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RESEARCH ARTICLE

The bean (*Phaseolus* spp.) landraces of the Lombardy Alps (Northern Italy): characterization and prospects for their valorization

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Abstract The loss of agrobiodiversity is a world damage both in biological and cultural aspects. Although mountainous areas in Italy still preserve many traditional cultivars (landraces), they face increasing risk from genetic erosion and disappearance. This study focused on the identification and multidisciplinary characterization of 16 previously undocumented bean landraces (*Phaseolus vulgaris* and *P. coccineus*) from the Lombardy Alps (Italy) using genetic, morphological, nutritional and ecological approaches. Genetic analyses based on simple sequence repeat (SSR) markers revealed moderate but structured diversity among 18 bean genotypes, with 1–5 alleles per locus and polymorphism information content (PIC) values ranging from 0 to 0.772. The principal coordinate analysis (PCoA) explained 66.01% of total genetic variation and, together with the unweighted pair group method with arithmetic mean (UPGMA) clustering, clearly separated landraces from commercial controls and distinguished *P. vulgaris* from *P. coccineus*, highlighting high intra-specific variability likely linked to geographic origin and absence of formal breeding. In contrast, morphological outline analysis and nutritional profiling showed that each landrace possesses unique and distinctive traits without major intra-specific variation. All beans showed high levels of proteins (20–29%) and some accessions (pigmented seeds) had a good quantity of antioxidants and other functional compounds, reinforcing their value as nutritious and health-promoting products. Furthermore, the ecological assessment indicated a shared competitive/competitive-ruderal strategy while morphometric seed analysis explained 90.9% of total shape variation (LD1 = 60.5%; LD2 = 30.4%) and identified three main morphotypes (reniform, elliptic, roundish), without clustering consistent with species or genetic groups. The results underscore the remarkable intra-genus and intra-specific diversity within *Phaseolus* landraces suggesting that this variability is genetic, nutritional and phenotypic. Their cultivation (on farm conservation) and integration into local value chains

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could support sustainable development in marginal areas and bring new opportunities for mountain economies. Moreover, the data collected provide a scientific basis for the registration of these landraces in Italian and European agrobiodiversity registers, a key step for their protection and promotion.

Keywords Plant diversity · Conservation · Traditional cultivars · Mountain resources · Nutritional composition · Biodiversity loss

Introduction

In the last few decades, the principles and methods of biodiversity conservation have become some of the most crucial and debated issues, due to the alarming fact that over a third of known species are now at risk of extinction, including those of agri-food interest (agro-biodiversity). A report issued by The Food and Agriculture Organization of the United Nations (FAO) showed that 75% of global agrobiodiversity has been lost in just a century, and today, three-quarters of the world's food supply comes from just twelve plant species and five animal species (Esquinas-Alcázar 2005; FAO 2010; CBD 2025; Hailu 2025).

This decline poses a serious threat not only to the planet's biodiversity but also to the variety of foods available to humans and other species (Spataro and Negri 2013). Plant genetic resources for food and agriculture include modern cultivars, crop wild relatives, and landraces (Villa et al. 2005; Spataro and Negri 2013). Landraces, also called local or traditional cultivars, are defined as dynamic populations of cultivated plants with a historical origin, a distinct identity, and no formal crop improvement (Spataro and Negri 2013). They are locally adapted and are closely tied to traditional farming systems (Villa et al. 2005; Piergiovanni and Lioi 2010; Almeida et al. 2023; Romero-Astudillo et al. 2024).

Additionally, the erosion of these resources undermines the cultural heritage linked to agri-food traditions, which play a crucial role in shaping the identity of specific communities and regions (Losa et al. 2025). As genetic erosion intensifies, the sustainable farming practices are at risk of disappearing, taking with them centuries-old knowledge that could hold the key to tackling upcoming agricultural issues (Frison et al. 2011; Giupponi et al. 2020a, 2021a; Raggi et al. 2022).

In response to these challenges, the European Union has developed a series of strategic initiatives aimed at protecting agrobiodiversity, Key initiatives include the EU Biodiversity Strategy 2020 (EU Commission 2010), the 2030 Agenda for Sustainable Development (United Nations 2015), the National Recovery and Resilience Plan (PNRR), and the European Register of Conservation Varieties (EU Commission 2023). The latter is among the most advanced tools implemented by the EU to promote the in situ conservation of landraces (Spataro and Negri 2013).

Italy is rich in plant agrobiodiversity and it boasts a significant number of landraces, particularly in mountainous and hilly regions (Giupponi et al. 2020a, 2021a). However, it also faces the progressive loss of traditional cultivars (Pacicco et al. 2018; Negri 2003) and the Italian government established the National Register of Agrobiodiversity (Ministerial Decree 2019/39407 accessed on 1 September 2023; https://rica.crea.gov.it/APP/anb/) to protect and promote agricultural and food resources from the risk of genetic erosion and extinction. Created in December 2019 in accordance with Law No. 194/2015 ("Provisions for the conservation and enhancement of biodiversity of agricultural and food interest"), this register complies information on landraces submitted by the regions to the Italian Ministry for Agriculture and Forestry in recent years. The register indicated that 12 out of 20 Italian regions had no landraces, including Lombardy (Giupponi et al. 2021a), one of the most industrialized areas in the Alpine macro-region (EU Commission 2017) and among the most productive Italian regions for horticulture (ISTAT 2020; ISMEA 2014). Despite these efforts, regions like Lombardy still face significant challenges in identifying and protecting their unique landraces, which are essential not only for conserving biodiversity but also for fostering sustainable agricultural practices.

A previous study which assessed the presence of landraces currently cultivated in Lombardy (Giupponi et al. 2020a), mainly in alpine and hilly zones, revealed that the first Italian inventory of in situ maintained landraces only included eight herbaceous traditional cultivars. Based on the outcomes of this study, several actions were recommended to strengthen Lombardy's and Italy's efforts to protect plant agrobiodiversity. These actions include performing a comprehensive census and regular updates of both cultivated and conserved landraces, characterizing the agronomic and nutritional properties of landraces to promote the development of sustainable agri-food chains and implementing legislative measures to protect both the landraces and the territories from which they originate.

Among these, the *Fabaceae* family (legumes) stands out, both for its agricultural importance and for its role in traditional diets (Ceccarelli 2012; Giupponi et al. 2021a). In fact, they might represent one of the main food and income sources in marginal and mountain areas (Alcázar-Valle et al. 2020; Rodríguez Madrera et al. 2021; Aquino-Bolaños et al. 2021). In these areas, legumes such as beans (*Phaseolus* spp.) have historically been a primary source of food and income, offering high-protein content (around 20 g/100 g) and serving as a meat substitute for rural communities (Alicandri et al. 2024), including that of Lombardy.

In developed countries like Italy, the nutritional properties of bean landraces are important for promoting their integration into local agri-food chains and supporting their cultivation and *on-farm* (in situ) conservation (Pedrali et al. 2022). Nevertheless, most Italian and Lombardy bean landraces remain largely undocumented in terms of distinctness traits, such as nutritional composition, genetic structure, morphological variability, and ecological characteristics, limiting their potential for valorization (Losa et al. 2025). Exploring and disseminating this information is essential for safeguarding these resources and enhancing their role in sustainable agri-food systems (Alicandri et al. 2024).

Landraces are indeed genetic resources of particular interest for both the technical and scientific sectors (for example, for the development of products or food ingredients with high added value and in plans for the genetic improvement of crops) in socio-economic areas, especially marginal areas, since an intensive farming model is not applicable for several physical, social, cultural or economic limitations (Giupponi and Leoni 2020; Raggi et al. 2022; Fenzi and Couix 2022).

In recent years, a renewed interest in local bean cultivars has emerged in Northern Italy, driven by consumers seeking traditional and high-quality products. However, despite their nutritional and agronomic value, many traditional Lombardy bean cultivars remain undocumented and at risk of genetic erosion (Giupponi et al. 2020a). Most are not preserved in germplasm banks but are still cultivated by a handful of small-scale farmers and hobbyists, making them particularly vulnerable to extinction (Rossi et al. 2019; Giupponi et al. 2020a).

For these reasons, this research aims to genetically, morphologically, ecologically, and nutritionally characterization of 16 previously undocumented bean landraces cultivars (*P. vulgaris* and *P. coccineus*) cultivated and preserved for decades in the Lombardy region. The objective is to assess their diversity and distinctive traits in order to deepen knowledge of plant agrobiodiversity in Northern Italy, support the inclusion of these landraces in national and European registers dedicated to agrobiodiversity protection, and promote their use in crop improvement programs and in high-value, sustainable agri-food systems.

