	241	GTA23	F CTCTGATGGAAGAAAAAATAGGTCGG
				R AGGAGGGGAGTTAGAGTTTGATG
TSR 15	BH016043	212	ATT(ATG)7	F GCACTAAGCATCTCTCTTCTAAC
				R ACTTCGCATTTGTGCTCATC
TSR 18	LEU63117	246	TA15	F TGCATGGACAAATCTTGAGG
				R CGGCACATCAAATTATTATATCTCG
TSR 20	LSTPRPF1	158	CCA7	F TAATACCACCACCCTACGTGCC
				R CACCTAGCTTGAGAGCATCAATGG
TSR 23	AQ367511	222	AT30	F TGGCTCTCGCTAACTCAAGAACTAC
				R GGTTTTCGGTTAGAGAATCTCCCAC

Initially, 27 SSR markers were constructed based on tomato sequence information from GeneBank (National Center for Biotechnology Information, USA).

Ten microsatellite markers were selected based on amplification and reproducibility in all accessions.

Statistical Analysis

- **The length of the polymorphic SSR alleles were measured and standardized with the DNA size marker (PUC/19) following by the exponential equation by computer.**

- **It was calculated the average number of alleles per polymorphic loci {A=A_i /n), where A_i is the number of alleles at the i^{th} locus, n is the total number of loci.**

- **The diversity levels of SSR loci were calculated with the genetic diversity index by Nei (1973) formula.**

- **Cluster analysis was carried out to construct a dendrogram based on the unweighted pair group method with arithmetic averages (UPGMA) in NTSYS-pc (Numerical Taxonomy System, version 2.0, Rohlf 2000).**

- **Analysis of molecular variance (AMOVA) was conducted in GENALEX 6 (Peakall and Smouse 2006).**

- **Principal component analysis (PCA) was performed to reveal genetic similarity and diversity among the genotypes.**

Amplification profile of different alleles and gene diversity in tomato accessions for ten microsatellite markers.

Locus	Size of Alleles (bp)	Total alleles	Unique alleles [1]		Gene diversity [2]	
			Myanmar	Gene bank	Myanmar	Gene bank[3]
TSR1	306-352	10	4	2	0.515	0.640
TSR2	219-301	20	6	6	0.883	0.814
TSR5	148-291	18	1	7	0.835	0.893
TSR6	312-374	13	4	4	0.0.786	0.816
TSR10	188-244	17	1	10	0.678	0.891
TSR14	241-293	12	2	4	0.726	0.830
TSR15	215-329	13	2	6	0.313	0.837
TSR18	264-334	11	2	5	0.668	0.798
TSR20	115-168	9	0	3	0.753	0.821
TSR23	192-230	10	0	6	0.591	0.820
Average	----	13.2 (133)	2.2	5.3	0.675	0.816

