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Architectural and Agronomic Evaluation of Some Wild Italian Genotypes of *Olea europaea* L. From Sardinia in High-Density Planting

Enrico Maria Lodolini | Matteo Zucchini | Costantino Pacilli | Davide Neri | Veronica Giorgi

Department of Agricultural, Food and Environmental Sciences, Marche Polytechnic University, Ancona, Italy

Correspondence: Veronica Giorgi (v.giorgi@staff.univpm.it)

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ABSTRACT

The olive (*Olea europaea* L.) germplasm of the Mediterranean basin is very rich and is characterized by a huge number of cultivars, more than 1200 already identified. The aim of our study was to evaluate these genotypes to be considered for further breeding programs or eventually for direct cultivation in super-high-density (SHD) planting systems. Some spontaneous, wild, and locally neglected genotypes from Italy (Sardinia), not previously and fully described, were collected and in the Autumn of 2015, 14 genotypes were planted in Apulia (Foggia province), the main Italian region for olive growing. In 2017, 2018, and 2019, several architectural parameters of the canopy were measured, and the fruits were characterized. Results identified two possible genotypes suitable for SHD cultivation or to be included in future breeding programs. These selected genotypes showed good architectural characteristics and high average fertility index. This study showed that spontaneous, wild, and local relict genotypes can represent a huge germplasm resource to identify interesting genotypes for cultivation and parentals for breeding programs.

1 | Introduction

From the original area of the first cultivation, corresponding roughly to the Middle-East Mediterranean coast (Syria, Lebanon, etc.), the olive (*Olea europaea* L.) spread to all the countries of the Mediterranean basin. A secondary diversification center in the central part of the Mediterranean (Greece, Italy, Tunisia, and North Africa) and a tertiary diversification center in the western part of the Mediterranean have been identified (Besnard et al. 2018).

The olive germplasm of the Mediterranean basin is very rich and characterized by a huge number of cultivars; the existence of more than 2600 has been outlined (FAO, 2010; Belaj et al. 2016), even though several cases of homonymy and synonymy were reported (Bartolini et al. 1998; Muleo et al. 2016) and the real consistency of the cultivated olive heritage still remains controversial (Baldoni et al. 2023). Due to the domestication and hybridization process with wild relatives, the local diffusion or the geographical redistribution over time, it is very difficult to identify the number of varieties so that the correct estimation of the amount of the genetic resources in olive is very complicated (D'Agostino et al. 2018; Julca et al. 2020; Belaj et al. 2022).

More than two-thirds of the olive cultivars are found in southern European countries: more than 500 in Italy (it has been reported 631), 427 in Spain, 88 in France, and between 80 and 100 in Greece (Bartolini et al. 1998; Khadari et al. 2003; Barranco et al. 2005; Muzzalupo et al. 2014; Gómez-Gálvez et al. 2024; Koubouris and Stournaras 2024). Moreover, a rich genetic heritage is still preserved in other olive-growing countries outside Europe, such as in Syria, Turkey, Tunisia, Morocco, and Iran (Belaj et al. 2003; Noormohammadi et al. 2007; Khadari et al. 2008; Fabbri et al. 2009; Fendri et al. 2010; Isk et al. 2011; Hosseini-Mazinani et al. 2014).

Based on estimates by the FAO's Olive Germplasm Production and Plant Protection Division (Bartolini 2008), the world's olive germplasm would contain many local varieties and ecotypes contributing to an increase in the amount of genetic diversity already described. Many reasons are at the base for the high genetic variability of the olive tree: the allogamy and self-incompatible floral biology, the traditional propagation by seeds, the domestication process and hybridization, the trade, and the great longevity of the tree (Baldoni and Belaj 2009; Beghè et al. 2011; D'Agostino et al. 2018; Julca et al. 2020).

The Italian olive germplasm includes, in addition to 631 cultivars, 827 incompletely identified accessions maintained in 26 collections (Bartolini 2008). The National Register of Fruit Plant Varieties, periodically updated by the Ministry of Agriculture, currently includes 750 olive cultivars. The number is probably underestimated due to the lack of information on local minor cultivars that are widespread in different olive-growing areas. Most of these are ecotypes that have been propagated at farm level since ancient times (Cruz et al. 2016).

A relevant importance is given by researchers to the high genetic diversity found in the two main Italian islands (Sardinia and Sicily). In fact, if geographical isolation reduces the spreading of many wild species, it can increase at the same time the development of endemic individuals (Passeri et al. 2023). In Sardinia, for example, oleaster (*Olea europaea* var. *sylvestris*) has been studied for its high distribution and wide phenotypic variability (Mulas 1999; Mulas et al. 2001, 2002). The genotypic and phenotypic study of these cultivated, wild, and less common genotypes is particularly important today to select interesting characteristics for breeding programs, for example, low tree vigor and high level of ramification, early and constant fruit production, self-fertility, big fruit size, high oil yield and quality, as well as suitability to changing climatic conditions and high resistance to pests and diseases (Rugini et al. 2011).

In the last decades, new and traditional olive-producing countries are adopting the high-density (HD, 300–1000 trees/ha) or super-high-density (SHD, >1000 trees/ha) systems to facilitate mechanization of harvesting and pruning (Marino et al. 2017; Diez et al. 2017) and significantly reduce management and production costs compared to traditional low-yield, hand-harvested orchards (Lo Bianco et al. 2021). Some cultivars, such as Arbequina, Arbosana, and Koroneiki, have proven to be more suitable than others for SHD orchards that require small trees (Camposeo et al. 2008; Tous 2011). These cultivars constitute the majority of orchards planted in hedgerow systems in Spain (Tous 2011), Italy (Godini et al. 2011), and Tunisia (Larbi et al. 2011).