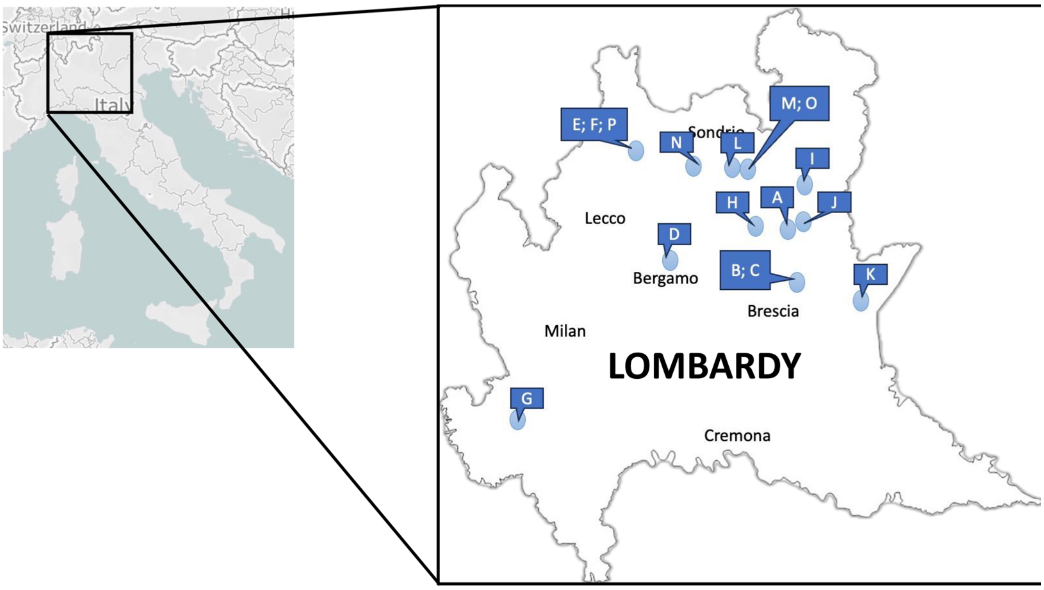
Materials and methods

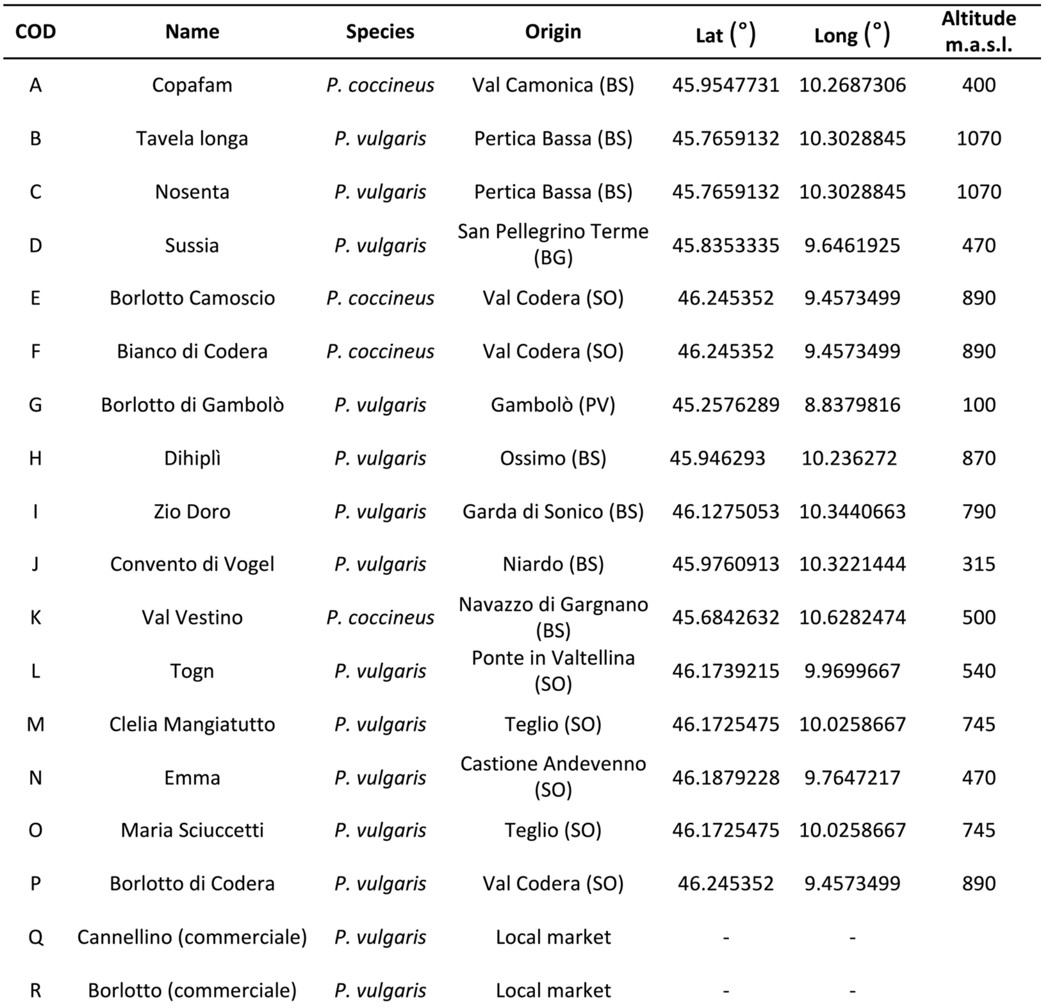
Plant material

Based on the census of Lombardy landraces by Giupponi et al. (2020a), 16 bean landraces were identified in Lombardy (Northern Italy); between 2020 and 2022 (Fig. 1).

These landraces have been cultivated in mountainous areas for over 30 years by local farmers, mainly hobbyists, primarily for self-consumption. Twelve landraces are *P. vulgaris* L. while only four are *P. coccineous* L. Plant identification was conducted using the dichotomous keys of Pignatti (2017) and the landrace data collected was verified to ensure it matched the characteristics outlined by Camacho Vila et al. (2005).

In 2023, the seeds of the 16 landraces were cultivated again in their original fields, following traditional farming practices under the supervision of researchers. This approach aimed to prevent potential hybridizations or phytopathological issues and allowed for the collection of morphological and agronomic data for each landrace. Approximately 500 g of each landrace were allocated for genetic analysis, and for morphometric and nutritional assessments of the seeds. For comparison, two commercially available





COD	Name	Species	Origin	Lat (°)	Long (°)	Altitude m.a.s.l.
A	Copafam	*P. coccineus*	Val Camonica (BS)	45.9547731	10.2687306	400
B	Tavela longa	*P. vulgaris*	Pertica Bassa (BS)	45.7659132	10.3028845	1070
C	Nosenta	*P. vulgaris*	Pertica Bassa (BS)	45.7659132	10.3028845	1070
D	Sussia	*P. vulgaris*	San Pellegrino Terme (BG)	45.8353335	9.6461925	470
E	Borlotto Camoscio	*P. coccineus*	Val Codera (SO)	46.245352	9.4573499	890
F	Bianco di Codera	*P. coccineus*	Val Codera (SO)	46.245352	9.4573499	890
G	Borlotto di Gambolò	*P. vulgaris*	Gambolò (PV)	45.2576289	8.8379816	100
H	Dihiplì	*P. vulgaris*	Ossimo (BS)	45.946293	10.236272	870
I	Zio Doro	*P. vulgaris*	Garda di Sonico (BS)	46.1275053	10.3440663	790
J	Convento di Vogel	*P. vulgaris*	Niardo (BS)	45.9760913	10.3221444	315
K	Val Vestino	*P. coccineus*	Navazzo di Gargnano (BS)	45.6842632	10.6282474	500
L	Togn	*P. vulgaris*	Ponte in Valtellina (SO)	46.1739215	9.9699667	540
M	Clelia Mangiatutto	*P. vulgaris*	Teglio (SO)	46.1725475	10.0258667	745
N	Emma	*P. vulgaris*	Castione Andevenno (SO)	46.1879228	9.7647217	470
O	Maria Sciuccetti	*P. vulgaris*	Teglio (SO)	46.1725475	10.0258667	745
P	Borlotto di Codera	*P. vulgaris*	Val Codera (SO)	46.245352	9.4573499	890
Q	Cannellino (commerciale)	*P. vulgaris*	Local market	-	-	
R	Borlotto (commerciale)	*P. vulgaris*	Local market	-	-	

◂**Fig. 1** Bean (*Phaseolus* spp.) samples and their cultivation areas

Phaseolus vulgaris market classes (Cannellino and Borlotto), purchased from a local food market, were cultivated in two experimental fields.

Genetic analysis

The genetic analysis was performed on the DNA extracted from the leaves of the 18 cultivars (16 landraces and the two commercials' beans) (Fig. 2) using 20 simple sequence repeat (SSR) markers (Table 1). Out of 20 SSRs with high polymorphism information content (PIC) values (Grisi et al. 2007; Panzeri et al. 2011), we selected 15 markers that showed the most robust amplification throughout the study; five markers (PV128, PV131, PV167, BM153, and BM187) were discarded.

For each cultivar, two seeds were germinated in the laboratory under controlled conditions and their leaves were sampled and crushed and then used for DNA extraction following the Steve1 method modified (Ghidoli et al. 2024). Genomic DNA quantity and purity were assessed by spectrophotometry by measuring absorbance at 260 and 280 nm.

For each PCR reaction, 5–10 ng of genomic DNA were used as template. PCR reactions were performed in a thermocycler, where the amplification conditions consisted of a first denaturation cycle at 94°C for 2' followed by 35 denaturation cycles for 1' at 94°C, primer annealing at the reported annealing temperature in Table 1 (Tm) for 1' and extension for 1' at 72°C, with a final extension cycle for 5' at 72°C. To verify successful amplification and the presence of single specific bands, the amplified fragments were analyzed by electrophoresis on a 4% agarose gel stained with ethidium bromide.

After verifying successful amplification using unlabelled primers, PCRs were repeated using 6-FAM–labelled primers to enable fragment sizing and determination of the base-pair length of each amplicon. Sizing analysis was performed as an outsourced service by BMR Genomics (Padova, Italy).

The results were used to construct a binary data matrix for Principal Coordinate Analysis (PCoA), performed using GenAlEx version 6.5 (Peakall and Smouse 2012). Genetic diversity parameters, including the number of alleles (Na), effective number of alleles (Ne), Shannon's information index (I), and polymorphic information content (PIC), were also calculated using GenAlEx. In addition, a cluster analysis based on the UPGMA (Unweighted Pair Group Method with Arithmetic Mean) algorithm was carried out to assess genetic similarity among landraces and commercial cultivars.

Ecological and agronomic analysis

The analysis of the competitor, stress-tolerator, ruderal (CSR) functional strategy of Grime (Grime 2001) of all 18 genotypes was performed according to the method proposed by Pierce et al. (2017). In detail, 10 fully expanded leaves of each genotype were collected in the experimental fields during July 2023. The leaf samples were collected from different plants considering those without disease. All the 10 leaf samples collected were wrapped in moist paper and stored at 4 °C overnight. Leaf fresh weight was measured (Precisa XB 220A, 0.0001 g), digitized (Samsung X3280NR) and it was calculated their area using ImageJ software (Schneider et al. 2012). Beans' dry weight was measured after oven-drying at 105 °C overnight. CSR values and functional strategy of beans samples were determined using 'StrateFy' spreadsheet (Pierce et al. 2017) and were plotted in the CSR ternary graph using R software (R Core Team 2025).

In field, phenotypic data were collected for all landraces through the completion of UPOV morphological descriptors. These forms provide essential information for the potential registration of these cultivars in official biodiversity or conservation registers.

