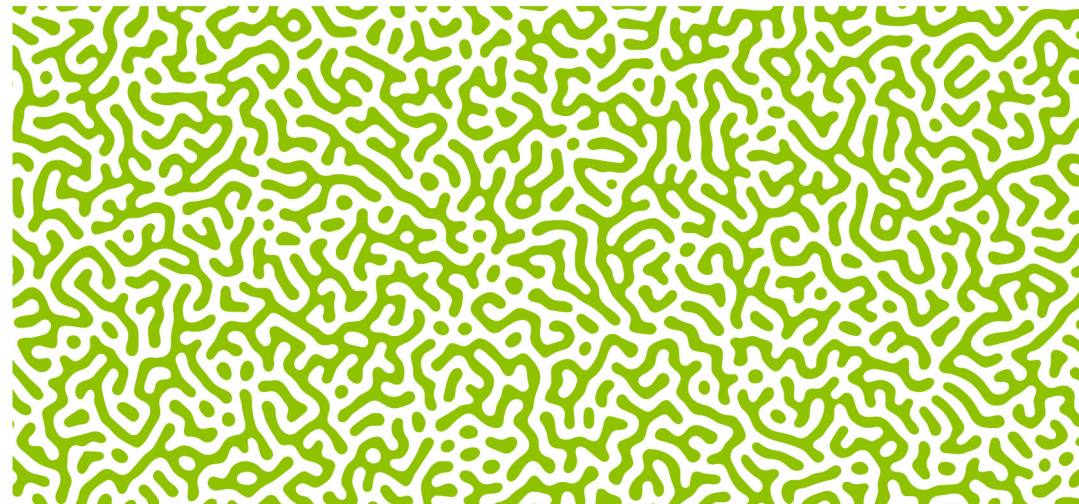




Settimana  
della  
Biodiversità  
Pugliese

Agricoltura  
Alimentazione  
e Ambiente

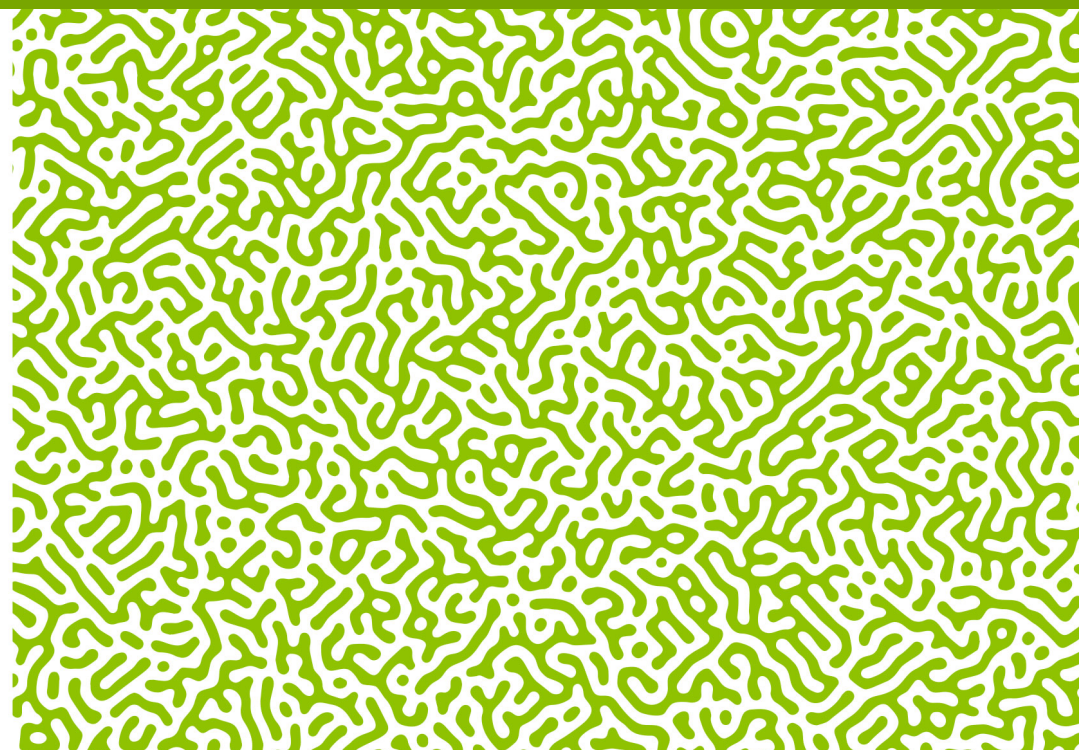
**17-21**  
**MAGGIO**  
**2021**



## ELENCO PUBBLICAZIONI BIODIVERSITÀ FRUTTIFERI RE.GE.FR.U.P.



PROGETTO  
**Re.Ge.Fru.P.**



**AKKAK, A., DE CHIARA, M.L., SAVASTANO, M., LUCHETTI, L., VENERITO, P.** *Genetic and chemical characterization of pomegranate (*Punica granatum L.*) cultivars grown in southern Italy. (2019) Acta Horticulturae, 1254, pp. 73-76. DOI: 10.17660/ActaHortic.2019.1254.11*

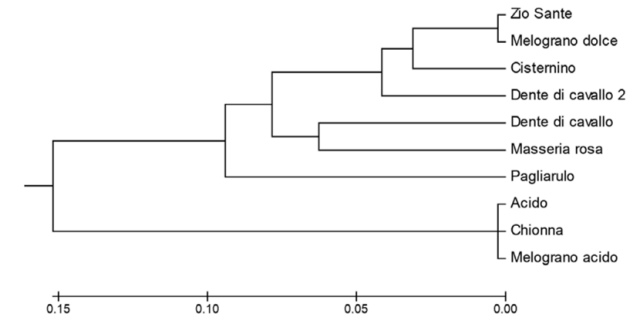


Figure 1. Dendrogram obtained by cluster analysis of 10 accessions, studied at 8 SSR loci.

**M. CHIUMENTI, B. NAVARRO, P. VENERITO, F. CIVITA, F. DI SERIO AND A. MINAFRA, 2019.** *Molecular variability of apple hammerhead viroid from Italian apple varieties supports the relevance in vivo of its branched conformation stabilized by a kissing loop interaction. Virus Research*

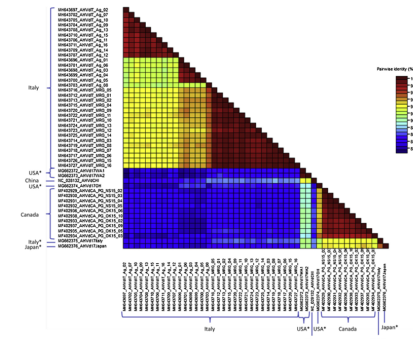


Fig. 1. Identity matrix generated by aligning HHVd sequence variants from AG and MBG isolates with those reported in literature. The geographic origin of the isolates is reported on the left and below the names of the variants. Asterisks denote isolates from germplasm collection.

**SUMMO, C., PALASCIANO, M., DE ANGELIS, D., PARADISO, V.M., CAPONIO, F., PASQUALONE, A.** *Evaluation of the chemical and nutritional characteristics of almonds (*Prunus dulcis* (Mill). D.A. Webb) as influenced by harvest time and cultivar. (2018) Journal of the Science of Food and Agriculture, 98 (15), pp. 5647-5655. DOI: 10.1002/jsfa.9110*

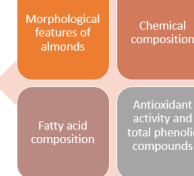
**Evaluation of the chemical and nutritional characteristics of almonds (*Prunus dulcis* (Mill). D.A. Webb) as influenced by harvest time and cultivar**

10 almond cultivars selected among the most widespread in the top producing countries (Australia, California, Italy, and Spain)

2 harvest time:

when the fruits were orange, but already edible, and showed green and moist hull;

when the fruits were ripe, with dry brown hull;



Lipid content  
Antioxidant activity and bioactive compounds  
Effect of the genotype