Other cultivars need to be evaluated for their adaptability to SHD planting models. Among previous studies, the Italian cultivars Maurino and Piantone di Mogliano were reported to be suitable for SHD orchards in Central Italy (Farinelli and Tombesi 2015; Lodolini et al. 2018, 2022). In Southern Italy (Sicily), the cultivar Calatina confirmed an exceptional performance at the highest planting density (Massenti et al. 2024 and Marino et al. 2019). In Apulia, only Urano resulted to be suitable for SHD systems (Godini et al. 2011 and Camposeo et al. 2022).

All the cultivars that showed good adaptability to SHD have low intrinsic vigor and so we can consider this characteristic as the key factor of suitability to very HD orchards (Camposeo et al. 2008). Therefore, plant architecture can be considered suitable for SHD when it features a conical canopy shape, uniform distribution of lateral branches, and greater branching ability associated with smaller trunk, branch, and shoot diameters. This results in higher yield efficiency and a greater number of fruiting shoots, which are essential within the limited canopy volume (CV) of hedgerow systems (Rosati et al. 2013; Lodolini et al. 2017; Famiani et al. 2023). The low vigor of these cultivars is usually associated with the ability to produce more and earlier, approximately from the third year after planting (Camposeo et al. 2008; Tous 2011). It is possible, therefore, that the low vigor may result from early bearing and higher productivity combined with high level of ramification (Rosati et al. 2017) instead of the possibility to reduce it with agronomic practices (Paoletti et al. 2023).

Breeding programs in the last decades focused on obtaining new cultivars with the abovementioned characteristics: FS17 (Patent IRO-CNR1165/NV) (Fontanazza et al. 1990), Sikitita (Rallo et al. 2008), Don Carlo (Patent CNR-RM 99 NV 000020) (Tombesi et al. 2011), Oliana (Camposeo 2017), Lecciana (Camposeo et al. 2021), and Sultana (Valverde et al. 2024). Nevertheless, the huge germplasm resources represented by local and less common accessions or wild ones all over the Mediterranean basin need to be investigated to identify interesting parentals for breeding.

The objective of our study was to assess 14 genotypes from Mediterranean shrublands of Sardinia for their architectural and productive characteristics in the same cultivation conditions in order to identify those with suitable characteristics to SHD plantation and to be used for further breeding programs.

2 | Materials and Methods

2.1 | Experimental Site and Planting Material

The trial was carried out at the "Fratelli Fratta" farm located in Foggia, Apulia Region, Southern Italy (41°32' N, 15°30' E, 55 m a.s.l.). According to a private weather station placed in the farm (iMETOS 3.3, PESSL Instruments GmbH, Weiz, Austria), in the last 10 years the average rainfall was around 500 mm per year and the average annual temperature 16°C. August is the hottest month of the year, characterized by an average temperature of 27°C, while January shows the lowest average temperature of the year (7°C). Maximum and minimum temperatures and rainfall during the period of the trail are shown in Figure 1. There is a clear variability between the years, with different rainfall distribution and temperature values.

The soil of the farm is medium-textured and characterized by the presence of sand <50%, silt 30%–40%, and clay 10%–20% and integrated farming is applied.

The 14 olive genotypes were collected in 2014 by the Buccelletti nursery (Castiglion Fiorentino, AR, Italy) from the wild Mediterranean shrubland in two different locations of Sardinia Island (northern and central areas) where olive shrubs from open pollination and seedling are very common.

Sampled vegetative material was propagated by cuttings and when the plantlets were 40–50 cm height, they were planted at the "Fratelli Fratta" farm according to SHD planting system (1666 tree ha^{-1}, 4.0 × 1.5 m) in October 2015.

Plantlets were planted in one row of the orchard with five replicates per each of the 14 genotypes. The trees were grown

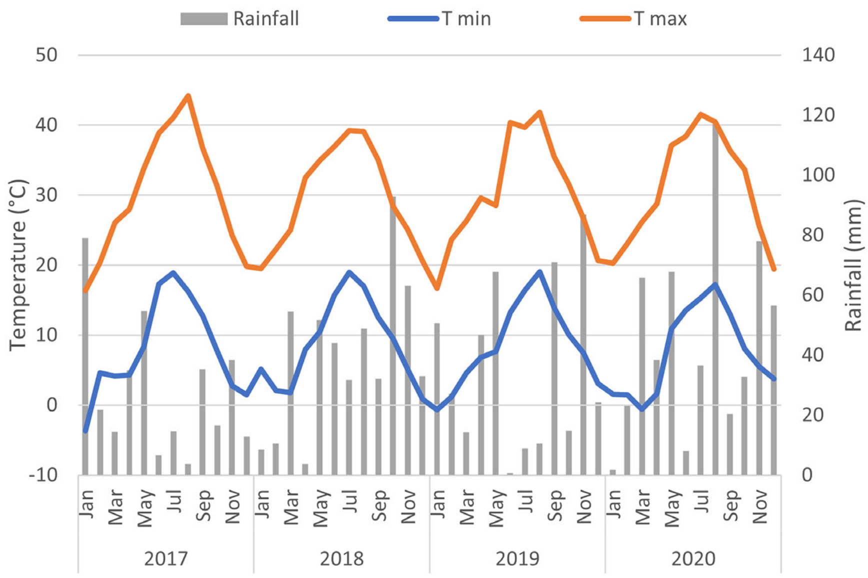

FIGURE 1 | Climatic trend data for the period of the trial. Maximum and minimum temperatures and rainfall.

maintaining a central leader by tying it to the stake, and pruning was limited to remove only suckers or branches in the trunk up to 50 cm from the ground in order to maintain the natural characteristics of each accession during the years of trial. Fertigation was used and nutrients and water were provided in accordance with integrated farming practices for olive cultivation (business as usual).