Geometric morphometric analysis

All landraces seed samples and those of the two commercial beans collected from local markets were employed to analyze the outline analysis (elliptical Fourier descriptors analysis) (Giupponi and Giorgi 2019a). For each genotype, 30 seeds were randomly selected. Each seed sample was positioned on a white table and photographed using a professional digital camera installed perpendicularly to the surface. The images of the beans were modified using Adobe Photoshop software removing the shadows and the images were transformed into black and white. The outline coordinates were extracted with Momocs

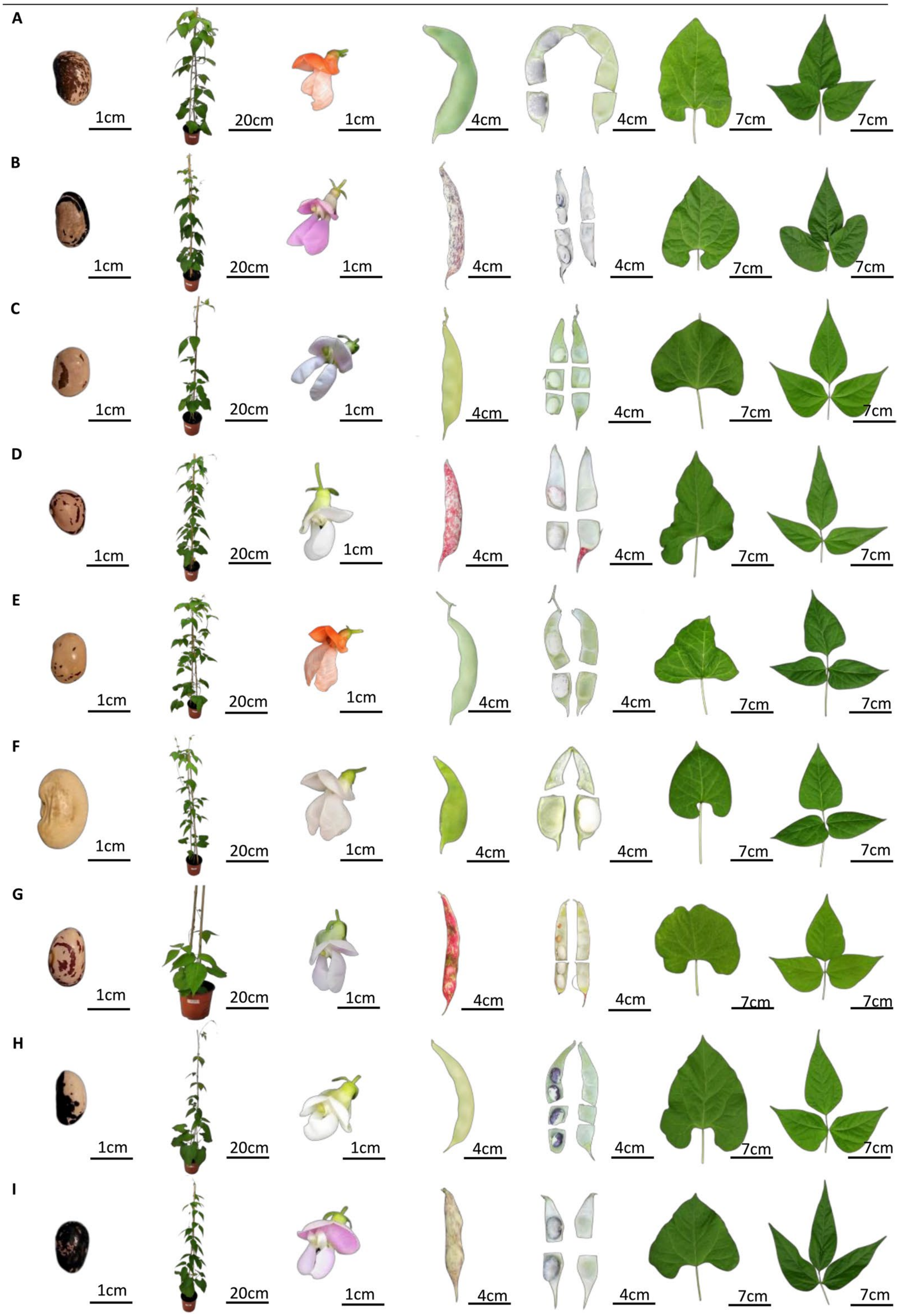


Fig. 2 Representative mature dry seeds, plants after one month, flowers, entire pods, sectioned pods, entire basal leaf and trifoliate leaf from each accession of Phaseolus spp. studied. The identification codes of bean samples (capital letter) are referred to in Fig. 1

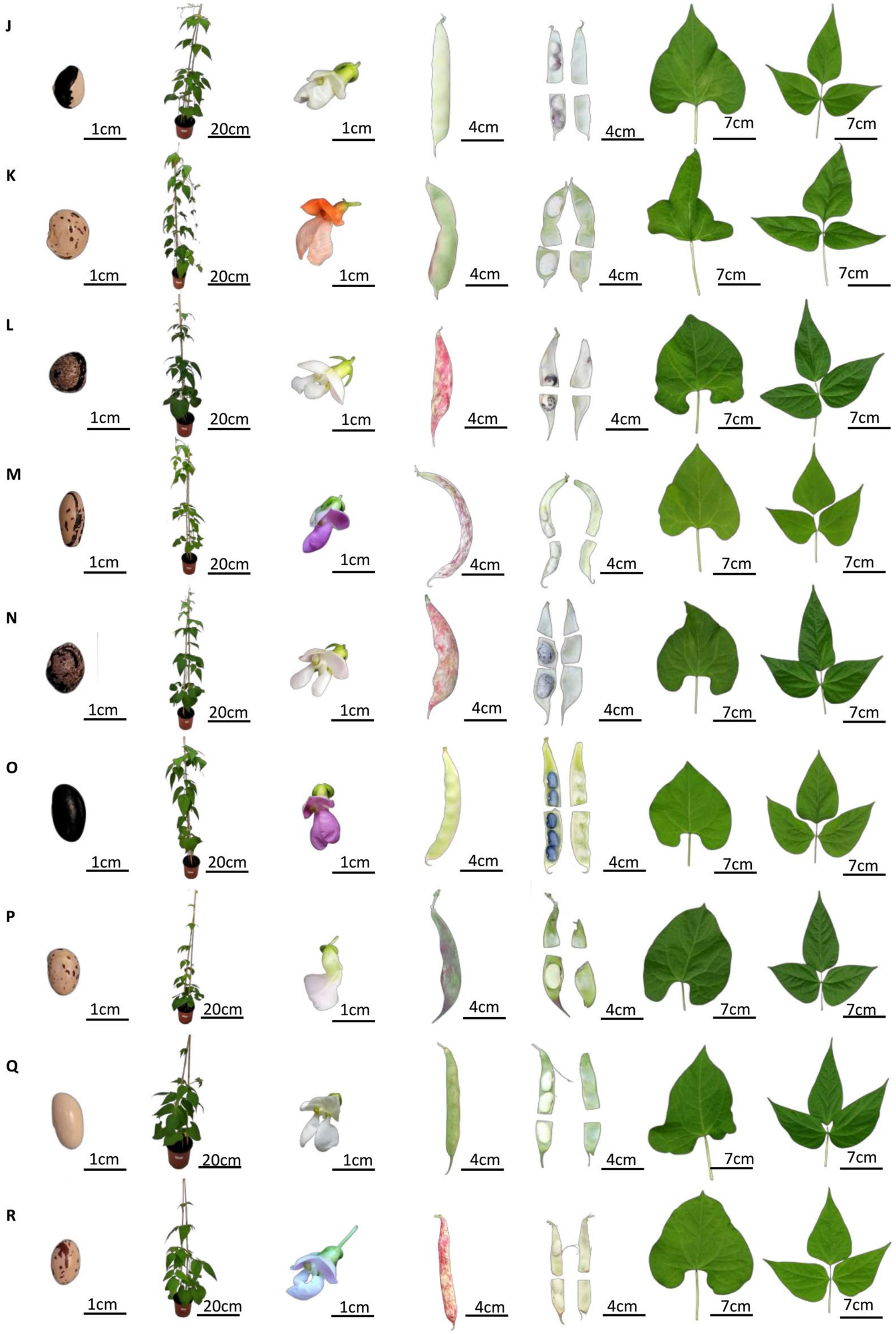


Fig. 2 (continued)

Table 1 Twenty simple sequence repeat (SSR) markers identified in bean and used for the molecular analysis (modified from Grisi et al. 2007)

SSRs	SEQ PRIMER FORWARD	SEQ PRIMER REVERSE	Tm (°C)
PV31	AATGGCAGGTCAGTGAAACA	ATGACCACGCAGTGACAGAfi	*56*
PV87	CTCATTGCGTCTACCAGTGC	CCTAGGTTCCGCAGCATGr	*56*
PV93	TGGGGTGAGAGAGAAAGGTA	TACWTAGCAG&CGTTGTTG	*56*
PV94	ACGACGGAGAGAGAGGTTGA	CCGTGTTCCTTCTGTCTGTG	*56*
PV106	CAACAACAAGGCTGAAAAACA	AAAAAGAGAGGAGAGAGAAGAGAGC	*56*
PV112	AACAACACCACCTGGAGAC	ACAAAAA&CGAGGAATC4CG	*56*
PV113	TGCATTCTTCCTCCCATCTT	TTGATTTGATTTGAGCAGTGGTG	*56*
PV123	SAAGAGCTCTCATCGCAACG	CTAGCTCCCTCCCCTCGTAA	*56*
PV131	GCGTCTGAGGAGAAGGAGGT	CTCCCAATCTCACCAAAACC	*56*
PV167	GGCAAAAACAAAACCATTTCA	GCCATTTCTCCACTGTCTGG	*56*
PV185	ᴛGGIMAGCAAAMCGATGG	GACA6AAGAGTGASGGTGTGAA	*56*
PV191	AATTTTGAACTGAAAGATAACAAAGC	CSCTTCATTCAACrDCGAAA	*56*
PV218	TGTAAATGGCAGGCAGTGAA	ATGACCACSCAGTGACAGAG	54
PV233	AGAGAGGGTTGTGGTTGGTG	TTAATCCtQCTTTACGCMC	56
PV269	TCGCCOCATATTCACTTTTC	TGGTGrGCAGAAAGTCTGTGA	56
BM141	TGAGGAGGMCAATGGTGGC	CTCACAAACCACAACGCACC	62
BM153	CCGTTAGGGAGTTGTTGAGG	TGACAAACCATGAATATGCTAA6A	63
BM154	TCTTGCGAOCGAGCTTCTCC	CTGAATCTGAGGAACGATGACCAG	68
BM160	CGTGCTTGGCGAATAGCTTTG	CGCGGTTCTGATCGTSACTTC	65
BM187	TTTCTCCAACTCACTCCTTTCC	TGTGTTTGTGTTCCGAATTATGA	63

1.4.0 (Claude 2008; Bonhomme et al. 2014) using R software (R Core Team 2025) and transformed into Fourier coefficients considering 8 harmonics that accumulated at least 99% of the total harmonic power (Bonhomme et al. 2014). To control the asymmetry, the samples were flipped in the same direction, and a landmark was defined as a starting point for importing outline coordinates. Principal Component Analysis (PCA) and Linear discriminant analysis of principal components (DAPC) (Jombart et al. 2010) was carried out was performed on the matrix of coefficients. The average bean shape was reconstructed using the MSHAPES function in Momocs (R software), and a multivariate analysis of variance (MANOVA) was performed to assess differences among beans' shapes. Subsequently, pairwise MANOVA was applied to identify specific differences between samples.

