

Genetic diversity of *Prunus domestica* selected from ten countries across Europe



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A total of 46 local plum accessions, presently conserved by partners in 10 different countries, were analysed in this study. Seven international reference cultivars were also included in the analyses. Young leaves were collected in the spring or summer from a single tree for each of the investigated accessions, and then sent to Balsgård, SLU in Sweden, where all DNA analyses were performed. The analyses were performed as part of the PRUNDOC project, approved by ECPGR following the call in 2014, and was carried out throughout 2015.

Table 1. Allele size range (bp) for all the analysed plum accessions, number of alleles per locus and gene diversity, based on 9 SSR loci, for all analysed accessions, 46 local European plum accessions and 7 reference cultivars.

Locus	All analysed accessions (N = 53)			Local European accessions (N = 46)		Reference cultivars (N = 7)	
	Size range (bp)	No. of alleles	Gene diversity	No. of alleles	Gene diversity	No. of alleles	Gene diversity
UDP98	164/231	20	0.89	19	0.89	11	0.94
PacA33	169/254	34	0.93	34	0.93	15	0.92
CP5CT026	165/216	21	0.92	21	0.92	13	0.92
BPPCT040	120/154	15	0.88	15	0.88	8	0.89
BPPCT007	123/152	16	0.91	16	0.91	11	0.91
BPPCT039	122/179	28	0.93	28	0.92	16	0.94
BPPCT014	186/283	37	0.93	37	0.93	16	0.94
BPPCT034	215/260	20	0.91	20	0.90	12	0.92
UDP96	92/165	27	0.93	26	0.93	12	0.90
Mean		24.2	0.91	24	0.91	12.7	0.92



SSR polymorphism

The highest number of different alleles was detected for BPPCT014, while BPPCT040 was the least polymorphic of all loci analyzed in our study. The gene diversity was very similar for local European accessions (0.91) and reference cultivars (0.92). Gene diversity calculated for all analyzed samples (0.91) was very similar or identical to the values reported by Halapija Kazija et al. (2014) and Sehic et al. (2015).

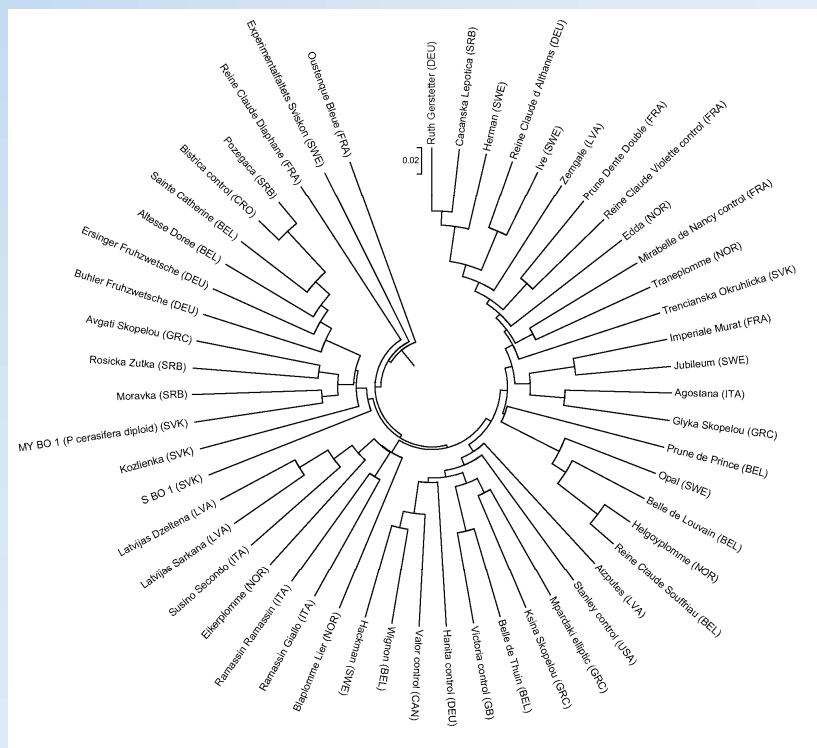
Figure 1. UPGMA cluster analysis based on polymorphisms of SSR data for 53 plum accessions using Jaccard's similarity coefficient.

Genetic relationships and differentiation

UPGMA cluster analysis grouped all 46 plum accessions and 7 reference cultivars into a dendrogram (Fig. 1). However, there was no notable separation in clusters of cultivars from different countries. No synonyms or homonyms were identified using the cluster analysis. Accessions 'Pozegaca' from Serbia and 'Bistrica' control from Croatia, which are supposed to be synonymous, clustered tightly together but were not identical.

Conclusions

European plum is a diverse crop, but the partitioning of variability does not appear to be related to the geographic origin. The 46 plum accessions of diverse genetic origin, with unique genetic profiles, documented with standard and agreed descriptors, will be candidates to be part of the AEGIS European Collection.



Literature cited

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