

# Genetic variability of feral almond (*Prunus dulcis* (Mill.) D.A.Webb) and walnut (*Juglans regia* L.) plants from northern Italy

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## BACKGROUND

Walnut and almond are long-lived trees, cultivated worldwide for edible seeds. Both two species were among the earliest domesticated fruit trees, with domestication centers very likely placed in Near and Middle East. The current distribution range of the two species can be viewed as the result of a long-standing, continuous, and complex interaction among various factors, including climate, human cultivation and usage, and biogeography. Their cultivation has been historically based, until recent times, on seedborne trees leading to a very complex genetic differentiation. This research was carried out with the main goal to characterise the genetic variability of feral or very old cultivated accessions of these two species as a first step in the identification of valuable genetic resources to be preserved and to enhance commercial varieties.

## MATERIALS AND METHODS

- Samples:
  - 64 feral or century old cultivated almond accessions
  - More than 100 walnut accessions, both spontaneous or old cultivated plants
- Sampling area (Figure 1):
  - Oltrepò Pavese (PV) (Figure 2) for both species
  - Valchiavenna (SO) (Figure 3) exclusively for walnut
- DNA analysis:
  - The almonds DNAs were analysed by using the AxiomTM60K-SNP-Almond array. 51,537 variants were initially detected, after filtering 11,223 variants were retained and used
  - The walnut DNAs were analysed by using 12 SSR markers
- Morphological characterization ((Figure 4,5) :
  - For both species according to UPOV guidelines



Figure 1. Lombardy map and the two sites of interest

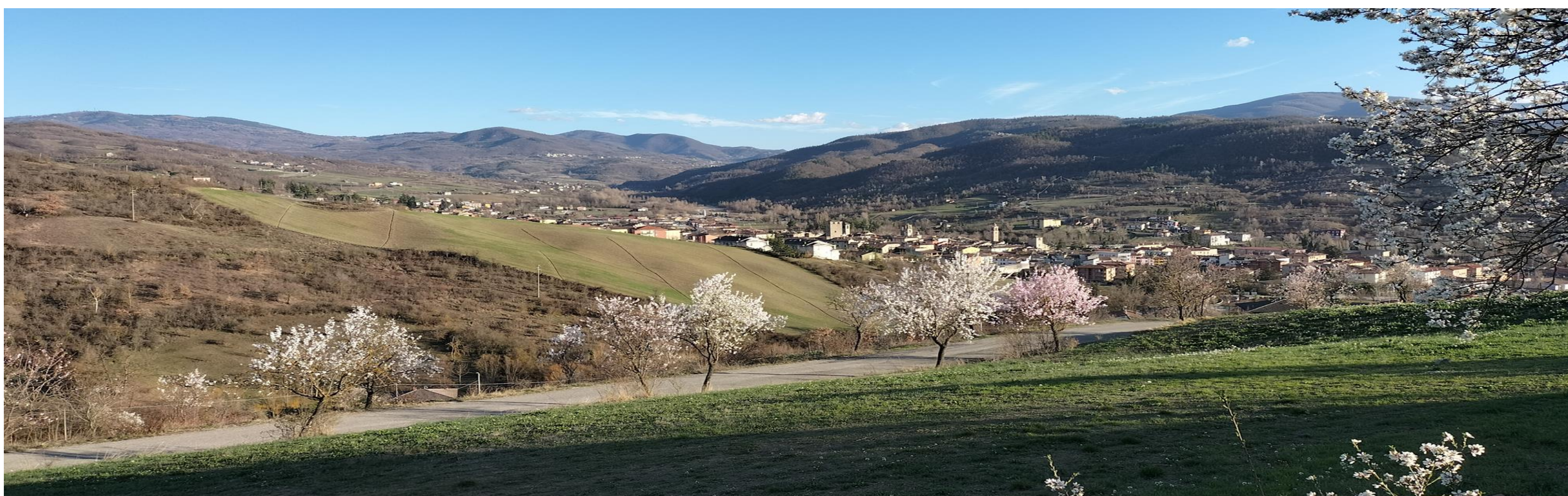


Figure 2. View of an almonds sampling site over the town of Varzi (PV)