Proximate composition of the seeds

Approximately 300g of seeds collected from the field were milled into flour for nutritional analysis. A blender (IKA A10 basic, Werke GmbH & Co.KG, Staufen, Germany) was used to obtain a bean whole flours. All plant material was collected in compliance with national and international mandatory regulations.

The measurement of the total starch content was done according to the AACC 76-13.01 method, following the manufacturer's instructions. Values were expressed as g/100 g of flour.

The Kjeldahl method was utilized to the protein content determination, in according to International Standard ISO 20483:2013 (AOAC 2005). Nitrogen was converted into protein using a conversion factor of 6.25 and the results were expressed as g/100g.

To determine the total lipid content, 0.5 grams of flour were extracted with 5 mL of pentane under agitation at 37°C for 2 hours and 30 minutes. This process was repeated twice. After extraction, the samples were placed in an oven at 40°C overnight to ensure complete evaporation of the pentane. The lipid content was then calculated using the following calculation:

$$\%lipids = \frac{mi - mf}{mi} \times 100 \tag{1}$$

where *mi* is the initial mass, and *mf* is the final mass.

Folin-Ciocalteau spectrophotometric method (Singleton et al. 1999) was used to analyze the total polyphenol content. Quantification was expressed as gallic acid equivalents (mg GAE/g bean flour) after measuring the absorbance at 765 nm.

The determination of total flavonoids was performed by aluminum chloride test (Alcázar-Valle et al. 2020). The absorbance was measured at 415 nm in a spectrophotometer, and the results were expressed as mg of catechin/g of flour.

The antioxidant activity of beans was evaluated using the Fe (III)/tripyridyltriazine complex (FRAP), following the procedure of Benzie and Strain (1996). Ferric sulfate (FeSO4) concentrations in the range 100–1000 µmol/l were used for calibration. Results were expressed in µmolFe2+/g based on the calibration curve.

Trypsin inhibitor activity (TIA) was carried out following the ISO 14902:2001 assay (AOAC 2005).

The phytic acid and Raffinose Series Oligosaccharides content were determined using K-PHYT and K-RAFGL Megazyme assay kit, respectively, (Megazyme International Ireland Ltd, Wicklow, Ireland) following the manufacturer's instructions. The results were measured by milligrams of phytic acid per gram of bean flour and Galactosyl-sucrose oligosaccharides (GSO) g/100 g, respectively.

One-way ANOVA and a Tukey post-hoc test were used to analyze the data for proximate analysis. The Levene and Shapiro-Wilk's tests were used to verify the assumption that variances were homogeneous, and group data was normal. Values are reported as mean ± standard deviation (SD) from three replicates, with statistical difference set at $P < 0.05$.

Results

SSR analysis revealed moderate genetic diversity among the 18 cultivars (Fig. 1). The number of alleles per locus (Na) ranged from 1 to 5 and PIC values from 0.000 to 0.772, with BM160 and PV87 being the most informative markers, while PV106 and PV191 were monomorphic (Table 2).

Table 2 Genetic diversity parameters of 18 cultivars assessed using 15 simple sequence repeats

Locus	N	Na	Ne	I	PIC
PV31	18	3.000	1.976	0.849	0.494
PV87	18	5.000	3.057	1.292	0.673
PV93	18	2.000	1.906	0.668	0.475
PV94	18	2.000	1.800	0.637	0.444
PV106	18	1.000	1.000	0.000	0.000
PV112	18	4.000	3 000	1.215	0.667
PV113	18	2.000	1.117	0.215	0.105
PV185	18	3.000	2.219	0.934	0.549
PV191	18	1.000	1.000	0.000	0.000
PV218	18	3.000	1.976	0.849	0.494
PV233	18	2.000	1.976	0.687	0.494
PV269	18	2.000	1.906	0.668	0.475
BM141	18	3.000	1.742	0.730	0.426
BM154	18	3.000	2.945	L.089	0.660
BM160	18	5.000	4.378	1.534	0.772

N number of cultivars, Na number of different alleles, No number of effective alleles, I Shannon's information index, PLC (polymorphic in formation content), Expressed as Expected Heterozygosity (He)

Furthermore, the PCoA (Percentage of variation explained by the two axes = 66.01%) and UPGMA analyses clearly demonstrated the presence of three main clusters. It was possible to highlight the differences not only between the two different species (*P. vulgaris* vs. *P. coccineus*) but also within *P. vulgaris*, distinguishing the two commercial benchmarks ("Cannellino" commercial (Q); "Borlotto" commercial (R)) from the traditional cultivars or landraces.

In Table 3 were represented the results of the ecological analysis (functional strategy). CSR functional strategy revealed that most samples had a competitor/competitive-ruderal strategy (C/CR). The genotypes do show less o no adaptation to stress, understood as phenomena which restrict photosynthetic production such as shortages of water, light, mineral nutrients or suboptimal temperatures (Grime 2001).

Also from the results of the functional strategy, no differences are observed between the two species considered (*P. vulgaris* and *P. coccineus*), nor between landraces and commercial cultivars. The only two genotypes that exhibit a slightly different functional strategy (CR) from the others are "Tavela longa" (B) and "Zio Doro" (I) (Table 4). Both are, in fact, more

Table 3 Results of Grime's competitor, stress-tolerator, ruderal (CSR) functional strategy

coD	C (%)	S (%)	R (%)	Strategy
A	67.98	0.00	32.02	C/CR
B	60.33	0.00	39.67	CR
C	73.41	0.00	26.59	C/CR
D	70.99	0.28	28.73	C/CR
E	70.12	o.oo	29.88	C/CR
F	61.27	6.68	32.05	C/CR
G	72.05	0.58	2737	C/CR
H	69.99	8.64	21.37	C/CR
1	56.09	0.00	43.91	CR
J	65.42	037	34.21	C/CR
K	69.19	0.00	30.81	C/CR
L	68.96	0.00	31.04	C/CR
M	64.66	5.47	29.87	C/CR
N	70.63	3.18	26.19	C/CR
0	63.91	O.OO	36.09	C/CR
P	69.34	O.OO	30.66	C/CR
Q	72.12	4.90	22.98	C/CR
R	68.16	1.82	30.02	C/CR

C, competitor; S, stress-tolerator; R, ruderal. The identification codes of bean samples (capital letter) are referred to in Fig. 1

ruderal ($R > 39\%$) and less competitive than the others ($C < 61\%$), which suggests that these landraces may be more resistant to disturbances (understood as the set of biotic and/or abiotic phenomena capable of destroying plant biomass), and therefore more resilient to potential mechanical damage (such as attacks by phytophagous insects or herbivores and/or hailstorms and wind damage, etc.) compared to the other genotypes.

Drawing on the data collected during fieldwork, a UPOV morphological descriptor form was filled out for each bean landrace, providing a standardized description of their phenotypic traits. The results of UPOV forms were reported in supplementary material (Supplementary Information SI 1).

The mean shapes of the eighteen bean samples returned by the outline analysis are shown in Fig. 4a, while Fig. 4b presents the Linear Discriminant Analysis of principal components (LDA) results. Along the horizontal axis ($LD1 = 60.5\%$), the seed shapes transition from more elliptic to more rounded, while along the vertical axis ($LD2 = 30.4\%$), moving from top to bottom, the seed shapes shift from less reniform to more reniform. Figure 4 illustrates the considerable morphological variation in seed shape

