

MOLECULAR CHARACTERIZATION OF ONION (*Allium cepa* L.) SPANISH LANDRACES AND RELATED *ALLIUM* USING MICROSATELLITE MARKERS



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Onions (*Allium cepa* L.) are the second most valuable vegetable in the world. Despite its global culinary and economic significance, knowledge about onion genetic diversity and resources is limited.

The Vegetable Germplasm Bank of Zaragoza (BGHZ) (Spain) holds an important number of *Allium cepa* L. accessions, where most of the Spanish onion variability is represented (Carravedo and Mallor, 2007). In order to investigate the diversity of Spanish onion germplasm, a total of 85 onion Spanish landraces (*Allium cepa* L.) and 6 related *Allium* outgroups (*A. cepa* L. *aggregatum* group, *A. schoenoprasum*, *A. christophii*, *A. sphaerocephalon*, *A. ramosum*, and *A. senescens*) from the BGHZ collection were studied by means of simple sequence repeats (SSRs) markers.

The origin of studied accessions are shown in Figure 1 and the SSRs markers used are listed in Table 1.

Results showed that 12 from the 18 SSRs markers amplified were polymorphic and useful to distinguish all the studied accessions, being 11 SSRs of them polymorphic for onion landraces.

Within onion accessions, the variation for allele size ranged from 172 to 299 bp. The total number of detected alleles was 47, ranging from 2 for ACM006, ACM124, ACM146, and ACM235 to 7 for ACM045, with an average of 3.9 alleles per locus (Table 1).

Within related *Allium* accessions, the variation for allele size ranged from 158 to 299 bp. The total number of detected alleles was 45, ranging from 1 for ACM006 and ACM124 to 10 for ACM300, with an average of 3.75 alleles per locus.

Table 1. Allele size and SSR amplicons observed in Spanish onion accessions

Marker	Repeat motif	Allele number reported		Allele number observed	Expected size (bp)		Observed size (bp)	Heterozygosity observed
		Jakše et al. (2005)	McCallum et al. (2006)		Jakše et al. (2005)	McCallum et al. (2006)		
ACM004	(CAA) ⁴	3	3	3	203-213	227-236	220-230	0.53
ACM006	(CTC) ⁷	4	4	2	220-232	221-233	217-224	0.41
ACM045	(TC) ⁵	4	5	7	264-271	226-275	255-280	0.72
ACM101	(TCC) ⁵	4	8	5	209-221	227-248	227-239	0.68
ACM119	(AAT) ⁵	4	3	5	252-265	241-259	242-260	0.61
ACM124	(AAA) ⁵	3	5	2	220-245	224-250	217-225	0.41
ACM134	(GA) ⁵	4	5	5	192-204	198-212	192-206	0.81
ACM138	(CTGC) ¹¹	5	1	6	235-268	242-286	242-274	0.80
ACM146	(ACA) ⁵	2	2	2	213-216	239-242	230-233	0.98
ACM187	(GT) ⁵	4	5	4	228-264	225-262	228-266	0.84
ACM235	(TTTG) ⁴	-	4	2	-	292-304	288-299	0.41
ACM300	(GCA) ⁷	-	3	4	-	170-177	172-181	0.00

The molecular variability detected in this study agrees with the fact that Spain is part of the secondary centre of onion diversification.

This is the first study on genetic diversity assessment involving Spanish landraces.

References

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 Jakše J, Martin W, McCallum J, Havey MJ (2005) Single nucleotide polymorphisms, indels, and simple sequence repeats for onion cultivar identification. *J Amer Soc Hort Sci*, 130: 912-917.
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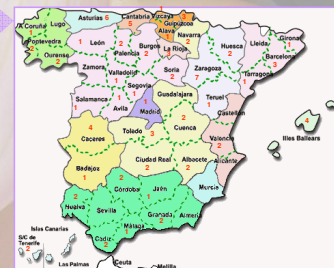
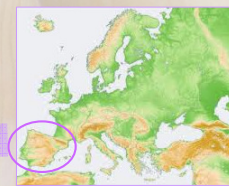


Figure 1. Origin of Spanish onion landraces (the number in red indicates total accessions studied for each province)

The resulting UPGMA dendrogram grouped the 91 *Allium* accessions according to their taxonomical classification, producing 6 main clusters (Fig 2).

Besides, within the *A. cepa* cluster, the *cepa* group (onions) and the *aggregatum* group (shallots) were correctly separated in two neighbour clusters.

The biggest cluster corresponded to onion landraces and was divided in seven subgroups, distinguishing all the accessions. The range of genetic distance was 0.69 – 0.95.

The subgroups were not clearly defined according to most relevant onion characteristics or their specific origins, previously reported for these accessions (Mallor et al., 2011).

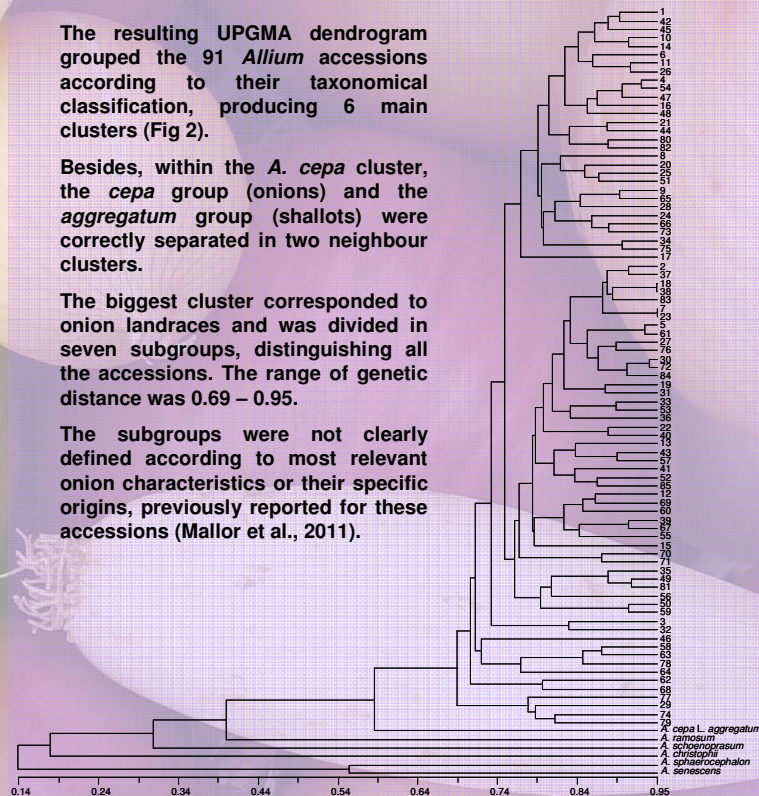


Figure 2. Dendrogram of 85 Spanish onion cultivars and 6 related *Alliums* revealed by UPGMA cluster analysis based on Dice's genetic similarity index estimates derived from SSR data.

ONION COLLECTION DIVERSITY