Preliminary molecular analyses and analysis of plastidial markers (Pontikis et al. 1980; Bassi et al. 2002; Rallo et al. 2000; Caruso et al. 2014) were commissioned to CNR-IBBR of Perugia in November 2017 to verify if the collected genotypes had a correspondence with their database, which includes over 2000 olive genotypes (Fabbri et al. 1995; Baldoni et al. 2000). All the analysis were carried by CNR-IBBR of Perugia following the protocols in the cited references and the complete dataset can be consulted upon request.

None of the examined samples correspond to cultivars previously recorded in the database of the CNR-IBBR of Perugia. In some genotypes, chloro-type E2 appeared. This is very rare among the cultivated varieties (only Canino, Kerkira, Pisciottana, Ouslati), but it is widespread in many populations of wild olive trees (*Olea europaea* L. ssp. *europaea* var. *sylvestris* Brot). Therefore, the studied genotypes are confirmed to be originated from the dissemination of wild olive trees and in some cases of the cv. Canino.

Regarding the kinship analysis, the possible direct relatives were identified for each accession, both among the same group of supplied samples and the cultivars registered in the database of the CNR-IBBR of Perugia (Table 1).

TABLE 1 | Molecular and kinship analysis of the studied olive genotypes.

Genotype	Chlorotype E2	Kinship based on molecular studies
BA01		Direct relative BA014
BA02	x	Possible seedling of the cv. CANINO (E2)
BA03	x	Direct relative BA08
BA04	x	Direct relative of another accession collected but not reported in this study
BA05		Direct relative cv. NOCELLARA MESSINESE (Sicily, Italy)
BA07	x	Direct relative BA013
BA08		Direct relative BA03
BA09		Direct relative cv. BORGIONA (Umbria, Italy)
BA10	x	Direct relative cv. SEMIDIANA (Sardinia, Italy)
BA11	x	Direct relative cv. LECHIN DE SEVILLA (E2; Spain)
BA12		Direct relative cv. BOSANA (Sardinia, Italy)
BA13	x	Direct relative BA07
BA14		Direct relative BA01
BA15		Direct relative cv. ITRANA (Lazio, Italy sinonime cv. Nera di Villacidro or Nera di Oliena, Sardinia, Italy)

2.2 | Tree Architecture and Tree Size

In 2017, to determine the architecture of the canopy and the branching density of the 14 genotypes, the measurement of the insertion height, the basal diameter, and the length of each primary branch was executed along the central leader starting from the base up to the top in five trees (replicates) per accession. A manual ruler and a digital caliper were used.

To determine the growth of the trees in 2017, 2018, and 2019, the diameter of the trunk was measured at 20 cm from the ground using a digital caliper along the two axes (longitudinal and transverse) in order to calculate the trunk cross-sectional area (TCSA).

To determine the height of the tree, the distance between the collar and the top of the plant was measured. Moreover, the in-row width and the cross-row width of the canopy were measured using the point of maximum expansion of the branches projected on the ground in both directions. The biometrical measurements were used to calculate the volume of the canopy assimilating it to a cone with elliptical base. Measurements of the reported parameters were performed in all the trees (replicates) of each accession in 2017, 2018, and 2019.

A canopy shape index (CSI) was calculated as canopy height/canopy transversal diameter (CH/TD), considering the canopy transversal diameter as an average of the cross-row and in-row width.

To assess the canopy architecture of the 14 olive tree genotypes, we developed a composite metric called Olive Tree Suitability Index (OTSI) and in particular to study the suitability for SHD orchard systems, we named it OTSI-SHD. This index integrates four structural parameters: plant height (H), CV, lateral branch frequency (LBF), and CSI.

For plant height (H), the optimal range for SHD suitability in our study case was considered between 2.5 and 3.5 m, with maximum suitability centered at 3.0 m. Trees outside this range were penalized accordingly. A compact canopy, with a CV ideally around 5.0 m^3, was considered the most suitable for the SHD system of our study case, whereas canopy with volumes above 10 m^3, indicating an excessive vegetative development, scored the lowest. LBF was quantified as the average internodal distance (in cm) between two consecutive lateral shoots along the main axis. A shorter distance reflects a higher branching density, which indicates a higher suitability for SHD systems. An ideal LBF was set at 5 cm, with a maximum acceptable value of 20 cm for our study case. For the CSI, a value of 1.5 was considered ideal for our study case, indicating an upright canopy growth habit, suitable for SHD hedgerow systems.