Table 4 Phytochemical and nutritional composition of samples beans

COD	Starch (g/lOOg)	Protein (g/lOOg)	Lipid (g/lOOg)	Polyphenols (mg GAE/g)	Flavonoids (mg/g)	FRAP (μmol Fe2 + /g)	TIA (mg/g)	Phytic acid (g/lOOg)	RSO (g/100 g)
A	35.84 ± 1.5^{defg}	21.76 ± 1.58^{abc}	2.98 ± 0.00^{def}	1.16 ± 0.05^{fghi}	0.31 ± 0.01^{ab}	$0.74\ 10.1^{cde}$	2.40 ± 0.02^{ef}	1.01 ± 0.02^{efg}	4.82 ± 0.07^{f}
5	40.08 ± 0.1^{bjk}	23.28 ± 0.99^{cde}	3.22 ± 0.11^{def}	1.08 ± 0.04^{efgh}	0.49 ± 0.04^{bc}	1.43 ± 0.04^{g}	2.35 ± 0.15^{ef}	0.90 ± 0.00^{cde}	4.54 ± 0.3^{lf}
c	42.03 ± 1.41^{k}	23.02 ± 0.61^{cd}	$2.41 \pm O.02^{bcd}$	1.06 ± 0.07^{efgh}	0.33 ± 0.16^{ab}	0.72 ± 0.16^{cde}	$3.24 \pm O.04^{g}$	1.06 ± 0.01^{gh}	1.13 ± 0.10^{a}
D	39.70 ± 0.18^{ijk}	23.57 ± 0.89^{cde}	2.72 ± 0.11^{cde}	0.91 ± 0.02^{cdefg}	0.31 ± 0.04^{ab}	0.67 ± 0.04^{cde}	$0.S5 \pm O.02^{b}$	1.17 ± 0.01^{hi}	$3.32 \pm O.05^{cde}$
E	39.51 ± 0.82^{hij}	$20.18 + 0.72^{ab}$	3.45 ± 0.12^{ef}	1.20 ± 0.01^{ghij}	0.33 ± 0.01^{ab}	1.13 ± 0.01^{f}	3.61 ± 0.02^{b}	$0.S9 \pm O.03^{cd}$	5.79 ± 0.02^{g}
F	35.36 ± 0.27^{def}	$21.96 \pm O.50^{bc}$	3.15 ± 0.11^{def}	0.60 ± 0.00^{ab}	0.41 ± 0.36^{abc}	0.39 ± 0.36^{a}	$3.13 \pm O.08^{g}$	1.19 ± 0.03^{i}	2.06 ± 0.00^{b}
G	37.65 ± 1.58^{fghij}	21.90 ± 0.09^{bc}	3.78 ± 0.22^{fg}	1.43 ± 0.12^{ij}	0.16 ± 0.05^{a}	0.79 ± 0.05^{de}	2.22 ± 0.03^{e}	$1.20 \pm 0.00ij$	3.52 ± 0.12^{cde}
H	32.42 ± 0.19^{bc}	27.78 ± 0.05^{f}	4.50 ± 0.18^{gh}	1.31 ± 0.09^{hij}	0.27 ± 0.11^{ab}	0.58 ± 0.11^{bc}	1.81 ± 0.06^{d}	$0.93 \pm 0.03cdef$	3.15 ± 0.19^{cd}
I	38.94 ± 0.74^{hij}	24.94 ± 0.58^{e}	3.52 ± 0.04^{ef}	0.73 ± 0.07^{bc}	0.20 ± 0.10^{a}	0.47 ± 0.10^{ab}	3.94 ± 0.09^{j}	$1.32 \pm 0.O3i$	3.74 ± 0.20^{e}
J	31.17 ± 0.47^{ab}	$20 \pm 23 \pm 0.23^{ab}$	2.80 ± 0.40^{cde}	0.85 ± 0.01^{bcde}	0.47 ± 0.22^{bc}	0.64 ± 0.22^{cd}	0.11 ± 0.00^{a}	0.71 ± 0.01^{b}	3.33 ± 0.0^{cde}
K	29.39 ± 0.32^{a}	20.01 ± 0.41^{a}	6.00 ± 0.40^{i}	1.02 ± 0.01^{defgh}	$1.3.3 \pm 0.12^{d}$	3.42 ± 0.00^{j}	3.38 ± 0.01^{gh}	$0.85\ 10.02^{c}$	4.90 ± 0.02^{f}
L	$35.05 \pm 0\ 30^{de}$	29.28 ± 0.10^{fg}	1.20 ± 0.40^{a}	1.28 ± 0.05^{hij}	0.41 ± 0.09^{abc}	0.81 ± 0.09^{e}	0.69 ± 0.03^{bc}	0.83 ± 0.00^{bc}	3.78 ± 0.03^{e}
M	46.55 ± 0.56^{l}	28.11 ± 0.14^{fg}	5.20 ± 0.4^{hi}	1.20 ± 0.09^{hij}	0.42 ± 0.09^{abc}	2.02 ± 0.09^{i}	$0.84 \pm O.01^{c}$	1.04 ± 0.01^{fg}	3.03 ± 0.03^{c}
N	39.12 ± 11^{hij}	28.20 ± 0.45^{fg}	2.80 ± 0.40^{cde}	1.40 ± 0.08^{ij}	0.61 ± 0.06^{c}	0.35 ± 0.06^{a}	0.08 ± 0.03^{a}	0.51 ± 0.00^{a}	3.25 ± 0.03^{cde}
0	34.74 ± 0.3^{cd}	28.97 ± 0.22^{fg}	2.00 ± 0.40^{hc}	0.89 ± 0.05^{bcdef}	0.31 ± 0.01^{ab}	0.62 ± 0.01^{cd}	1.83 ± 0.21^{d}	0.91 ± 0.01^{cde}	3.24 ± 0.06^{cde}
P	37.87 ± 0.4^{ghij}	29.68 ± 0.01^{g}	5.20 ± 0.40^{hi}	1.46 ± 0.33^{j}	0.30 ± 0.03^{ab}	1.90 ± 0.03^{h}	$0.78 + 0.09^{bc}$	1.00 ± 0.00^{defg}	3.04 ± 0.03^{c}
Q	37.08 ± 0.47^{defgh}	24.36 ± 0.09^{de}	1.85 ± 0.11^{ab}	0.32 ± 0.02^{a}	0.27 ± 0.24^{ab}	$0.39 + 0.24^{a}$	2.35 ± 0.13^{ef}	1.31 ± 0.02^{i}	3.59 ± 0.53^{cde}
R	37.37 ± 1.35^{efghi}	$2\ 2.83 \pm 0.45^{cd}$	$2.50 \pm 0.11b^{cd}$	0.76 ± 0.04^{hcd}	0.32 ± 0.06^{a}	0.73 ± 0.06^{cde}	$2.63 \pm O.20^{f}$	1.07 ± 0.14^{gh}	3.66 ± 0.27^{de}

The identification codes of samples, capital letter, are mentioned in Fig. 1. TIA (Trypsin inhibitor activity); FRAP (Ferric Reducing Antioxidant Power); RSO (Raffinose Series Oligosaccharides) among the analyzed genotypes, with each accession displaying a distinct and specific shape profile. However, in contrast to the genetic analysis, the results of the morphometric analysis do not allow for any clear clustering of accessions, neither according to species (*P. vulgaris* and *P. coccineus*) nor between the 16 traditional landraces and the two commercial cultivars.

The landraces “Bianco di Codera” (F), “Borlotto Camoscio” (E) and “Fagiolo della Val Vestino” (K), placed in the left part of the graph LDA, had the most elliptic seeds, the landraces “Togn” (L), “Convento di Vogel” (J) and “Zio Doro” (I), placed on the right side of the graph, presented the roundish seeds, while the “Clelia mangiatutto” (M) and “Borlotto di Codera” (F), placed at the bottom of the graph, have the most reniform seeds. The other cultivars have morphometric characteristics intermediate between those mentioned above. These results were based on the data reported in supplementary material (SI 2). Multivariate analysis of variance (MANOVA) showed that the only cultivars among which there are no statistically significant differences in seed shape are “Dihipli” (H), commercial “Borlotto” (R), “Sussia” (D) and “Fagiolo Emma” (N).

Finally, based on LDA and PCA results (Fig. 4c), three main shapes of bean seeds emerged: reniform, elliptic, roundish.

Table 4 shows the nutritional and phytochemical characteristics of bean samples. The analysis of bean samples reveals significant variability in their nutritional and phytochemical composition, making it challenging to establish clear groupings or identify consistent patterns of similarity among genotypes.

Regarding the proximate composition, “Clelia Mangiatutto” (M) sample has the highest starch content (46.55 g/100 g), while “Val Vestino “bean (K) has the lowest (29.39 g/100 g).

All beans had a protein content above 20%, with sample P reaching 29.68 g/100 g and the lowest amount was found in K (20.01 g/100 g) and in the other *P. coccineus* beans.

Lipid content varies among samples, with “Val Vestino bean”sample (K) (6.00 g/100 g), (M) “Clelia Mangiatutto” and “Borlotto di Codera” (P) (5.20 g/100 g) having the highest and “Togn” bean (L) the lowest (1.20 g/100 g).

The highest polyphenol content was found in *P. Vulgaris* samples, particularly “Emma” (N), “Borlotto di Codera” (P), “Togn” (L), and “Maria Sciuccetti” (O). The flavonoid level was higher in K and N samples (1.33 and 0.61 mg/g, respectively), suggesting a strong presence of functional and bioactive compounds. G has the lowest flavonoid content (0.16 mg/g), indicating a limited antioxidant potential.

Sample K has the highest antioxidant capacity (3.42 μmol Fe^{2+}/g), making it potentially beneficial for oxidative stress protection, while N, Q and F beans had the lowest mean value (less than 0.4 μmol Fe^{2+}/g).

“Zio Doro” bean (I) has the highest TIA value (3.94 mg/g), which may reduce protein digestibility, while “Emma” (N) has the lowest activity (0.08 mg/g), making it a more digestible cultivar. Generally, *P. coccineus* samples showed a higher value of trypsin inhibitor activity than the other beans. The same trend was shown in phytic acid content, where sample I scored a mean value of 1.32 g/100 g in contrast to “Emma” bean (N) which had the lowest content (0.51 g/100 g), making it a better choice for those with mineral deficiencies. This antinutrient was high in commercial beans too.

In the dataset, *P. coccineus* samples displayed the highest oligosaccharide (α-Galactosides) content, with “Borlotto Camoscio” (E) reaching 5.79 g/100 g. In contrast, samples C and F exhibit the lowest value (1.13 and 2.06 g/100 g, respectively), potentially making them more digestible for individuals with intestinal issues related to oligosaccharides.

The Multidimensional Scaling (MDS) analysis (Fig. 5) showed distinct patterns in the distribution of the analyzed bean accessions, as far as nutritional and phytochemical parameters concerns. The commercial cultivars lie in the center of the principal component plot, reflecting their uniformity and lack of extreme traits, while the landraces had a broader dispersion highlighting their diversity. The *P coccineus* landraces are concentrated in the upper left quadrant (first quadrant) an area associated with elevated levels of RSO, flavonoids and strong antioxidant activity. Conversely, several *P. vulgaris* landraces were found in the lower region of the plot. These genotypes exhibit the highest levels of both protein and polyphenols among all accessions analyzed.

