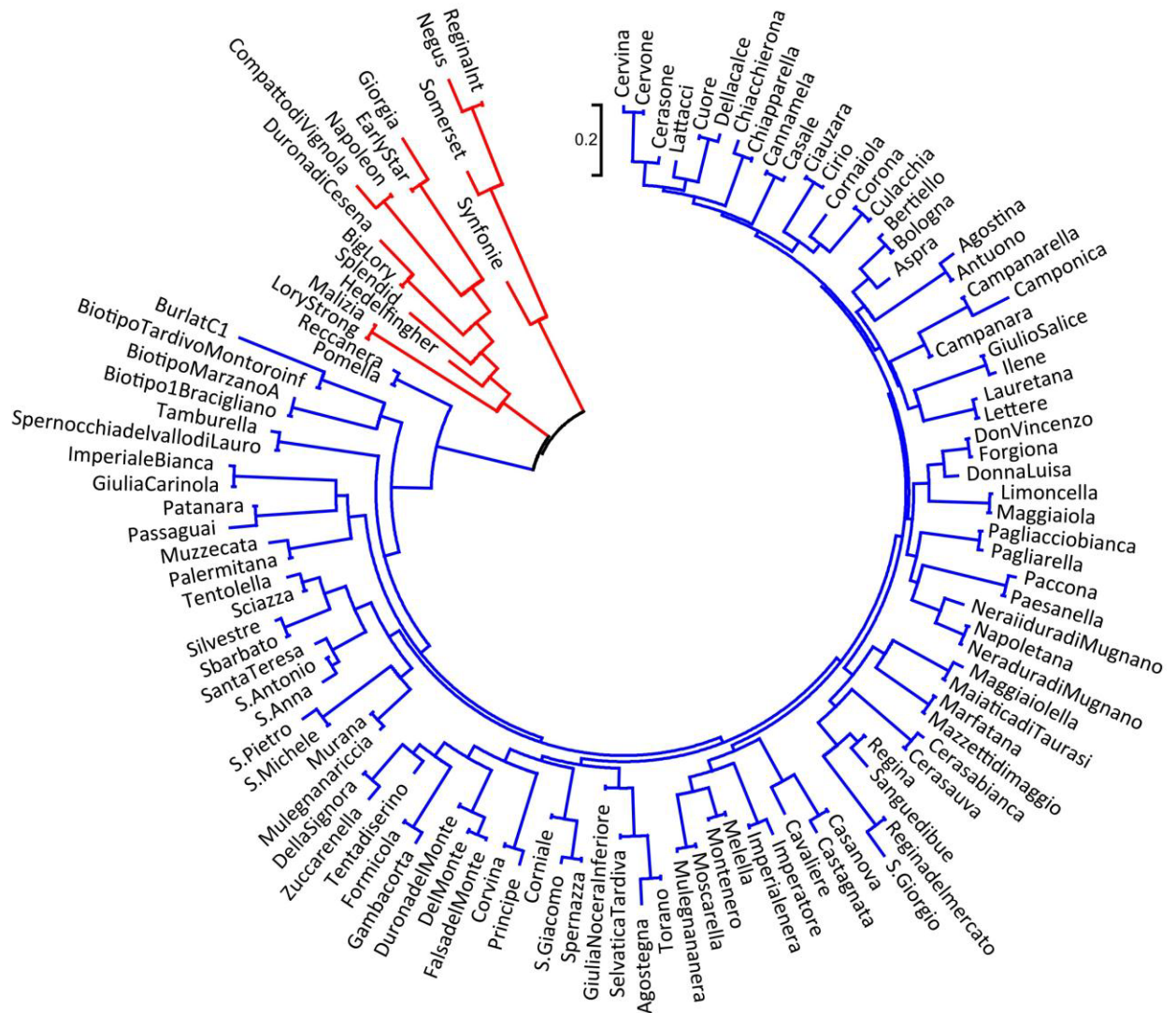


Molecular and environmental analysis of Campania (Italy) sweet cherry (*Prunus avium* L.) cultivars for biocultural refugia identification and conservation