Each of the four parameters was normalized to a score ranging from 0 (least suitable) to 1 (most suitable), using tailored linear scaling functions. The final OTSI-SHD value was calculated as the arithmetic mean of the four standardized scores:

$$\mathrm{OTSI}-\mathrm{SHD}=0.25\cdot \mathrm{Hs}+0.25\cdot \mathrm{CVs}+0.25\cdot \mathrm{LBFs}+0.25\cdot \mathrm{CSIs} \tag{1}$$

where:

- Hs = standardized height score
- CVs = standardized canopy volume score
- LBFs = standardized lateral branch frequency score
- CSIs = standardized canopy shape index score

2.3 | Fertility Evaluation, Fruit Production, and Fruit Characteristics

A visual index considering the level of fruit load was used to estimate the reproductive attitude, as in Neri et al. (2020). The "fertility index" is not influenced by canopy dimensions and was assigned every year to each tree of the studied olive genotypes by the same person using the same parameters and methodology in order to reduce subjectivity. The index consisted in values from 0 to 5 assigned according to the presence of the fruits on the tree: 0 = absence, 1 = low, 2 = low-medium, 3 = medium, 4 = high, and 5 = very high. The evaluation was performed for all genotypes in 2017, 2018, and 2019 while in 2020, data for BA01, BA02, BA13, and BA14 genotypes are missing because the trees were uprooted due to a high attack of olive knot. In 2020 (5 years after planting), the fruits were collected from each tree of the studied genotypes to determine the fruit yield per tree and calculate the fruit yield per hectare.

In 2019, a characterization of the fruits was performed. A sample of 30 fruits per tree was collected and weighted as a single sample to calculate the average fruit weight. Pit fresh weights were weighted as a whole (30 pits) and single pit weight was then calculated. Fruits and pits were characterized following the indication of a previous study (Barranco et al. 2000).

2.4 | Statistical Analysis

One-way ANOVA was performed for biometrical measurements of the canopies and for SHD aptitude index (OTSI) and in case of significant differences the Tukey–Kramer (HSD) test at $p < 0.05$ was used for mean separation.

Data of OTSI-SHD index and production parameters (2019 fruit weight and fertility index, average of the 3 years) were used for a hierarchical clustering (Ward method) of the 14 genotypes for a better visualization of the patterns. All statistical analyses were performed with JMP 13.0 software (SAS Institute, Cary, NC, USA).

3 | Results and Discussion

During the 3 years of assessment (2017, 2018, and 2019), the genotypes showed their architectural and productive characteristics being subjected to pruning only to remove suckers or branches in the trunk up to 50 cm from the ground without any other manipulation of the canopy, so that it was possible to classify them according to their suitability for HD plantations.

It is worth noting that some genotypes were excluded from the study in 2020 (trees uprooted) because strongly attacked by the olive knot. Even though the symptoms of the disease were not recorded on the trees and pathogenic tests were not executed, a susceptibility of the remaining studied genotypes cannot be excluded, especially in limiting climatic conditions (Valverde et al. 2020).

3.1 | Tree Architecture and Tree Size

In 2017, after two growing seasons from planting, the trees showed an average number of 43.3 ± 11 primary branches on the central leader. The maximum value was 74.6 ± 13 in

BA04, and the minimum was 26.6 ± 9 in BA08. In each genotype, the branches with the biggest diameters were also the longest and inserted on the central leader not higher than 100 cm from the ground. BA01, BA02, BA03, BA04, and BA05 showed the longest lateral branches, over 180 cm (Figure 2). Some genotypes showed a very regular branching along the central leader and a self-organization of the canopy according to an appreciable narrow conical shape. These characteristics are reported to be important