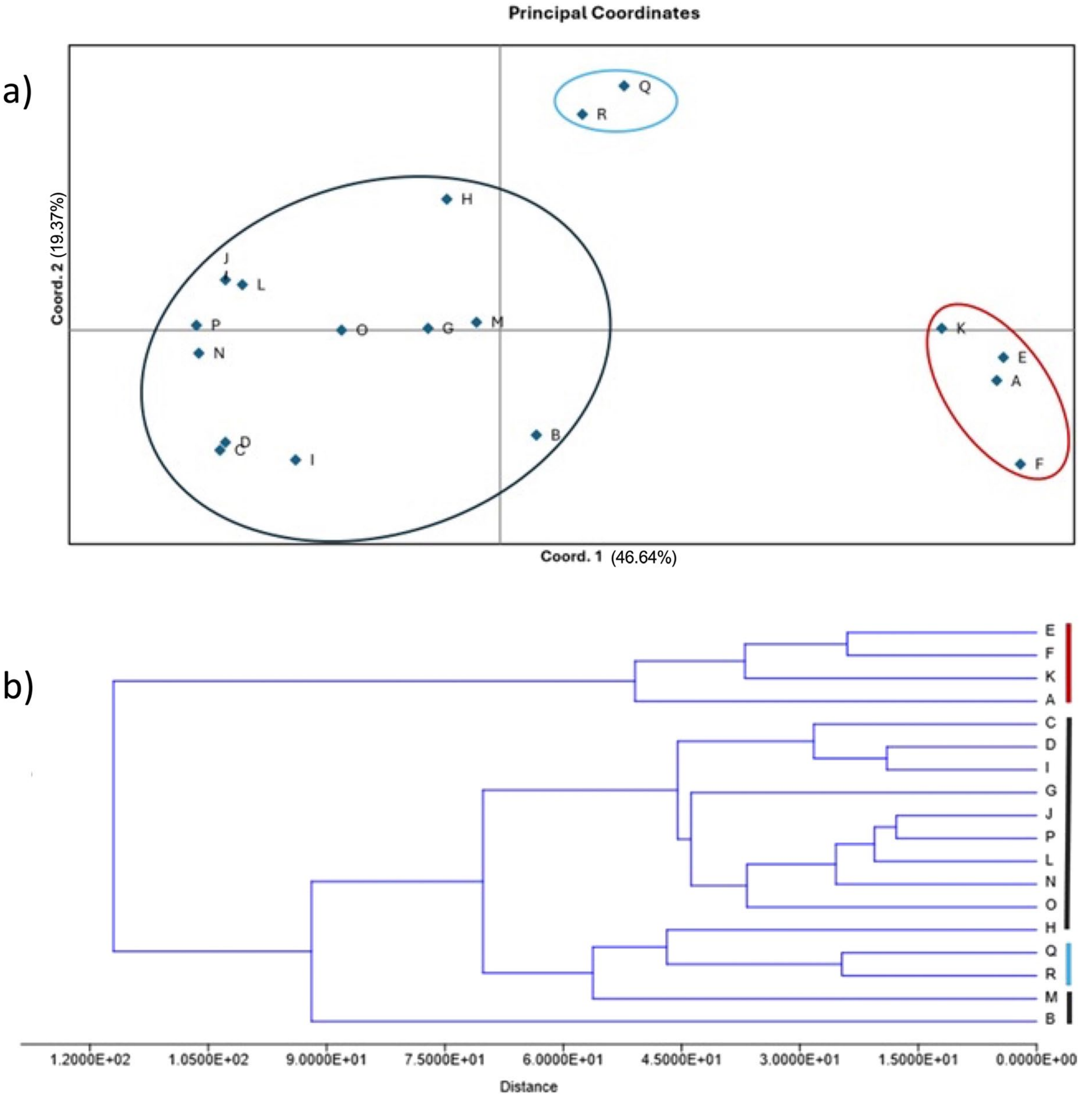


Fig. 3 Molecular analysis. **a** Principal coordinate analysis (PCoA) (Eigenvalue scaling) and **b** Unweighted pair group method with arithmetic mean (UPGMA) clustering using 15 simple sequence repeat (SSR) markers across 18 different cultivars. *Phaseolus coccineus* is shown in red, *P. vulgaris* commercial cultivars in light blue, and *P. vulgaris* landraces in black. K-means = 3 was used for the clusterization. The identification codes of bean samples (capital letter) are referred to in Fig. 1

Discussion

This research contributed to knowledge on characterizing several previously undocumented Lombardy bean landraces, bridging the lack of scientific data.

The SSR-based analyses revealed a clear genetic differentiation between Phaseolus vulgaris and *P. coccineus*, as consistently shown by both PCoA and UPGMA clustering (Fig. 3). This pattern agrees with recent studies on European Phaseolus landraces, which highlight strong species-level separation linked to contrasting mating systems and evolutionary histories (Bosmali et al. 2024; Ciaffi et al. 2024). The predominantly allogamous reproduction of *P.*

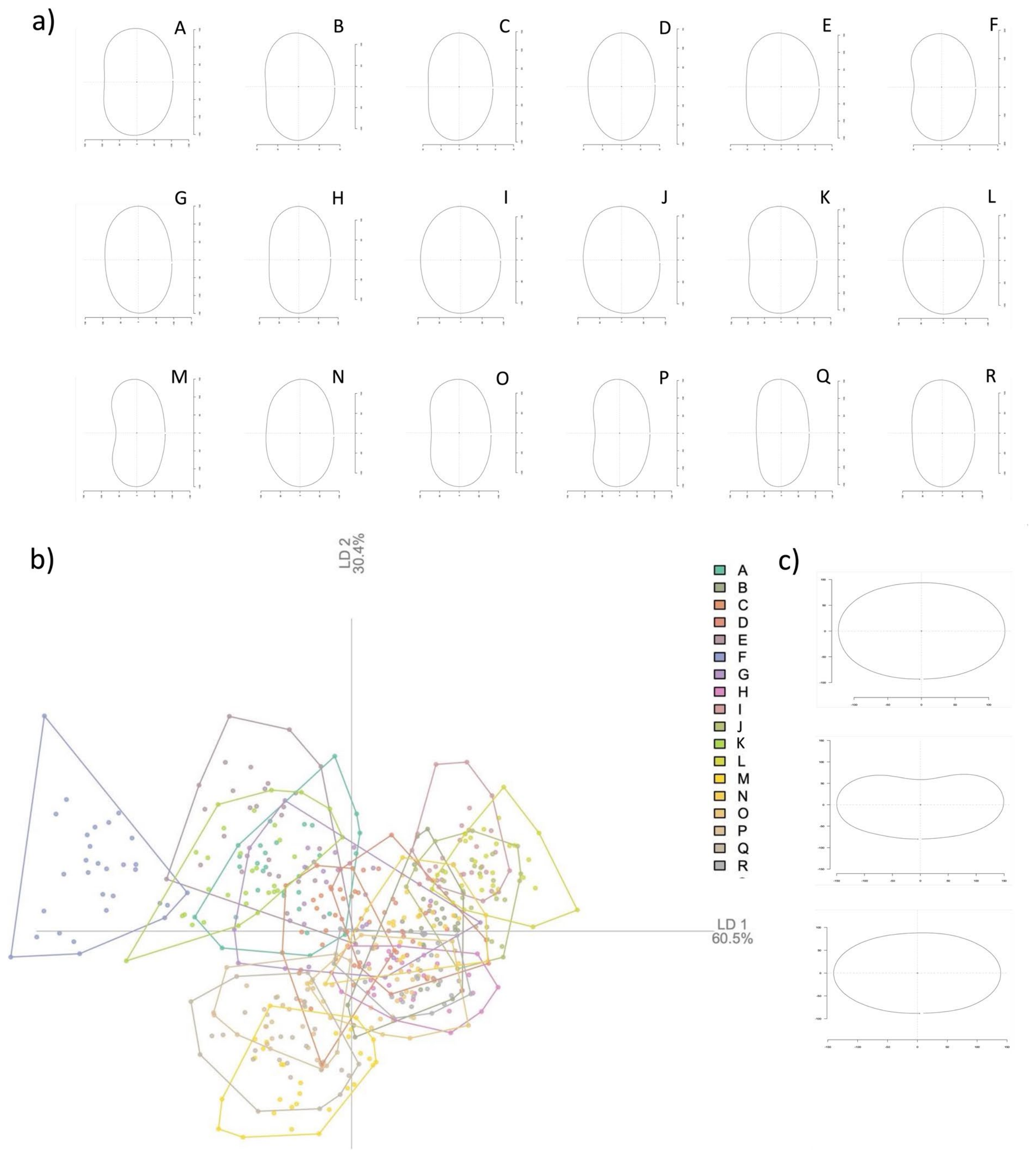


Fig. 4 **a** Mean seed outlines of the 18 bean samples obtained from geometric morphometric analysis; **b** Linear discriminant analysis (LDA) of seed shape, with points colored according to bean samples; axes represent the first two discriminant functions (LD1 and LD2); **c** Main seed morphology types identified in the dataset (reniform, elliptic, and roundish). Sample identification codes (capital letters) correspond to those reported in Fig. 1

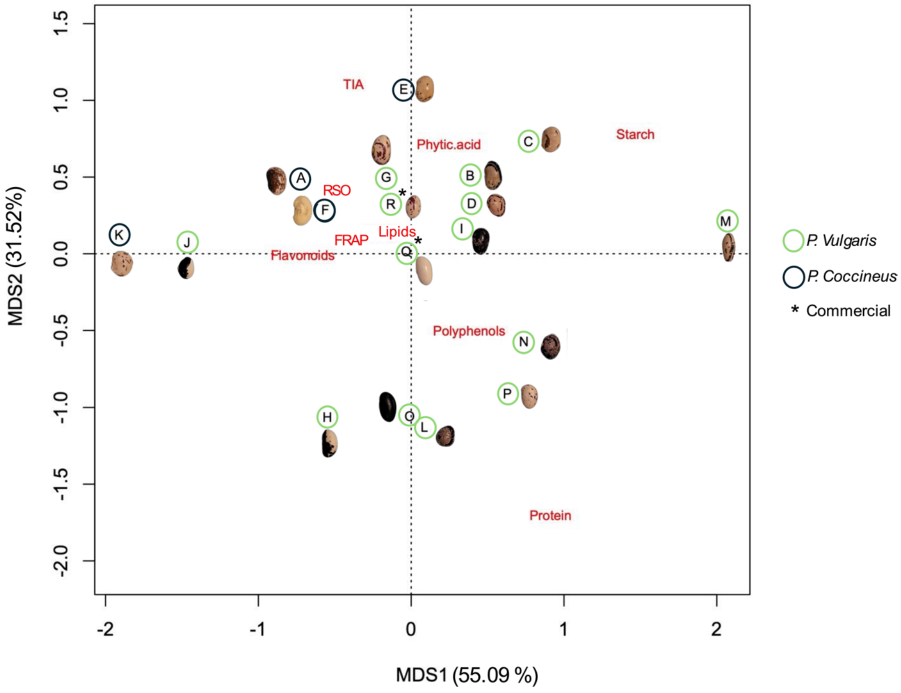


Fig. 5 MDS (Multidimensional Scaling) biplot of beans samples associated with nutritional and phytochemical parameters. The identification codes of bean samples (capital letter) are referred to in Fig. 1. Key: TIA (Trypsin inhibitor activity); FRAP (Ferric Reducing Antioxidant Power); RSO (Raffinose Series Oligosaccharides)

coccineus, compared with the autogamous behavior of *P. vulgaris*, likely contributes to the higher genetic dispersion observed within species, as previously reported by Mercati et al. (2015) and more recently by Romero-Astudillo et al. (2024).

Within *P. vulgaris,* traditional landraces were clearly separated from commercial cultivars, supporting the notion that modern breeding has reduced genetic variability through selection for uniformity. Similar trends have been described for Italian and Mediterranean common bean germplasm, where landraces retain higher levels of structured genetic diversity compared to formal cultivars (Alicandri et al. 2024; Losa et al. 2025). The presence of loci with moderate to high PIC values further confirms the effectiveness of SSR markers for landrace discrimination and genetic resource characterization (Table 2).

Overall, the observed moderate but well-structured genetic diversity reflects long-term on-farm conservation under geographically fragmented mountain conditions. These results confirm that Lombardy bean landraces represent distinct and valuable genetic resources, providing a solid molecular basis for their conservation and potential registration as conservation varieties (Landoni et al. 2024). Based on K-means clustering (K = 3), the SSR data clearly distinguished three main genetic groups corresponding to *Phaseolus coccineus*, commercial *P. vulgaris* cultivars derived from breeding programs, and *P. vulgaris* traditional landraces. The genetic structure observed within the *P. vulgaris* landrace group suggests a complex background that can be discussed in light of the well-known dual domestication of common bean in the Andean and Mesoamerican gene pools (Bitocchi et al. 2012, 2013). However, it should be emphasized that the aim of this study was not to discriminate between Andean and Mesoamerican origins. Rather, the presence of multiple genotypes within a single landrace cluster is consistent with a history of multiple introductions into Europe followed by local diversification and admixture, as widely reported for European bean germplasm. Therefore, no further subdivision within the landrace group is proposed, as such an interpretation would not be sufficiently supported by the available molecular data and would go beyond the scope of this study.