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SUPPLEMENTARY FIGURES AND TABLES

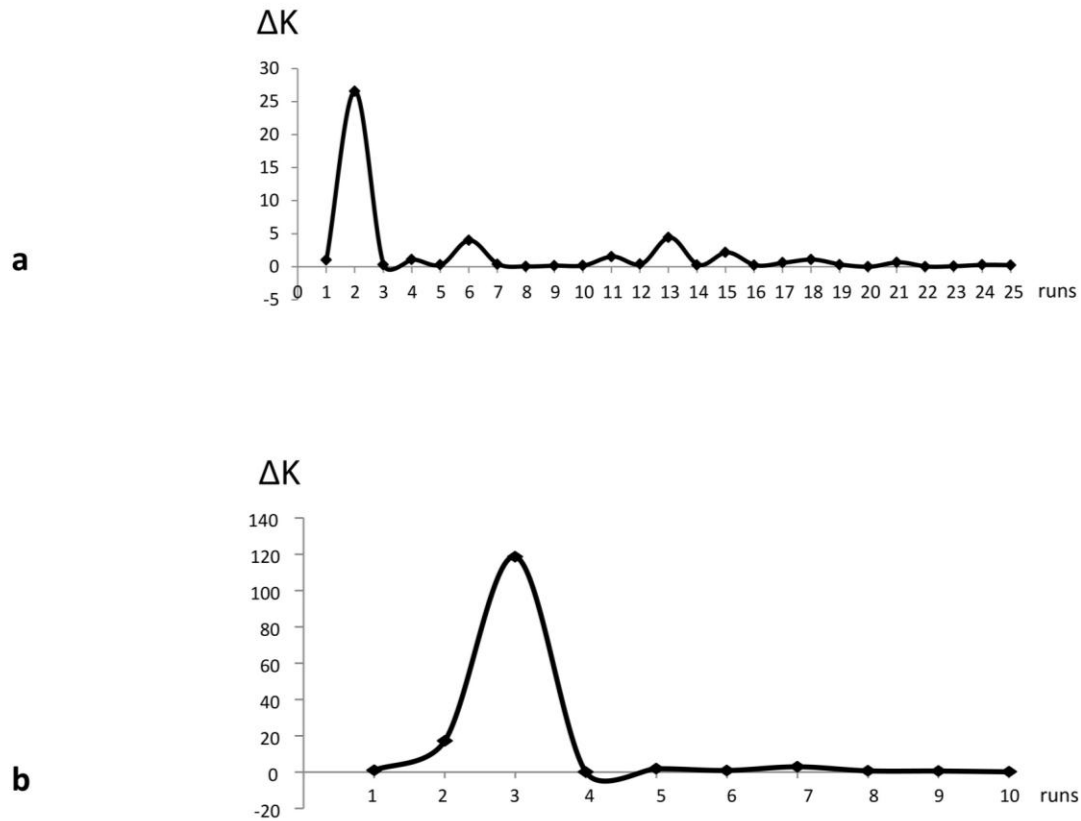
Supplementary Figure S1



Supplementary Figure S1. Genetic relationships of Campania sweet cherry cultivars with

International reference cultivars. The dendrogram was inferred using the the UPGMA method ⁵⁶.