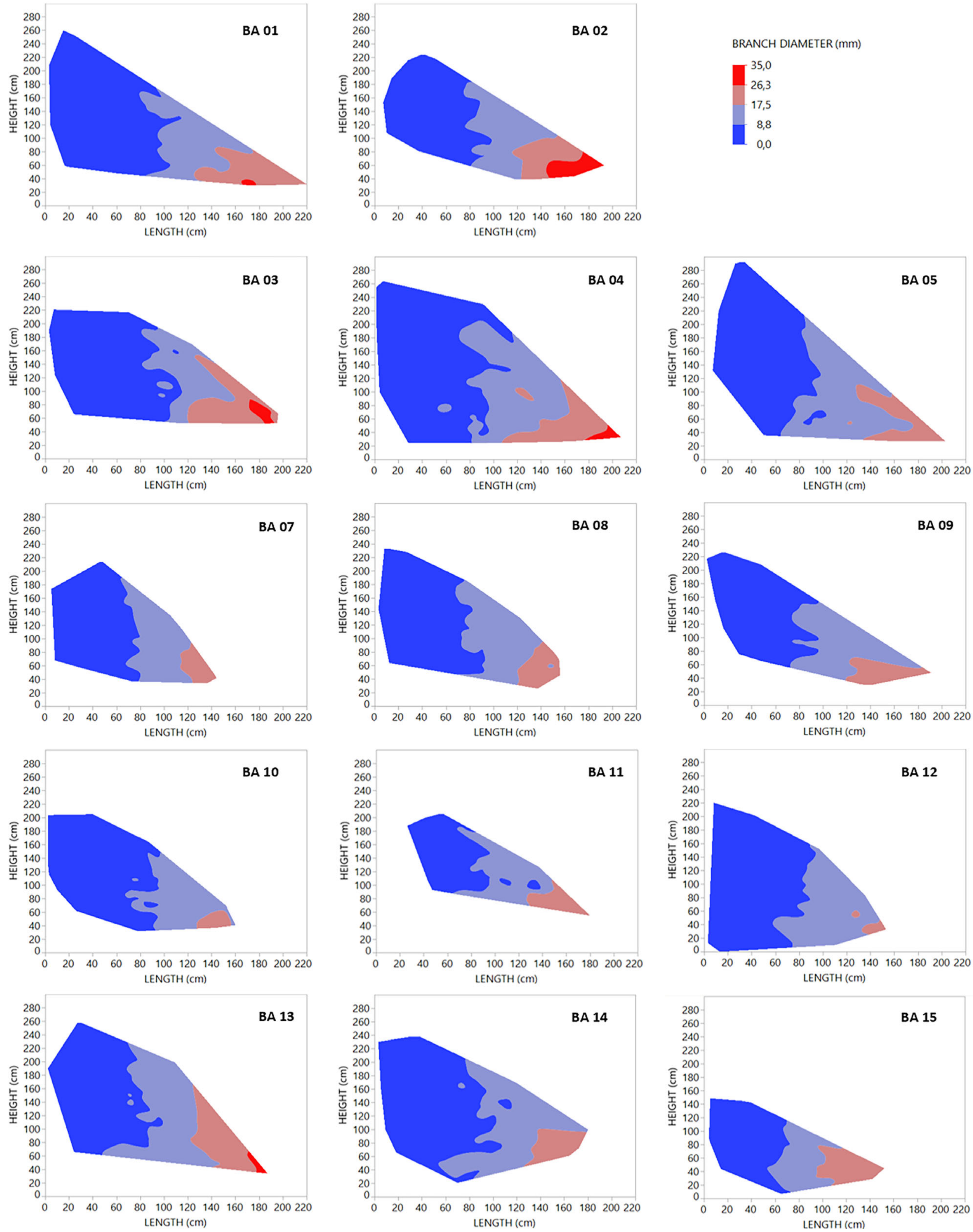

FIGURE 2 | Distribution of the branch diameter according to the length and in relation to the height of insertion from the ground along the central leader in 14 studied genotypes.

for the selection of cultivars or planting material to be used in HD and SHD olive orchards (Marino et al. 2019; Rosati et al. 2013; Neri et al. 2020; Lodolini et al. 2023a, 2023b).

The trees showed different behaviors regarding the canopy growth. In the fourth year after planting, 6 genotypes out of 14 (BA01, BA02, BA03, BA04, BA13, and BA05) had exceeded the height of 3.5 m with BA04 reaching the maximum tree height of 3.7 ± 0.1 m. BA10 recorded the lowest tree height in 2019 (2.73 m). The other studied olive genotypes had an average height between 3.0 and 3.5 m (Figure 3). Considering the relative height increase, BA08, BA10, and BA14 recorded the lowest growth increase over the years (20% of the initial height) (Table 2). These characteristics preclude the possibility of adaptation of some cultivars to SHD systems as reported by Farinelli and Tombesi (2015). In fact, the hedgerow should have a 3 m maximum height (with additional 0.5 m flexible shoots) to allow the use of over-the-row harvesting machines (Valverde et al. 2020), whereas the total height of these genotypes was higher than 3.5 m (Figure 3).

The average TCSA varied between the genotypes too, indicating a different vigor, but the relative increase during the trial was not significantly different (Table 2).

The CV showed differences among the genotypes in 2019. BA01, BA02, and BA03 were significantly higher than the other genotypes, confirming the greater vigor (Figure 3). On the contrary, BA09 and BA10 showed the lowest volumes (about 4 m^3). BA07 recorded the greatest relative increase in volume (170%), whereas BA14 showed the lowest one (20%) (Table 2).

Regarding the OTSI-SHD the best average record was showed by BA07 and BA09, while BA01 and BA03 the lowest (Table 2).

3.2 | Fertility, Fruit Production, and Fruit Characteristics

The fertility index (from 0 to 5) per tree in the 4 years of assessment (from 2017 to 2020) showed a strong variability between the considered genotypes. BA01, BA02, BA05, BA11, BA12, BA13, and BA14 recorded an increasing fruit load (based on the fertility index) over the years compared to the other genotypes which, on the other hand, showed an alternating fertility index trend (Table 3).

BA03, BA09, BA12, and BA14 registered the greatest fruit load over the years; on the contrary, BA15 and BA13 showed the lowest average values. BA13 presented a very low fertility index in 2017 which increased in the following years. BA09 and BA12 showed a very high fruit production at harvest in 2020: 17.4 and 14.0 kg $tree^{-1}$, corresponding to 29.0 and 23.0 t ha^{-1}, respectively. BA07 recorded the lowest fruit production in the same