Furthermore the molecular analysis shown in Fig. 3 highlighted the differences between the species *P. coccineus* and *P. vulgaris*. Considering the phenotypic differences, growth environments, and reproductive cycles of the two species, these results confirm previous studies on the genetic differences between these two species (Bosmali et al. 2024). It is well known that *P. coccineus* is predominantly an allogamous species that requires pollinating insects for fruit set and seed production, whereas *P. vulgaris* is capable of self-pollination (Ciaffi et al. 2024). Additionally, *P. coccineus* thrives in environments with lower average temperatures compared to *P. vulgaris*, favoring hilly or mountainous regions (Aquino-Bolaños et al. 2021). Within the *P. vulgaris* species, it is possible to distinguish the two commercial cultivars used (Q: “Cannellino” commercial; R: “Borlotto” commercial), employed as benchmarks, from the traditional cultivars studied. This result is particularly important for future work on the characterization and conservation of the germplasm of this species, as it allows for the rapid identification of newly synthesized commercial cultivars that might be mistaken for traditional cultivars or landraces (Landoni et al. 2024). Modern newly synthesized cultivars, having been subjected to improvement programs, exhibit a modified genetic structure with alleles conferring superior traits related to resistance to biotic and abiotic stresses, enabling their distinction from traditional genetic materials (Mercati et al. 2015).

Unlike the results of the genetic analysis, those concerning seed morphology, functional strategy, and nutritional traits did not reveal clear distinctions between the two species (*P. vulgaris* and *P. coccineus*) or between the landraces and the commercial bean varieties. Each genotype exhibited unique and specific characteristics, which, particularly in terms of seed shape and nutritional composition, clearly differentiated it from the others. These findings highlight the high intra-genus and intra-specific diversity within *Phaseolus* and suggest that this variability is both intrinsic (genetic, eco-physiological, and phytochemical) and phenotypic (seed shape and morphological traits, see Fig. 2).

In this research, the outline analyses demonstrated differences in the beans assessed, which present more variable shapes. This might be because landraces are not commercial cultivars having not been subjected to strong morphological selection (and genetic depletion) to produce standardized products. The morphometric analysis has revealed three main shapes of bean seeds: reniform, elliptic and roundish (Fig. 4c).

Modern geometric morphometric methods, such as outline analysis, provide a powerful approach for analyzing and comparing shapes in biological studies. These techniques evaluate the spatial relationships of landmarks and outlines to measure form and size and have been successfully applied in plant biology, for example, to distinguish leaf shapes (Chitwood and Otoni 2017; Giupponi and Giorgi 2019a) or to characterize landraces (Giupponi et al. 2019b, 2020b; Pedrali et al. 2024). These analyses offer an objective (based of statistical analysis), cheap and modern method for the characterization and identification of landraces, reducing subjectivity and human error. They could support or even replace traditional morphological descriptors used in Distinctness, Uniformity, and Stability (DUS) testing, as defined by the Community Plant Variety Office (CPVO) and the International Union for the Protection of New Varieties of Plants (UPOV) which are imperative for the enrollment of cultivars in the register of conservation varieties and the plant agrobiodiversity register (https://www.upov.int/resource/en/dus_guidance.html).

The CSR functional classification of the studied beans revealed a prevailing C/CR strategy, with no particular differences among the genotypes considered. The observed C/CR profile suggests that bean plants combine the ability to efficiently exploit available resources with a certain degree of tolerance to disturbances. In particular, the presence of competitive traits in the analysed genotypes indicates that the different bean cultivars share the ability to thrive in environments where plants do not experience stress from factors such as insufficient light, nutrients, or water in the soil. This occurs in cultivated or managed fields where humans, even in mountainous regions, have contributed to the development of agroecosystems with more favorable soil characteristics compared to natural soils, for example, through regular fertilization and stone removal (Sicard et al. 2005).

Moreover, the ruderal traits highlighted in the various genotypes studied indicate that beans, in general, are fairly tolerant to disturbances, meaning they are capable of good vegetative recovery following mechanical damage caused, for instance, by insect attacks or adverse weather events. This characteristic explains the presence of many bean landraces in Italian mountain environments (Giupponi et al. 2021a), where there is a higher likelihood of adverse weather conditions (storms, strong winds, tempests) capable of destroying plant biomass. In fact, the landrace “Copafam” (sample A) in the Italian Alps is cultivated even above 1,000 m a.s.l. (Giupponi et al. 2018) and can produce shoots, flowers, and fruits late in the season.

Although the analysis of CSR functional strategy has been mainly applied to wild plants (Pierce et al. 2017), it has also been assessed for a few Italian landraces (Giupponi et al. 2019b; Zuccolo et al. 2023), one of which, "Ciuenlai" (*Cyclanthera pedata* (L.) Schrad.) (Zuccolo et al. 2023), exhibits a CSR strategy similar (C/CR) to that of the beans considered in this research and is cultivated in Val Camonica (Lombardy Alps) in the same fields where some bean landraces, including "Copafam", are also grown.

In the future, it would be advisable to apply this methodology to other plants of agricultural and food interest, if only to investigate intra-specific ecological variability and gather information on the functional/adaptive traits of cultivars, useful for those who cultivate and/or conserve them in situ (*on-farm*).

Moreover, the nutritional composition was similar in all landraces analyzed but they exhibited equal or superior phytochemical profiles compared to commercial cultivars especially those with pigmented seeds that demonstrated high levels of functional molecules and antioxidant activity. Starch is the primary energy source in beans but it hadn't showed strong variation among traditional cultivars as well as compared with the commercial samples. Its content ranged from 46.55 g/100 g to 31.17 g/100 g (sample M and K, respectively), indicating that certain landraces may be more suitable for energy-dense diets, while others, the *P. coccineus* beans, may cater to low-glycemic nutritional needs. A similar carbohydrate content (45.66 ± 0.3 to 55.24 ± 0.4 g/100 g) was found by Nor Azmah (2023) that studied four underutilized legumes in Malaysia and confirmed literature data (Maphosa and Jideani 2017; Serventi 2020).

The protein content is a key nutritional feature in legume seeds. With protein levels exceeding 20 g per 100 g across all samples, these legumes are particularly well-suited for vegetarian and vegan diets. "Borlotto di Codera" sample (P) displayed the highest protein concentration at 29.28 ± 0.01 g/100 g. The MDS analysis results showed a group of traditional cultivars (all belonging to *P. vulgaris*) that are particularly rich in protein content, more than the commercial ones.

These results are congruent with previous findings by Pedrali (2022), which compared a mountain bean landrace ("Copafam bean", which is included in this research too) to three other commercial beans. All these samples had a protein content ranging from 21.9 to 26.48 g/100 g dw and the *P. coccineus* beans had a lower value than the *P. vulgaris* ones.

As expected, lipid content was low in all samples, with limited variability. Each sample exhibited a lipid level below 10%, confirming that these beans represent a healthy food choice aligned with World Health Organization (WHO) dietary recommendations. The WHO advises limiting the intake of high-fat foods to help combat the rising prevalence of overweight and obesity worldwide. This result is according to Maphosa (2017) and Pedrali (2022), who found a total lipid content ranging from 1 to 5% in beans (Maphosa and Jideani 2017).

Anti-nutritional compounds such as trypsin inhibitor activity (TIA) and phytic acid, which can impair protein digestion and mineral absorption, were lower in the traditional landraces compared to the commercial cultivar analyzed (Alcázar-Valle et al. 2020; Cominelli et al. 2022). This suggests that landraces may offer improved digestibility and be more appropriate for individuals with mineral deficiencies or sensitive digestive systems.

In the dataset, *P. coccineus* samples exhibited the highest oligosaccharide content, with "Borlotto Camoscio" (E) reaching a peak value of 5.79 g/100 g. This suggests a greater presence of these sugars, which are often associated with the anti-nutritional effects of legumes. Due to the lack of α-galactosidase, these oligosaccharides remain undigested until they reach the lower intestine, where they are fermented by gut microbiota producing gases such as methane, which can result in flatulence. Consequently, the presence of galactosyl-sucrose oligosaccharides could represent a factor limiting these beans use in human diets (Han and Baik 2006). In contrast, "Nosenta" (C) and "Bianco di Codera" (F) samples showed the lowest oligosaccharide levels (1.13 and 2.06 g/100 g, respectively), potentially making them more suitable for individuals with digestive sensitivities to these compounds.

Phytochemical analysis highlighted significant differences among samples. Some samples belonging to the *P. vulgaris* genus recorded the highest polyphenol (1.46 ± 0.33 mgGAE/g) suggesting a strong antioxidant profile. In contrast, *P. coccineus* samples had a high flavonoid level and antioxidant capacity, measured by the FRAP assay. Although flavonoids are a subset of total polyphenols, a strong correlation with TPC was not consistently observed, likely due to the non-specific nature of the Folin–Ciocalteu assay, which also detects other reducing compounds. Likewise, seed color did not strictly reflect phenolic content, suggesting that colorless phenolics and genetic variability among landraces contribute substantially. The lack of a clear relationship between FRAP and TPC or flavonoids further indicates that antioxidant activity depends on the chemical nature and redox properties of individual compounds rather than on total concentration alone.

This trend was confirmed by MDS biplot graph (Fig. 5). In fact, the MDS analysis revealed the *P. coccineus* landraces cluster in the upper left quadrant (first quadrant), an area associated with higher levels of flavonoids and antioxidant activity indicating an ability to counter oxidative stress and potentially lower chronic disease risk. However, these samples also show elevated concentrations of trypsin inhibition activity and oligosaccharides.

In contrast, several *P. vulgaris* landraces are found in the lower portion of the plot. These genotypes exhibit the highest levels of both protein and polyphenols among all accessions analyzed.

Previous studies have shown that seed weight is negatively correlated with crude protein and ash contents and positively correlated with starch content (Wang et al. 2017). Accordingly, this relationship may explain the higher protein and mineral contents and the lower starch observed in *P. vulgaris*, as well as the opposite pattern found in the larger-seeded *P. coccineus* accessions in this study, given that *P. vulgaris* beans are generally smaller than *P. coccineus*. Their nutritional profiles suggest a strong potential for valorization within the context of functional food development, especially in developed countries where plant-based protein sources and bioactive compounds are increasingly in demand (King et al. 2024). These landraces could therefore serve as a valuable basis for promoting high-quality, locally adapted bean cultivars that support both agrobiodiversity conservation and the growing interest in health-oriented diets.