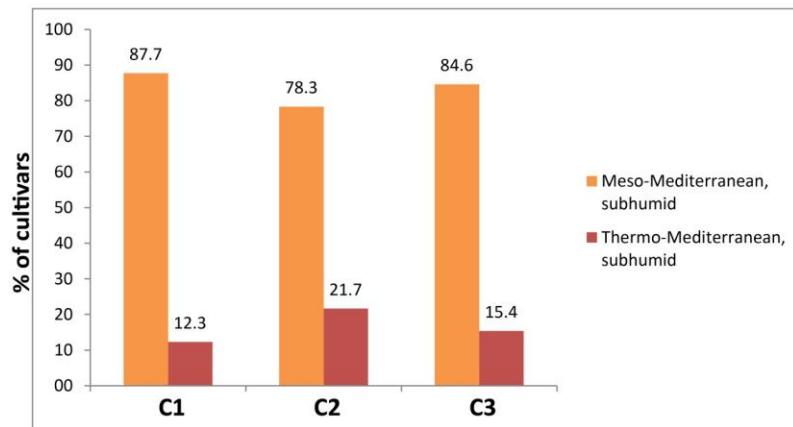
Supplementary Figure S2



Supplementary Figure S2. Graph representation of the ΔK values obtained using STRUCTURE analysis.

(a) Best $\Delta K=2$ was obtained with a burning period ranging from 5000 to 50000 with biased k from 1 to 25; **(b)** Best $\Delta K=3$ was obtained with a burning period ranging from 500000 to 750000 with biased k from 1 to 10.

Supplementary Figure S3



Supplementary Figure S3. Correlation of sweet cherry varieties' locations with bioclimate distribution.

83,5% of the analysed samples are exposed to the Meso-Mediterranean and the remaining 16,5% to the Thermo-Mediterranean bioclimate.

Supplementary Table S1

Locus	Accession No.	Repeat motif	Forward and Reverse primer sequences (5'-3')	Size range (bp)
EMPA001	AJ564644	[AG] ₄ GGGT[AG] ₂₆	F: FAM-GCTCTGCTGCTTCAACCATT R: TTCCAACACATTACCCC	144-164
EMPA004	AJ564647	[GA] ₄ AA[GA] ₄ AA[GA] ₁₅	F: NED-TACGGTAGGCTTCTGCAAGG R: TTGGCAGCCAACAAAATCA	168-192
EMPA005	AJ564648	[CT] ₂ CAT[CT] ₁₂ T[AC] ₂₃	F: PET-TGGGTTTGAGCAATATGCAA R: CACCAATACACATGCACACG	160-264
EMPA011	AJ564654	[AG] ₁₆	F: VIC-TGTGCTCACTCTCTGCTGCT R: TGTGTGGGGTTCACAGTCTCC	222-256
EMPA018	AJ564661	[AG] ₁₈	F: FAM-TCCAAGAACAAGCCAAAATC R: AATTTCAATGATTCTGGATAG	79-111
EMPA015	AJ56458	[GA] ₃₂	F: NED-TTTTGGTCAATCTGCTGCTG R: CTCTCATCTTCCCCTCCTC	193-252
EMPA012	AJ56455	[AG] ₁₃	F: PET-TGTGTGAAGGAAGCTTAAGAG R: TGGCTGATTGGGGTTAAGTC	227-237
EMPA506	ay526622	[CT] ₁₂	F: VIC-AAGCGGAAGCACAGGTAG R: TTGCTAGCATAGAAAAGAATTGTAG	190-226
EMPA502	ay526619	[TTG] ₂ CTGC[TG] ₁₀ [AG] ₈	F: FAM-CTACTTCCATGATTGCCTCAC R: AACATCCAGAACATCAACACAC	134-148
EMPA510	ay526626	[GA] ₂₈	F: NED-GCTAATATCAAATCCCAGCTCTC R: TGAAGAAGTATGGCTTCTGTGG	154-191
EMPA016	AJ564659	[AG] ₁₀	F: PET-CCAAACCAATTACCCAGAG R: GCCAATGTGCCAACCAATAAC	177-195
EMPA513	ay526629	[TC] ₁₁ [GT] ₃ AT[GT] ₅	F: VIC-GAATTGAAGCAACCAAGCAC R: TGGCACACTCTACCTAACATTC	203-223
EMPA512	ay526628	[TG] ₁₀ A[GA] ₁₀ AA[GA] ₁₃	F: FAM-TGTGCTAATGCCAAAATACC R: ACATGCATTTCAACCCACTC	123-149
EMPA501	ay526618	[GA] ₉ [GA] ₁₁	F: PET-CAAAATCAACAAAATCTAAACC R: CAAGAAGTCTCTAGCTCAAACC	224-242
EMPA514	ay526630	[TC] ₁₀ CCAT[TC] ₃ CCAT[TC] ₈	F: VIC-TCCGCATATCACAATCAAC R: TTCCACACAAAACCAATCC	173-212