Protein content and carbohydrates

MARCOTULI, I., MAZZEO, A., NIGRO, D., GIOVE, S.L., GIANCASPRO, A., COLASUONNO, P., PRGOMET, Ž., PRGOMET, I., TARANTINO, A., FERRARA, G., GADALETA, A. *Analysis genetic diversity of Ficus carica L. (Moraceae) collection using simple sequence repeat (SSR) markers (2019) Acta Scientiarum Polonorum, Hortorum Cultus, 18 (4), pp. 93-109. DOI: 10.24326/asphc.2019.4.9*

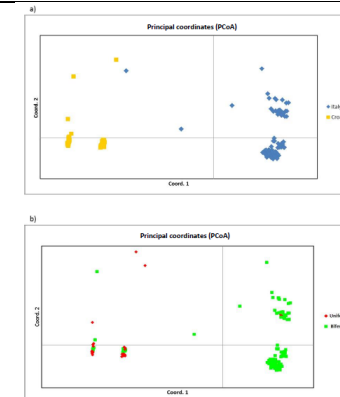


Fig. 1. Principal coordinates analysis (PCA) plot of the first two components obtained from 70 SSRs for 139 fig accessions. The first three axes explained the 63.40%, 6.95% and 7.40% of genetic variations, respectively for a total of 80.71%. The graph reported the subdivisions following to the geographical origin/location of the accessions and to the number of crops per year (underfive or biflorous).

FERRARA, G., MAZZEO, A., GALLOTTA, A., PACUCCI, C., MATARRESE, A.M.S., TARANTINO, A., INCERTI, O., MARCOTULI, I., NIGRO, D., BLANCO, A., GADALETA, A. *Fruit-set and SSR markers of fig cultivars from Puglia region, Southeastern Italy (2017) Acta Horticulturae, 1173, pp. 39-43. DOI: 10.17660/ActaHortic.2017.1173.7*

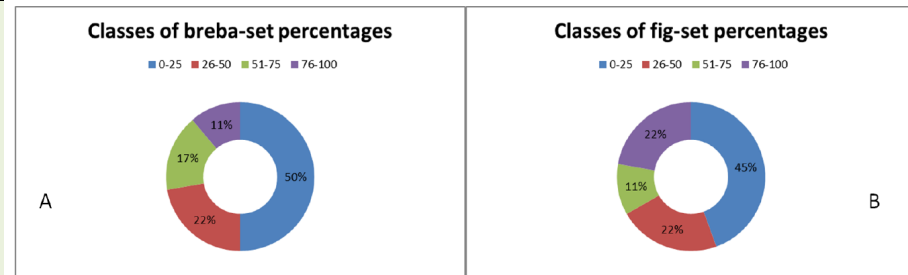


Figure 1. Breba-set (A) and fig-set (B) percentages of the examined cultivars in four classes of fruit-set, low (0-25), medium (26-50), high (51-75) and very high (76-100).

COSTA, F., MARCHESI, A., MAFRICA, R., DI VAIO, C., FERRARA, G., FRETTO, S., QUARTARARO, A., MARRA, F.P., MENNONE, C., VITALE, F., REALE, S., CARUSO, T. *Genetic diversity of fig (Ficus carica L.) genotypes grown in Southern Italy revealed by the use of SSR markers (2017) Acta Horticulturae, 1173, pp. 75-79. DOI: 10.17660/ActaHortic.2017.1173.13*

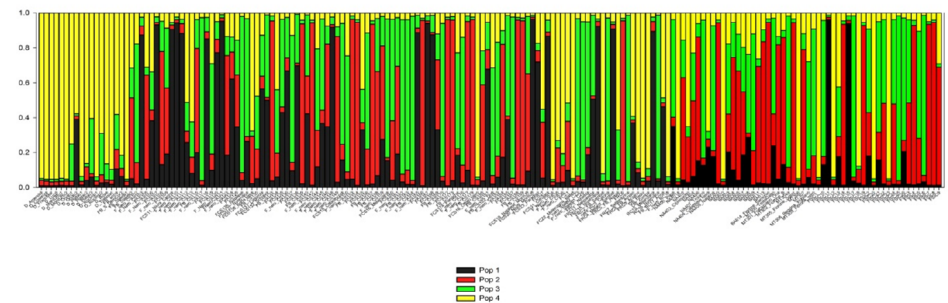


Figure 1. Inferred population structure for K=4 of 181 fig accessions from Southern Italy.