Figure 4. Almond perspective views

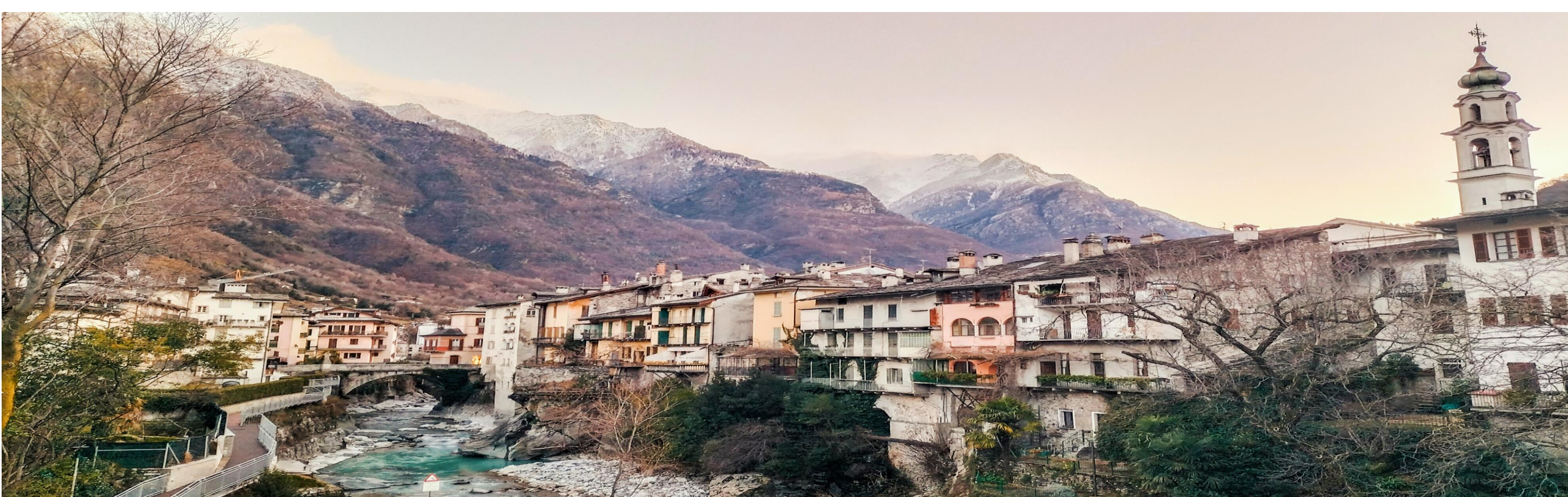


Figure 3. View of the town of Chiavenna (SO)



Figure 5. Walnut perspective views

## RESULTS

- Walnuts: The analyses revealed that, regardless of the sampling site, the walnut feral germplasm of Lombardy is characterised by high genetic variability, making it impossible to establish clusters based on the sampling locations. A comparison with Italian germplasm indicates that Lombardy accessions group with those from other northern regions of Italy, slightly distinguishing them from accessions found in southern Italy. Finally, a comparison with international germplasm reveals a gradient of genetic variability from Asia to Western Europe, with Lombardy accessions clustering closely with other Western European accessions (Figure 6).
- Almonds: A high level of genetic variability was observed, with the presence of four (Figure 7) main genetic backgrounds that may be indicative of a common origin of the corresponding accessions. In parallel, the presence of admixed individuals can be the consequence of spontaneous crosses among the different backgrounds.