Meanwhile, the commercial cultivars are positioned near the center of the principal component plot, indicating an absence of distinctive biochemical traits. This distribution likely reflects the effects of breeding programs aimed at standardization, which typically select for "average" characteristics to ensure uniformity and consumer acceptance. The limited extremes observed in commercial cultivars likely reflect breeding for agronomic uniformity and yield rather than selection for phytonutrient traits, resulting in reduced biochemical variability compared to genetically diverse landraces.

The presence of numerous traditional landraces in Italian mountain areas provides valuable opportunities to enhance food choices while preserving agricultural biodiversity. This diversity enables the selection of bean cultivars best suited to individual dietary needs and health goals, offering a wide range of nutritional and functional profiles. Promoting the cultivation and use of plant-based products, such as legumes as alternative protein sources, is one of the main objectives of the Farm to Fork strategy within the European Green Deal (NRP 2021–2027). This strategy supports the transition toward sustainable food systems by encouraging innovative and environmentally friendly solutions, including increased legume consumption (NRP 2021–2027; Falcione et al. 2022).

In light of this, the preliminary results of the multidisciplinary characterization of Lombardy bean landraces presented in this study could represent a first step toward the valorization of legumes in line with the goals of the Green Deal. Furthermore, as consumer awareness shifts towards the health-promoting properties of food, the demand for products rich in bioactive compounds continues to increase (Firoozzare et al. 2024). In this study we have shown that Lombardy bean landraces offer significant potential for the agri-food sector, particularly in the development of functional foods designed to increase protein, fiber, and antioxidant intake.

These landraces, therefore, have the potential to not only be consumed in their traditional form but also integrated as functional ingredients into processed foods, enhancing both their nutritional quality and health-promoting properties (Pedrali et al. 2022; King et al. 2024; Bosmali et al. 2025).

The production and consumption of food products from underutilized traditional cultivars strongly linked to specific territories and traditions offers a unique opportunity to create employment and revitalize rural and mountain communities (Giupponi et al.

2018, 2020a; Zuccolo et al. 2023; Pedrali et al. 2022, 2024).

Lombardy features a highly diverse landscape that has long supported the cultivation and conservation of numerous plant species (Rossi et al. 2019; Giupponi et al. 2020b;; Canella et al. 2022; Colombo et al. 2022). All the landraces included in this study were found in mountainous and hilly areas, as the lowland zones, particularly the Po Valley, have undergone intense urbanization and land degradation over the past century (Giupponi et al. 2013). Today, large-scale farms in these lowland areas mainly grow commercial cultivars, while the mountain regions remain hotspots of agro-biodiversity (Alicandri et al. 2024; Giupponi et al. 2020a, 2021a). These beans should be viewed as strategic resources for the sustainable development of rural and marginal areas (Giorgi and Scheurer 2015; Falcione et al. 2022). In this context, mountain territories could play a dual role, not only as economically and culturally significant areas, but also as key sites for the in situ conservation of bean landraces (Alicandri et al. 2024;).

However, the abandonment of agricultural activities, partly caused by a generational turnover in the Alps, remains an ongoing concern, leading to the loss of traditional practices and local genetic resources, including landraces (Nordregio 2004; Keenleisyde and Tucker 2010; Terres et al. 2013, Cislaghi et al. 2019, Didonna et al. 2024). To reverse this trend, greater support is needed to involve new farmers and/or young people in modern, sustainable agricultural systems, particularly those that include the cultivation of landraces (Puneeth et al. 2024).

Rural Development Programmes (RDPs) represent a valuable opportunity to engage and encourage the involvement of young and new farmers, offering financial support and training pathways that can help them start and sustain agricultural activities (https://agriculture.ec.europa.eu/common-agricultural-policy/rural-development/country_en). Part of these funds is specifically allocated to research and innovation activities, such as the project presented in this study, which contributes to the conservation and valorization of agrobiodiversity and supports more resilient and diversified agri-food systems.

In line with European directives aimed at the protection of genetic resources, Italy has also established a National Register of Agrobiodiversity, an innovative tool designed to safeguard traditional genetic resources (https://rica.crea.gov.it/APP/anb/anagrafe-nazionale-35.php). Article 3 of Law No. 194/2015 created this Register within the Ministry of Agricultural, Food and Forestry Policies. The Register includes all local genetic resources of food and agricultural interest, of plant, animal, or microbial origin, that are at risk of extinction or undergoing genetic erosion. Its purpose is to formally recognize and protect these resources, which are crucial for preserving agrobiodiversity and ensuring the resilience and sustainability of national agri-food systems (https://rica.crea.gov.it/APP/anb/anagrafe-nazionale-35.php).

A notable example of successful registration on the European register of conservation variety is the "Nero Spinoso" maize (Cassani et al. 2017), while "Grano Siberiano Valtellinese" (Giupponi et al. 2019b), "Ciuenlai" (Zuccoolo et al. 2023) and "Mais delle Fiorine di Clusone" (Giupponi et al. 2021a) landraces which are now protected under the National agrobiodiversity Registry. Their inclusion has led to an expansion of the cultivated area, thus enhancing their in situ conservation, and could promote their valorization through the development of new agri-food products (Alicandri et al. 2024).

Recently, some farmers have formed associations or consortia to conserve and promote landraces (Negri 2003; Piergiovanni and Lioli 2010; Montesano et al. 2012; Raggi et al. 2022; Fenzi and Couix 2022; Colombo et al. 2022), though most of the cultivars identified in this study are maintained by individual, often elderly, hobby farmers who are not affiliated with any formal network generations (Negri 2003; Colombo et al. 2022).

Although Italy has a lot of traditional cultivars (more than 1,650 only considering herbaceous plants), mainly discovered in mountain and submountain, the majority of them remains unknown to most farmers and only a small fraction was inscribed in the European Register of Conservation Varieties and/ or in the National Register of Agrobiodiversity (Giupponi et al. 2021b). So far, the use of these registers has been and still is limited. In fact, out of the 20 Italy's regions, only eleven, Calabria, Emilia Romagna, Lombardy, Piedmont, Umbria, Liguria, Marche, Tuscany, Apulia, Trentino Alto Adige and Veneto, have recorded conservation varieties. Combined, these registrations (1,148 varieties in total, considering both herbaceous and tree landraces, even if 80% of the landraces listed are tree species).

Of these, Tuscany stands out with 738 registrations (64.28%), while Lombardy has only 13 (1.13%) (https://rica.crea.gov.it/APP/anb/anagrafe-nazionale-35.php). This highlights the need for a better evaluation of the effectiveness and accessibility of such regulatory tools in the coming years and increase the awareness of citizens on biodiversity conservation connecting researchers, population, seed savers and farmers (Didonna et al. 2024; Bocci et al. 2025).

Gene banks and seedbanks are examples of tools has been born after the introduction of the "dynamic conservation" concept (as the "preservation of genetic diversity within and between cultivated plant species, including both in situ conservation and ex situ conservation, with the aim of a sustainable use of plant genetic resources and agrobiodiversity") and they are involved in seed saving, on-farm conservation and agro-biodiversity management (Didonna et al. 2024). To protect and conserve the seeds of the landraces studied in this research they have been entrusted to "Rete Semi Rurali" (RSR), the Italian seed network (https://rsr.bio/), which safeguards them in its seedbanks and it could distribute these traditional cultivars to farmers committed to cultivating them in purity promoting both ex situ and on-farm conservation (Alicandri et al. 2024; Bocci et al. 2025).

Following scientific characterization, the next crucial step for the conservation and protection of these bean landraces is to support farmers in registering their traditional cultivars in the Italian and European agrobiodiversity registers, thereby granting them the recognition and legal protection they deserve at both national and international levels. The data collected in this study are essential for this purpose, as the registration process requires a detailed description of the distinctive traits of each landrace (https://www.upov.int/resource/en/dus_guidance.html). The characterization of these Lombardy bean landraces and the RSR involvement contributes to their on farm conservation, recognizing them as foundational resources for resilient and sustainable agri-food systems (Losa et al. 2025).

This status not only safeguards the landrace itself but also supports the cultural and environmental value of the territory in which it has historically been cultivated (Pedrali et al. 2022; Zuccolo et al. 2023).

Without concrete support for the preservation and valorization of Lombardy beans landraces, and the others traditional cultivars generally, there is a tangible risk of losing valuable agro-biodiversity. This not only undermines conservation efforts but also limits the development of high-quality, low-impact agri-food chains that could play a pivotal role in promoting smart, inclusive, and sustainable growth in their origin areas (Fideghelli and Engel 2009; EU Commission 2010). Simultaneously, greater emphasis must be placed on deepening the understanding and promoting the role of agro-biodiversity in food security, cultural identity, and climate change resilience (Falcione et al. 2022; Pedrali et al. 2024; Losa et al. 2025). Raising awareness and educating younger generations on these issues will facilitate future efforts toward the conservation and valorization of agro-biodiversity, especially in mountain areas (Puneeth et al. 2024).

Conclusion

This research enabled the genetic, morphological, ecological, and nutritional characterization of 16 bean landraces from the Lombardy Alps, previously undocumented. The results highlighted that, from a genetic perspective, these landraces were clearly distinguishable not only by species (*P. vulgaris* and *P. coccineus*), but also from the two commercial cultivars for a comparison. Furthermore, a high level of genetic variability was observed within the landraces themselves, likely due to their origin from distinct mountain areas across Lombardy (often adjacent or overlapping) and to the absence of breeding or selection programs.

While the ecological analysis revealed that the Lombardy beans follow a C/CR functional strategy without substantial intra-genus or intra-specific differentiation, the outline and nutritional analyses demonstrated that each landrace exhibits unique and distinctive traits. These characteristics differentiate them not only from landraces of other species but also from those of the same species. Given the agri-food relevance of beans, the nutritional data obtained in this study are particularly valuable for promoting the cultivation, and thus the *on-farm* conservation, of these landraces in developed countries such as Italy, where mountain and marginal agricultural systems are increasingly oriented toward producing quality and niche products rather than quantity.

Nutritional assessments of the 16 landraces revealed that some possess high levels of bioactive compounds and antioxidant activity, along with excellent protein content, suggesting potential use in the development of functional foods. For these reasons, the studied landraces should be regarded as plant genetic resources with untapped potential for innovation in food production and new value chains. Their protection and valorization are essential, especially considering they are still grown by only a few farmers (mainly hobbyists) for self-consumption. To prevent the loss of agrobiodiversity, more research projects must be supported in the future to characterize plant agrobiodiversity, since scientific knowledge represents the fundamental starting point for promoting/valorizing, and conserving landraces.

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Declarations

Conflict of interest The authors declare no competing interests.

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