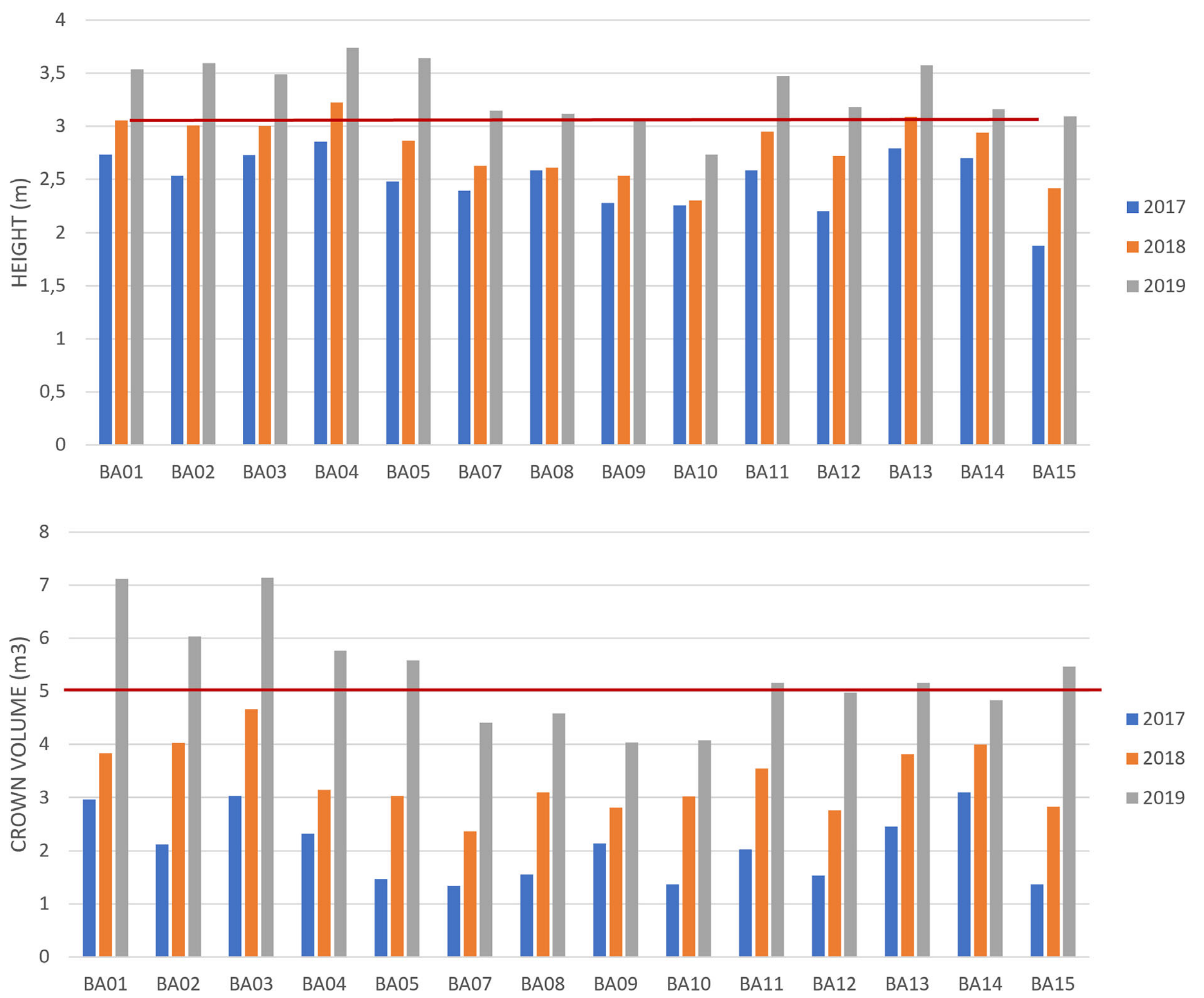

FIGURE 3 | Plant height and CV measured in 2017, 2018, and 2019. The red line indicates the height and volume limit for an efficient mechanical harvest.

TABLE 2 | Increase of the biometric measurements during the trial (2017–2019) presented as relative growth. OTSI-SHD index for suitability to HD planting (mean ± standard deviation). Different letters indicate significant difference, Student's *t*-test.

Genotype	Relative height growth	Relative volume growth	Relative TCSA growth	OTSI-SHD
BA01	0.3 ± 0.1 bcd	1.4 ± 0.6 abc	2.8 ± 0.2 a	0.68 ± 0.09 e
BA02	0.4 ± 0.2 abc	1.2 ± 0.6 abcd	2.0 ± 0.5 a	0.70 ± 0.19 cde
BA03	0.3 ± 0.2 bcd	0.8 ± 0.1 bcde	2.9 ± 1.2 a	0.67 ± 0.10 e
BA04	0.4 ± 0.2 abc	1.4 ± 0.8 abc	3.9 ± 2.3 a	0.79 ± 0.03 bcde
BA05	0.4 ± 0.2 abc	1.6 ± 0.7 ab	3.5 ± 1.0 a	0.74 ± 0.14 de
BA07	0.4 ± 0.2 abc	1.7 ± 0.8 a	2.8 ± 0.9 a	0.92 ± 0.11 a
BA08	0.2 ± 0.1 d	0.9 ± 0.3 bcde	2.7 ± 1.1 a	0.88 ± 0.07 abc
BA09	0.3 ± 0.1 abcd	0.5 ± 0.4 de	2.8 ± 0.7 a	0.92 ± 0.06 abc
BA10	0.2 ± 0.2 cd	0.7 ± 0.4 cde	2.7 ± 0.9 a	0.84 ± 0.04 abcd
BA11	0.3 ± 0.0 abcd	0.9 ± 0.8 abcde	2.4 ± 0.6 a	0.82 ± 0.08 abcd
BA12	0.5 ± 0.2 ab	1.2 ± 0.7 abcd	3.4 ± 0.9 a	0.89 ± 0.05 abc
BA13	0.3 ± 0.1 bcd	0.7 ± 0.7 cde	2.1 ± 1.4 a	0.78 ± 0.10 cde
BA14	0.2 ± 0.1 d	0.2 ± 0.2 e	2.8±0.4 a	0.83 ± 0.10 abcd
BA15	0.5 ± 0.3 a	1.4 ± 1.0 abc	2.6±1.3 a	0.88 ± 0.14 abc

TABLE 3 | Fertility index (visual estimation) of the 14 genotypes (from 0 to 5, where 0 is the absence of fruits and 5 is very high presence) in 2017, 2018, 2019, and 2020 (mean ± standard deviation). Different letters indicate significant differences among the years within the same genotype (Tukey HSD test). *p*-values from ANOVA analysis are shown for significant differences between years and genotypes.