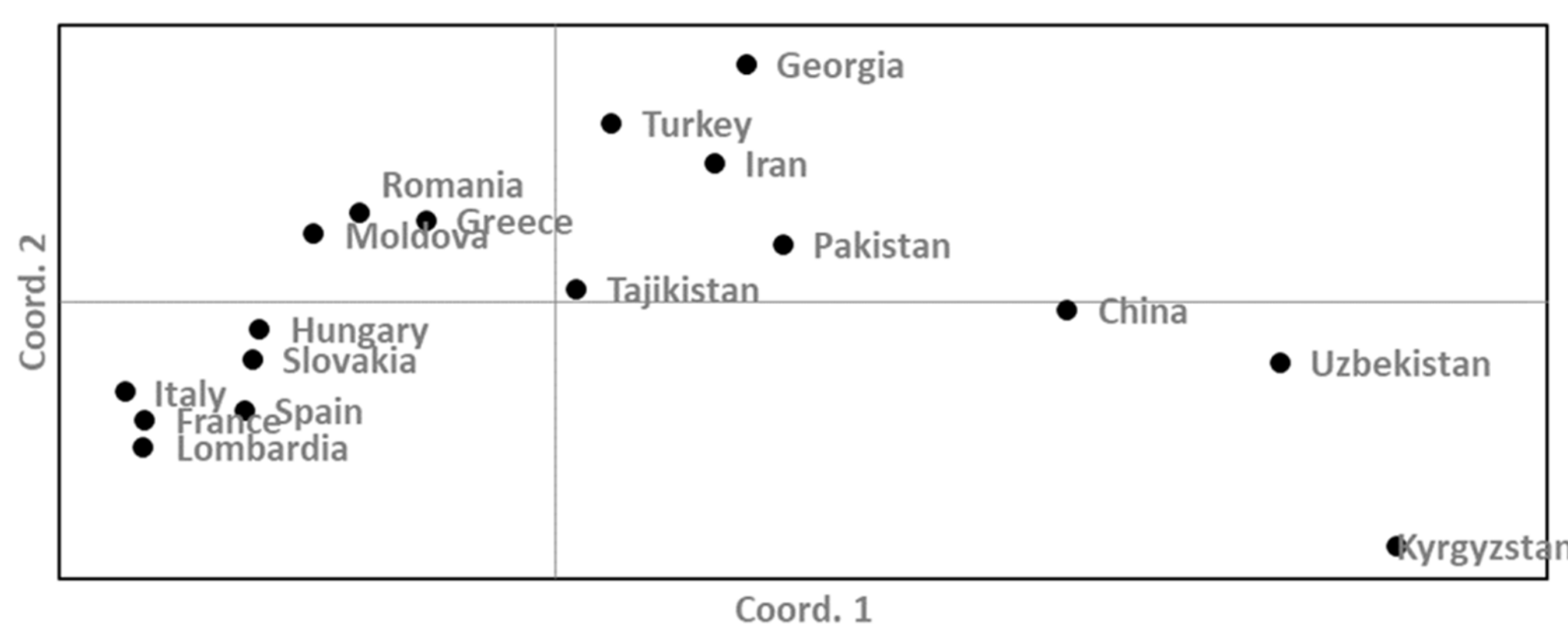


Figure 6. PCA of Lombardy and international walnut germplasm

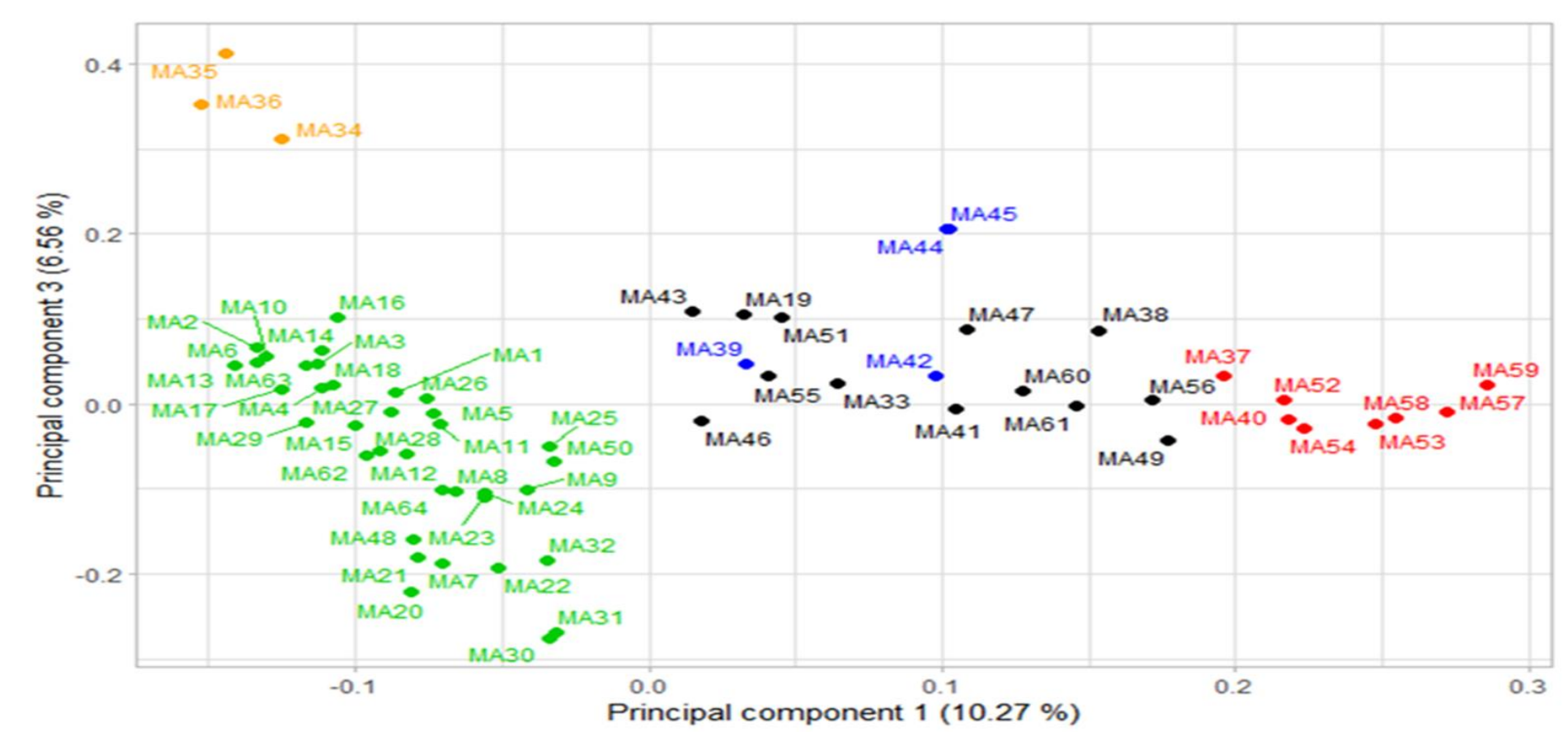


Figure 7. PCA of the almond accessions investigated

## ACKNOWLEDGEMENTS

Research activities were carried out in the frame of: VALHALLA, PSR RL Operazione 10.2.01-BIO 2022, CUP: J33C22003240009 (Survey and Genetic analysis) and CN\_00000033, Decreto Direttoriale MIUR n. 1034 17/06/2022 di concessione del finanziamento, CUP B43C21000920006, «National Biodiversity Future Center – NBFC» (Bioinformatic analysis).