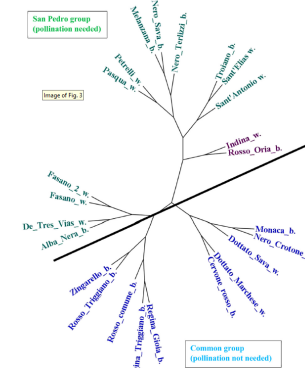


**GIANCASPRO, A., MAZZEO, A., GIOVE, L.S., ZITO, D., MARCOTULI, I., GALLOTTA, A., COLASUONNO, P., NIGRO, D., BLANCO, A., ARADHYA, M., GADALETA, A., FERRARA, G.** *Exploiting DNA-based molecular tools to assess genetic diversity in pomegranate (Punica granatum L.) selections and cultivars (2017) Fruits, 72 (5), pp. 292-305. DOI: 10.17660/th2017/72.5.5*



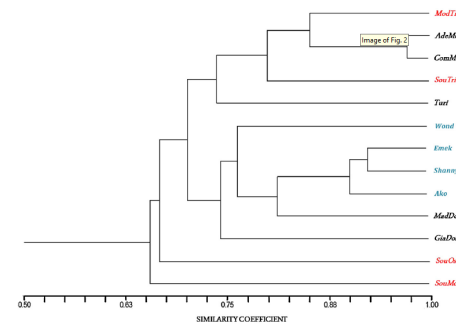
**FIGURE S1.** Tomb of the pomegranate at Egnazia (left) of the III century B.C. and a particular of the fruit close to the ceiling (right). Photos authorized by the National Archeological Museum of Egnazia - Polo Museale della Puglia, Italy.

**FERRARA, G., MAZZEO, A., PACUCCI, C., MATARRESE, A.M.S., TARANTINO, A., CRISOSTO, C., INCERTI, O., MARCOTULI, I., NIGRO, D., BLANCO, A., GADALETA, A.** *Characterization of edible fig germplasm from Puglia, southeastern Italy: Is the distinction of three fig types (Smyrna, San Pedro and Common) still valid? (2016) Scientia Horticulturae, 205, pp. 52-58. DOI: 10.1016/j.scienta.2016.04.016*



**Fig. 3.** Evolutionary relationships of figs. The evolutionary history was inferred using the Neighbor-joining method (Saitou and Nei, 1987). The tree is drawn to scale, with branch lengths in the same units as those of the evolutionary distances used to infer the phylogenetic tree. The upper and the lower part are the two groups determined by certification trials: San Pedro and Common, respectively.

**FERRARA, G., GIANCASPRO, A., MAZZEO, A., GIOVE, S.L., MATARRESE, A.M.S., PACUCCI, C., PUNZI, R., TRANI, A., GAMBACORTA, G., BLANCO, A., GADALETA, A.** *Characterization of pomegranate (Punica granatum L.) genotypes collected in Puglia region, Southeastern Italy (2014) Scientia Horticulturae, 178, pp. 70-78. DOI: 10.1016/j.scienta.2014.08.007*



**Fig. 2.** Dendrogram resulting from microsatellite (SSR) markers analysis showing genetic distance within a collection of 13 pomegranate ecotypes. In red are the sour genotypes; in dark-blue are the 4 Israeli varieties. Cluster analysis was performed using the UPGMA (unweighted pair group method with arithmetic averages) algorithm, and the jaccard coefficient in pairwise comparisons. (For interpretation of the references to color in this figure caption, the reader is referred to the web version of this article.)