1. Specifially found in Myanmar and Genebank population, respectively 2. According to Nei (1973)

3. Accessions from the Genebank of National Institute of Vegetable of Tea Science

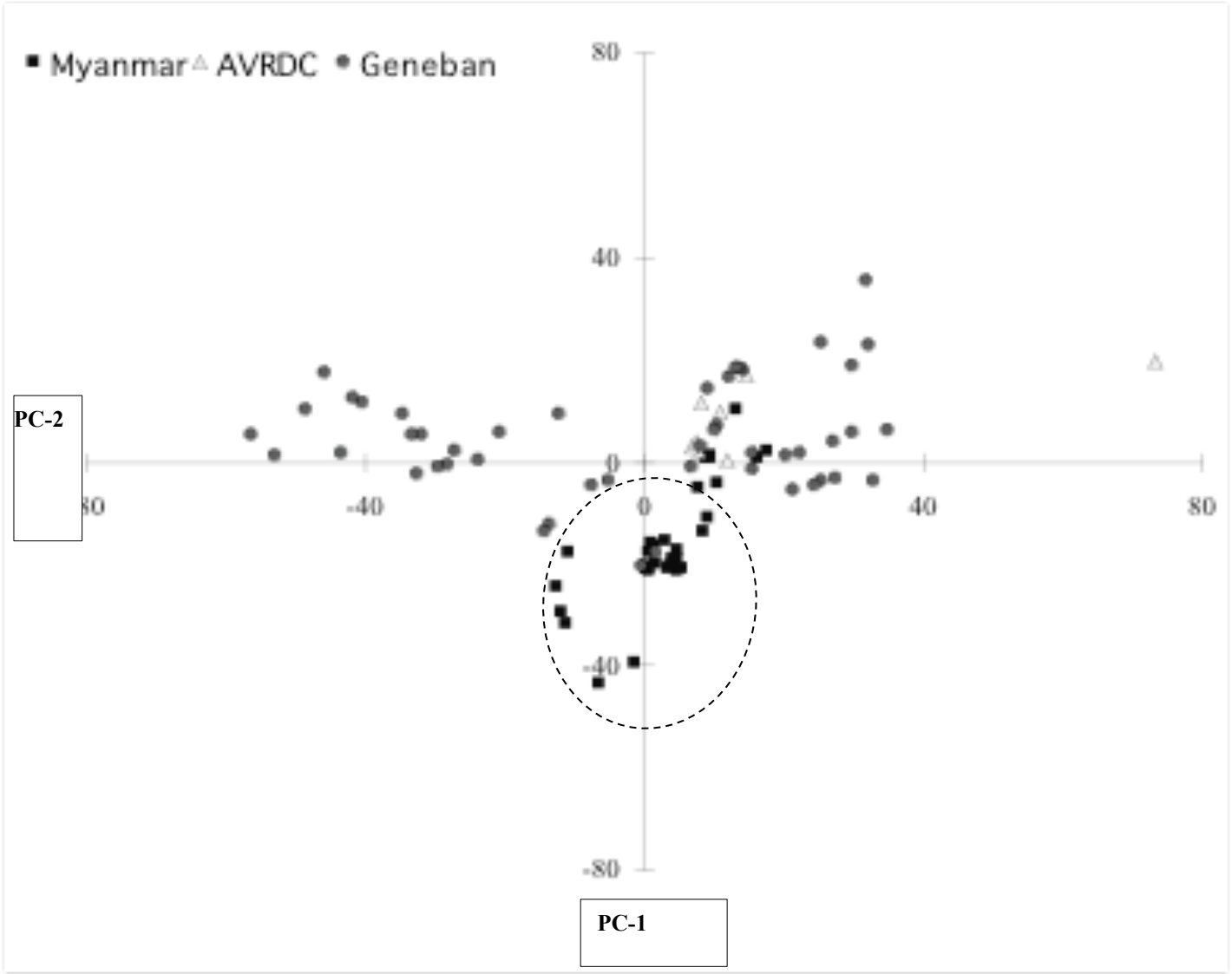
•The amplification of alleles specific to Myanmar and the Genebank populations demonstrate that these markers can discriminate tomato accessions at the intraspecific level.

Gene diversity

- **The mean gene diversity was higher in Genebank populations than in Myanmar landraces, reflecting the overall diversity in both groups.**