	Fertility index				
Genotype	**2017**	**2018**	**2019**	**2020**[a]	***p*-value**
BA01	1.4 ± 0.4 c	2.0 ± 0.0 b	3.7 ± 0.5 a		<0.0001
BA02	1.7 ± 0.4	2.2 ± 0.4	2.75 ± 1.0		0.1052
BA03	2.6 ± 0.5 b	2.2 ± 0.4 b	4.0 ± 0.5 a	4.1 ± 0.2 b	<0.0001
BA04	2.3 ± 0.9 b	2.2 ± 0.4 b	4.7 ± 0.6 a	1.6 ± 0.5 b	<0.0001
BA05	1.0 ± 0.6 c	2.8 ± 0.7 b	4.1 ± 0.6 a	3.1 ± 0.2 b	<0.0001
BA07	2.2 ± 0.5 c	3.2 ± 0.4 b	1.3 ± 0.4 d	3.9 ± 0.5 a	<0.0001
BA08	0.5 ± 0.5 c	3.2 ± 0.4 a	1.6 ± 0.6 b	3.6 ± 0.5 a	<0.0001
BA09	2.4 ± 1.0 c	3.6 ± 0.5 b	3.0 ± 0.9 bc	5.0 ± 0.0 a	0.0004
BA10	1.4 ± 0.8 b	3.6 ± 0.5 a	1.7 ± 1.1 b	2.8 ± 0.4 a	0.0015
BA11	1.5 ± 0.5 c	3.0 ± 0.0 b	4.7 ± 0.3 a	2.0 ± 1.0 c	<0.0001
BA12	3.3 ± 0.6 b	3.8 ± 0.4 ab	4.5 ± 0.5 a	3.4 ± 0.5 b	0.0129
BA13	0.3 ± 0.4 b	2.6 ± 0.8 a	2.9 ± 0.4 a		<0.0001
BA14	2.3 ± 1.0 b	3.0 ± 0.7 b	4.6 ± 0.2 a		<0.0001
BA15	1.0 ± 0.8 b	2.6 ± 0.5 a	1.3 ± 0.5 b	2.6 ± 0.4 a	0.0019
***p*-value**	<0.0001	<0.0001	<0.0001	<0.0001	

[a]Data of BA01, BA02, BA13, and BA14 genotypes are missing because the trees were uprooted due to a high attack of olive knot.

year: 4.25 kg tree^{-1}, corresponding to 7.0 t ha^{-1}, whereas the other genotypes had an average production of 7 kg tree^{-1}, corresponding to 12.0 t ha^{-1}.

The characterization of the pits (Table 4) showed that almost all the genotypes presented an elliptical shape with a slight asymmetry along the longitudinal axis. BA01 and BA04 presented an elliptical shape with a symmetry along the longitudinal axis for the first one and an asymmetry along the longitudinal axis for the second one. The pits of BA07 and BA09 appeared elongated with an asymmetry along the longitudinal axis, while BA10 showed similar shape with a slight asymmetry. The pit of BA08 was the only one with an ovoid symmetrical shape. BA15 resulted the genotype with the lowest fresh weight of the pit, while BA07 showed the highest value.

The shape of the fruits resulted diversified although the prevailing one was ellipsoidal with a slight asymmetry along the longitudinal axis (Table 4). BA07 and BA08 showed the biggest fruit (fresh weight higher than 4.0 g), with different shapes. BA04 and BA09 registered the lowest values, below 1.0 g. The other genotypes showed values included between 1.0 and 2.0 g. BA03, BA07, BA08, and BA13 showed the biggest pulp-to-pit ratio (more than 4), with BA08 registering the highest value (6.39) and making these genotypes very interesting for table olives production.

3.3 | Data Clustering

Data of canopy aptitude to SHD (OTSI-SHD) and production parameters (fruit fresh weight and fertility index, average of the 3 years) were used for a hierarchical clustering (Ward method) of the 14 genotypes (Figure 4). It is possible to group the studied genotypes into four clusters with distinct characteristics.

In the first cluster, the genotypes BA01, BA02, BA03, BA05, and BA13 showed low OTSI-SHD values. In fact, they were characterized by tall trees, not very compact in-row width, higher trunk diameter, and less regular distribution of the primary branches along the central leader. Therefore, they can be classified as genotypes with low aptitude for SHD, as previously indicated for other cultivars selected through breeding programs (Camposeo 2017). Moreover, they have good values of fertility with small fruits.

The second cluster included BA04, BA11, BA12, and BA14 which were characterized by medium–high aptitude to SHD, with medium-sized trees with small trunk diameter and medium–small CV. They showed also a high fertility and medium–large fruit dimension. Such genotypes could be therefore used as germplasm source for testing directly in pilot SHD orchards, or included in breeding programs, in order to perform controlled

TABLE 4 | Fruit and pit characteristics of the 14 studied genotypes measured on 30 fruits per genotype (total weight/30) in 2019.