**MARCHESE, A., GIOVANNINI, D., LEONE, A., MAFRICA, R., PALASCIANO, M., CANTINI, C., DI VAIO, C., DE SALVADOR, F.R., GIACALONE, G., CARUSO, T., MARRA, F.P.** *S-genotype identification, genetic diversity and structure analysis of Italian sweet cherry germplasm.* (2017) *Tree Genetics and Genomes*, 13 (5), art. no. 93. DOI: 10.1007/s11295-017-1176-2

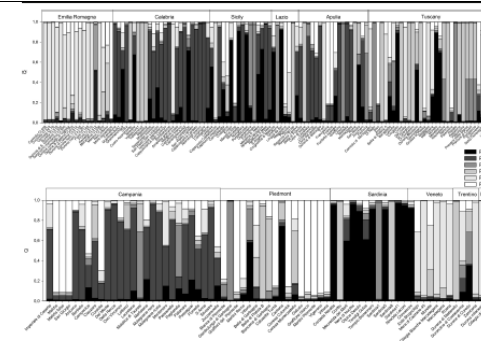


Fig. 1 Genetic structure of 186 Italian sweet cherry landraces, value. Sweet cherry accessions showing more than one colour may have an introgressed genetic makeup, originated from crossing. The vertical axis designates the membership value 1

**MARRA, F.P., BASSI, G., GAETA, L., GIOVANNINI, D., PALASCIANO, M., SIRRI, S., CARUSO, T.** *Use of phenoclimatic models to estimate the chill and heat requirements of four sweet cherry cultivars in Italy* (2017) *Acta Horticulturae*, 1162, pp. 57-64. DOI: 10.17660/ActaHortic.2017.1162.10

Table 2. Average estimated dates of beginning of CU and CH accumulation ( $\pm$  standard error/SE in days) and total chilling accumulation (Average  $\pm$  SE) according to Weinberger (CU) and Richardson (CH) within the end of February in the three Italian sites in the 1994-2013 period.

Location	Date (CU Model)	S.E. ( $\pm$ days)	Date (CH Model)	S.E. ( $\pm$ days)	CU ( $\pm$ SE)	CH ( $\pm$ SE)
Verona	Oct. 18	2.7	Oct. 9	2.5	1693 $\pm$ 51	1831 $\pm$ 34
Forli	Oct. 23	2.1	Nov. 1	2.4	1939 $\pm$ 38	1865 $\pm$ 63
Bari	Nov. 1	6.3	Oct. 31	6.5	1575 $\pm$ 48	1067 $\pm$ 59

The actual blooming date of each of the cultivars studied varied depending on the year and site. In terms of blooming time (Figure 1), Bari resulted in the earliest but also the more variable environment, while Verona was the least variable site.

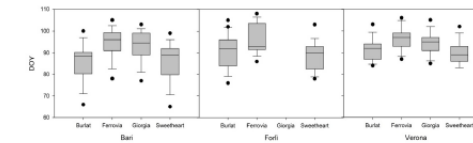


Figure 1. Box plot of BF dates of four sweet cherry cultivars in three contrasting sites environments.

**PALASCIANO, M., GAETA, L.** *Comparison of different models for chilling requirements evaluation of sweet cherry cultivars in a Mediterranean area.* (2017) *Acta Horticulturae*, 1161, pp. 405-410. DOI: 10.17660/ActaHortic.2017.1161.65

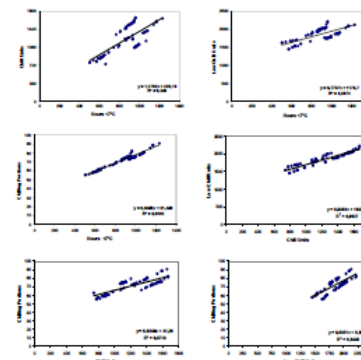


Figure 1. Correlation between the chilling requirements of ten sweet cherry cultivars, calculated as hours below 7°C, chill units, low chill units and chilling portions.