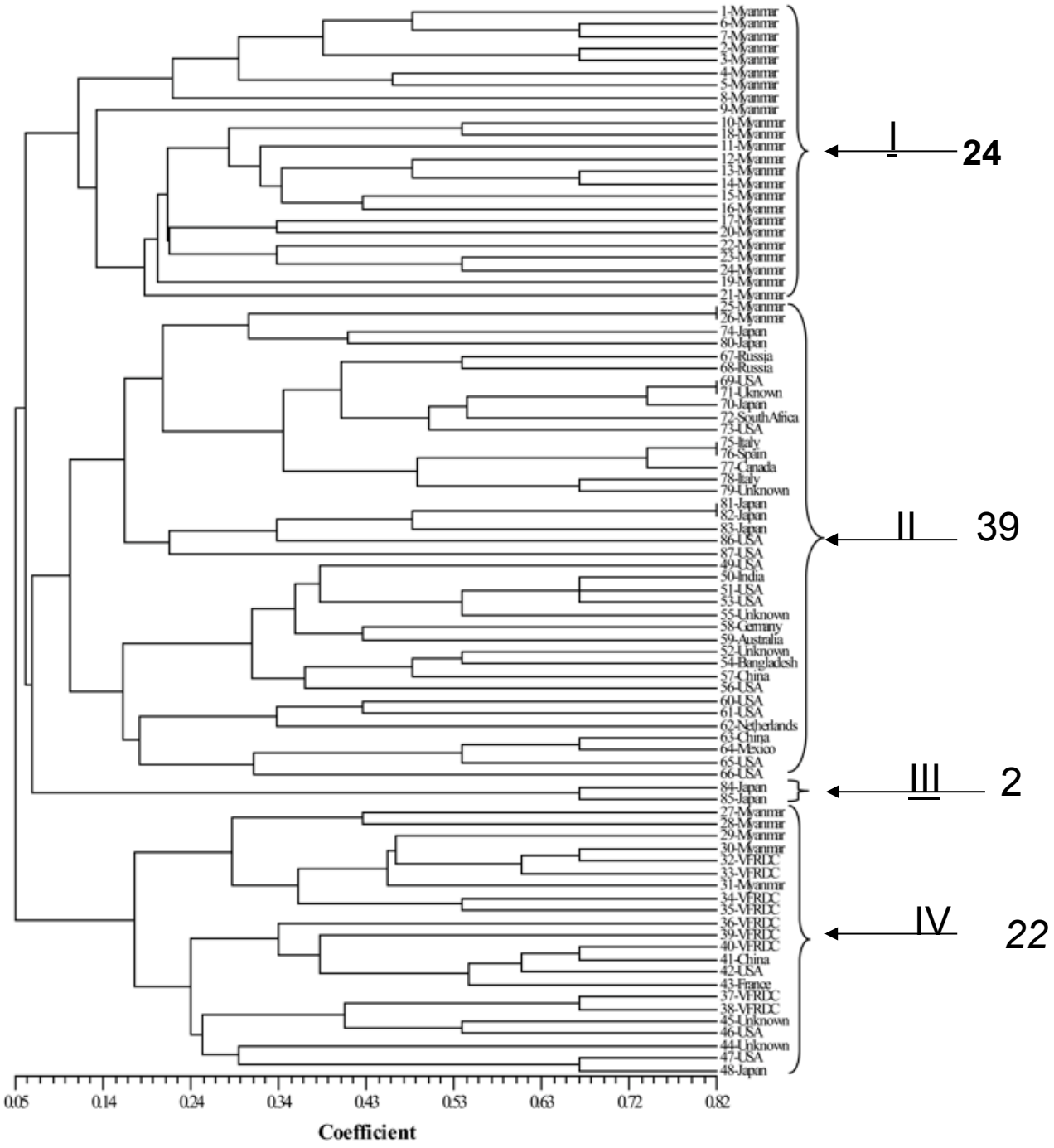
- **The lower gene diversity in Myanmar landraces was due to the fact that this collection was from one country compared to the Genebank populations that were a diverse collection from different continents.**

- **The current gene diversity is a good indicator of the broad genetic base of tomato landraces from Myanmar.**



Principles components analysis of showing distribution of tomato landraces from Myanmar, AVRDC, and Genebank. The contribution of the first and second principal components were 32 and 20% respectively.

Dendrogram showing the clustering pattern of 87 tomato accessions from Myanmar, Genebank, and VFRDC. **The coefficient matrix values ranged from 0.05 to 0.82.**



- **A dendrogram was constructed for the 87 accessions that resolved all genotypes into four main clusters**

- **In addition to being present in almost all clusters, the Myanmar landraces also constituted a separate cluster, showing their unique genetic structure**

- **The AVRDC and Genebank accessions, being worldwide collections, expectedly showed a scattered distribution in both the principal component and cluster analyses.**

- **However, the presence of Myanmar landraces in three major clusters of the dendrogram demonstrates their diverse genetic base.**

- **lack of variability is a concern in tomato cultivation due to its self-pollination (Foolad et al. 1993); however, the tomato landraces from Myanmar, even though not representative of the entire country, emerged as a diverse group and highlighted their uniqueness from the rest of the collections in both analyses.**

Diversity analysis in tomato landraces from Myanmar

- As a primary objective of our study was to evaluate the diversity status of tomato landraces from Myanmar, we analyzed diversity in world collections in a relative context and kept the major emphasis and focus on Myanmar collections.

- Analysis of molecular variance (AMOVA) was conducted to analyze variation in tomato landraces within and among groups (Table 4).