Supplementary Table S1. List of the fifteen simple sequence repeats (SSRs) employed for genotyping the 113 cultivars, including nucleotide sequences, Accession No., repeat motifs and allelic size ranges (in bp).

Supplementary Table S2. List of the Campania's sweet cherry accessions analysed reporting the individual identification code (ID), related cultivar name (CV name), STRUCTURE individual number (STRUCTURE nr), cultivar number (CV nr) and all the amplified alleles of the SSRs loci as reported in Supplementary Table S1.

Supplementary Table S3

Locus	k	N	HExp	HObs	PIC	PD	P. A.	ARR	F(Null)	Fis	Fst	Fit
EMPA001	7	200	0,684	0,635	0,635	0,854	0	ND	0,037	-0.719	0.462	0.076
EMPA004	7	204	0,687	0,657	0,628	0,753	2	0,286	0,028	-0.716	0.494	0.131
EMPA005	13	194	0,62	0,552	0,581	0,662	5	0,385	0,045	-0.709	0.580	0.283
EMPA011	10	197	0,185	0,107	0,180	0,412	4	0,400	0,260	-0.796	0.821	0.678
EMPA018	12	203	0,694	0,764	0,642	0,789	4	0,333	-0,056	-0.786	0.393	-0.084
EMPA015	19	196	0,747	0,408	0,784	0,861	6	0,315	0,307	-0.543	0.684	0.512
EMPA012	6	196	0,497	0,337	0,427	0,552	2	0,333	0,187	-0.587	0.634	0.419
EMPA06	12	205	0,81	0,737	0,710	0,711	1	0,083	0,042	-0.713	0.477	0.104
EMPA02	7	202	0,774	0,871	0,737	0,88	0	ND	-0,069	-0.806	0.418	-0.050
EMPA10	10	205	0,748	0,785	0,710	0,954	3	0,300	-0,027	-0.765	0.439	0.010
EMPA016	5	201	0,615	0,801	0,534	0,662	1	0,200	-0,140	-0.873	0.350	-0.218
EMPA13	7	206	0,538	0,583	0,438	0,623	1	0,143	-0,045	-0.817	0.458	0.016
EMPA12	10	203	0,715	0,828	0,672	0,845	2	0,200	-0,083	-0.790	0.406	-0.063
EMPA01	9	197	0,736	0,843	0,687	0,722	3	0,333	-0,077	-0.806	0.473	0.049
EMPA14	4	202	0,53	0,465	0,417	0,556	1	0,250	0,064	-0.669	0.520	0.198
Mean	9,20	200,7	0,639	0,625	0,585	0,722	0,233	0,238	0,032	-0.740	0.507	0.137

Supplementary Table S3. Statistical analysis' data obtained by genotyping both Campania's and International reference's 206 sweet cherry individuals corresponding to 113 cultivars, using the fifteen SSR microsatellite markers.

For each locus, the allele number (k), the number of amplified samples (N), the expected (He) and observed (Ho) heterozygosity, the Polymorphic Index Content (PIC), Power Discrimination (PD), the private (P.A.)/total Alleles Richness Ratio (ARR), null alleles frequencies, F (Null), Inbreeding coefficient (Fis), Fixation Index (Fst) and Fit (Fitness) were calculated.