**MARCHESE, A., MARRA, F.P., PRIOLO, D., CARUSO, T., GIOVANNINI, D., LEONE, A., MAFRICA, R., PANGALLO, S., PALASCIANO, M., DE SALVADOR, F.R.** *Identification of (in)compatible S-genotypes and molecular characterisation of Italian sweet cherry cultivars (2017) Acta Horticulturae*, 1161, pp. 41-46. DOI: 10.17660/ActaHortic.2017.1161.6

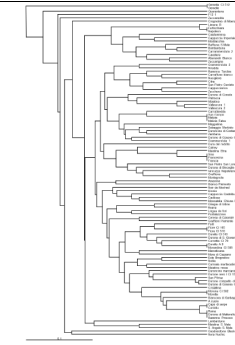
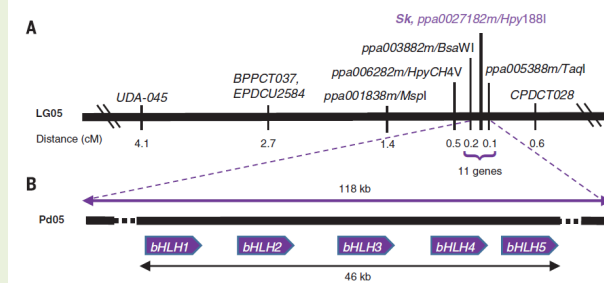


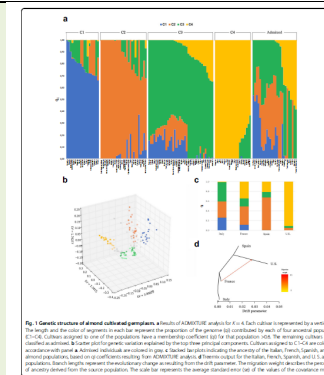
Figure 1. UPGMA dendrogram of 94 Italian sweet cherry accessions and six reference cultivars, based on 10 SSR loci and the 2-locus.

**SÁNCHEZ-PÉREZ, R., PAVAN, S., MAZZEO, R., MOLDOVAN, C., AIESE CIGLIANO, R., DEL CUETO, J., RICCIARDI, F., LOTTI, C., RICCIARDI, L., DICENTA, F., LÓPEZ-MARQUÉS, R.L., LINDBERG MØLLER, B.** *Mutation of a bHLH transcription factor allowed almond domestication. (2019) Science*, 364 (6445), pp. 1095-1098. DOI: 10.1126/science.aav8197



**Fig. 1. Map-based cloning of the Sk gene.** (A and B) Comparison of linkage group 5 (LG05) (A) and pseudomolecule 5 (Pd05) (B) in the region where the Sk locus is mapped. Approximate positions of the five bHLH genes present within that region are shown.

**PAVAN, S., DELVENTO, C., MAZZEO, R., RICCIARDI, F., LOSCIALE, P., GAETA, L., D'AGOSTINO, N., TARANTO, F., SÁNCHEZ-PÉREZ, R., RICCIARDI, L., LOTTI, C.** *Almond diversity and homozygosity define structure, kinship, inbreeding, and linkage disequilibrium in cultivated germplasm, and reveal genomic associations with nut and seed weight (2021) Horticulture Research*, 8 (1), art. no. 15. DOI: 10.1038/s41438-020-00447-1



**Fig. 1. Genetic structure of almond cultivars.** a) Results of ADMIXTURE analysis for 416 46k cultivars implemented by vertical bar. The height and the color of segments in each bar represent the proportion of the genome contributed by each of four ancestral populations. b) 3D-PCA. Cultivar assigned to one of the populations has a membership coefficient (K) for that population. c) K=4. The remaining cultivars were classified as admixed. d) Color and size of pie charts representing the four principal components of genetic structure (PC1, PC2, PC3, and PC4) associated with each cultivar. e) Ancestral individuals are colored in gray. f) Pie charts indicating the ancestry of the Italian, French, Spanish, and US almond populations based on a coefficient matrix from ADMIXTURE analysis of the reference cultivars. The pie charts represent the proportion of ancestry from each of the four populations. The size of the pie charts represents the average squared distance of the value of the membership matrix.