Genotype	Morphology of pit[a]	Pit fresh weight, g	Morphology of fruit[a]	Fruit fresh weight, g	Pulp-to-pit ratio
BA01	Elliptical Asymmetrical	0.42	Ellipsoidal Slightly asymmetrical	1.37	2.24
BA02	Elliptical Slightly asymmetrical	0.36	Ellipsoidal Slightly asymmetrical	1.06	1.90
BA03	Elliptical Slightly asymmetrical	0.33	Ovoid Symmetrical	1.77	4.35
BA04	Elliptical Symmetrical	0.30	Ovoid Slightly asymmetrical	0.96	2.24
BA05	Elliptical Slightly asymmetrical Mucro	0.34	Ellipsoidal Slightly asymmetrical	1.45	3.29
BA07	Elongated Asymmetrical Mucro	0.86	Ellipsoidal Slightly asymmetrialc	5.49	5.35
BA08	Ovoid Symmetrical	0.58	Spherical Symmetrical	4.80	7.21
BA09	Elongated Asymmetrical Mucro	0.26	Ellipsoidal Asymmetrical	1.01	2.82
BA10	Elongated Slightly asymmetrical Mucro	0.41	Ellipsoidal Asymmetrical	1.44	2.50
BA11	Elliptical Slightly asymmetrical	0.32	Ellipsoidal Slightly asymmetrical	1.11	2.41
BA12	Elliptical Slightly asymmetrical	0.35	Ellipsoidal Asymmetrical	1.15	2.30
BA13	Elliptical Slightly asymmetrical Mucro	0.52	Ovoid Symmetrical	3.10	4.99
BA14	Elliptical Slightly asymmetrical	0.29	Ellipsoidal Symmetrical	0.89	2.08
BA15	Elliptical Slightly asymmetrical Mucro	0.24	Ellipsoidal Slightly asymmetrical	0.88	2.61

[a]Descriptors used for pit and fruit morphology are the shape, the longitudinal symmetry, and the presence of mucro.

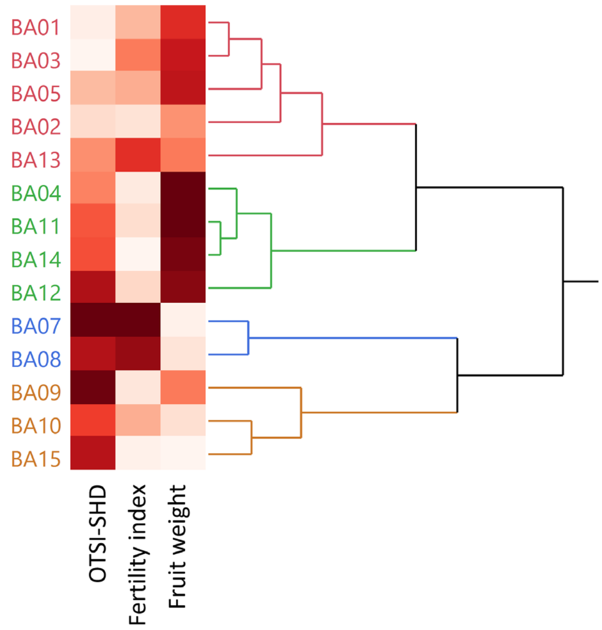

FIGURE 4 | Hierarchical clustering (Ward method) for the biometric parameters (OTSI-SHD index) and production parameters (fruit weight and fertility index) of the 14 genotypes considered.

cross-pollination to select new cultivars with higher suitable characteristics for SHD plantations.

The third cluster included the genotypes BA09, BA10, and BA15. They recorded high OTSI-SHD, in fact they have low values in all studied biometric parameters of the canopy and were hence considered to possess good aptitude for hedgerow systems. However, they showed a low level of fertility and small fruits.

The fourth cluster included BA07 and BA08 which were characterized by a high fruit weight and a high SHD aptitude (very high OTSI-SHD), which makes them very interesting genotypes for SHD plantations, even for table olives production.

Spontaneous and wild olive genotypes from free pollination all over the Mediterranean basin can represent a huge germplasm resource to identify interesting parentals for breeding programs (Godini et al. 2011). However, few studies, at our knowledge, reported about the use of spontaneous germplasm as starting material for breeding programs in olive (Klepo et al. 2013; Diaz-Rueda et al. 2020). The results of our study highlighted a high diversity of the studied genotypes, even though some of them can be grouped for similar descriptors. This is consistent with what previously reported by other studies (Lo Bianco et al. 2021; Camposeo et al. 2008; Tous 2011) and also confirmed the development of endemic individuals in geographical isolated regions, as for Sardinia. In particular, the genotypes BA09, BA10, and BA15 proved to be interesting due to their adaptability to SHD systems, especially BA09, which also exhibited a medium level of fertility. BA04, BA11, BA12, and BA14 can also be considered promising genotypes due to their high fertility, despite showing moderate adaptability to SHD. Finally, another noteworthy group includes BA07 and BA08, which demonstrated good suitability for SHD and large fruit size, making them ideal for table olive production. Such individuals can represent a starting point for controlled cross breeding programs.

4 | Conclusions

The olive intensification depends on the selection of cultivars with suitable architectural habit of the tree and early fruit production adapted to HD hedgerow planting systems with over-the-row mechanized harvest. Presented results suggest that at least five of the spontaneous, wild, and locally relict genotypes (BA07, BA08, BA09, BA10, and BA15) collected from olive shrubs in the northern and central areas of Sardinia have suitable architectural and productive characteristics to be used for further breeding programs in order to select suitable and improved cultivars, in HD and SHD planting models. Among the five mentioned genotypes, two were identified for their potential use in SHD plantations and as table olive varieties, showing high suitability for SHD and high fresh fruit weight and pulp-to-pit ratio. At the same time our results show the potential of the huge but very little known olive germplasm resource that can be found in many areas of the Mediterranean basin.

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Disclosure

The authors report there are no competing interests to declare.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data are available on request from the authors.

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