

Evaluation of Wild Plum Species for Their Potential as Clonal Rootstock for Apricot

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Apricot, plum, prunus, selection, rootstock

Abstract

This research was conducted between 2020 and 2024 in the Malatya and Elazığ regions, two important centers of stone fruit cultivation in Turkey, with the primary objective of identifying and selecting wild plum genotypes that could serve as potential rootstocks for apricot production. The study was designed within the framework of a systematic selection breeding program, emphasizing the evaluation of morphological and growth-related traits relevant to rootstock performance. A weighted ranking system was employed to ensure a comprehensive assessment of candidate genotypes, integrating multiple growth parameters into a unified scoring approach. In the initial stage of exploration and collection, a total of 159 wild plum accessions were identified and subjected to preliminary monitoring. Taxonomic classification revealed that these accessions comprised 37 genotypes of *Prunus cerasifera*, 16 of *Prunus spinosa*, 9 of *Prunus divaricata*, and 12 of *Prunus domestica*. This diversity reflects the rich genetic variation present in the natural plum populations of the studied regions. Following a two-year period of morphological and agronomic evaluation, 74 accessions displaying promising characteristics were retained as rootstock candidates for subsequent weighted ranking. Based on their cumulative performance scores, 64 genotypes were advanced to the Selection-II stage, thereby representing the most promising materials for further investigation and potential use in breeding programs. At the conclusion of the study, it was determined that approximately 50 of the 64 genotypes advanced to Selection-II exhibited dwarf or semi-dwarf growth characteristics, an attribute of particular importance for the development of rootstocks adapted to modern high-density orchard systems. The identification of such genotypes underscores the potential of wild plum populations as valuable genetic resources for rootstock breeding, offering opportunities to enhance both the sustainability and productivity of apricot cultivation in Turkey.

Kayısı İçin Klonal Anaç Olarak Potansiyellerine Göre Yabani Erik Türlerinin Değerlendirilmesi

Özet

Anahtar Kelimeler

Kayısı, erik, Prunus, seleksiyon, anaç

Bu araştırma, 2020–2024 yılları arasında, Türkiye'nin önemli sert çekirdekli meyve doğal yayılış alanlarından olan Malatya ve Elâzığ bölgelerinde yürütülmüştür. Çalışmadan temel amaç olarak kayısı üretiminde anaç olarak kullanılabilecek yabani erik genotiplerinin belirlenmesi ve seçilmesi hedeflenmiştir. Çalışma, sistematik bir seleksiyon ıslah programı çerçevesinde tasarlanmış, anaç performansı açısından önem taşıyan morfolojik ve gelişimle ilgili özelliklerin değerlendirilmesine odaklanılmıştır. İncelenen genotiplerin bütüncül bir şekilde değerlendirilmesi amacıyla, çok sayıda gelişim parametresini tek bir puanlama yaklaşımında bütünlükten ağırlıklı tartılı derecelendirme sistemi kullanılmıştır. Araştırmanın ilk aşaması olan survey ve koleksiyon sürecinde toplam 159 yabani erik materyali tespit edilerek ön gözleme tabi tutulmuştur. Taksonomik sınıflandırma sonucunda bu materyallerin 37'sinin *Prunus cerasifera*, 16'sının *Prunus spinosa*, 9'unun *Prunus divaricata* ve 12'sinin *Prunus domestica* genotiplerinden oluştuğu belirlenmiştir. Bu çeşitlilik, araştırma bölgelerindeki doğal erik popülasyonlarının zengin genetik varyasyonunu yansıtmaktadır. İki yıllık morfolojik ve tarımsal değerlendirme sürecinin ardından, ümitvar özellikler gösteren 74 materyal, sonraki ağırlıklı sıralama aşamasında anaç adayları olarak tutulmuştur. Kümülatif performans puanlarına göre 64 genotip Seleksiyon-II aşamasına aktarılmış ve bu genotipler, ileri değerlendirmeler ve ıslah programlarında potansiyel kullanım için en ümitvar materyalleri temsil etmiştir. Çalışma sonucunda, Seleksiyon-II aşamasına geçen 64 genotipin yaklaşık 50'sinin bodur veya yarı bodur gelişim özellikleri sergilediği saptanmıştır. Bu özellik, modern sık dikim bahçe sistemlerine uyum sağlayabilecek anaçların geliştirilmesi açısından özel bir önem taşımaktadır. Söz konusu genotiplerin belirlenmesi, yabani erik popülasyonlarının anaç ıslahında değerli genetik kaynaklar olarak potansiyelini ortaya koymakta ve Türkiye'de kayısı yetiştiriciliğinin sürdürülebilirliğinin ve verimliliğinin artırılmasına yönelik önemli fırsatlar sunmaktadır.

1. INTRODUCTION

Anatolia represents one of the most significant regions worldwide in terms of plant biodiversity. Numerous fruit species occur naturally in this area, providing valuable genetic resources for breeding programs (Asma, 2000). Among the stone fruit species naturally distributed across various geographical regions of Anatolia, plums hold a prominent position. Wild plum species such as *Prunus cerasifera*, *Prunus divaricata*, *Prunus domestica*, and *Prunus spinosa* are widely distributed throughout the country (Saglam et al., 2021; Kırca, 2025). These species are well adapted to extreme climatic and edaphic conditions in their natural habitats. Several studies have reported that wild plum species can be effectively utilized in rootstock breeding programs, highlighting their importance as a source of adaptability and resilience (Güleryüz and Ercişli, 1995; Gürkan et al., 2018; Gogorcena et al., 2004; Jiménez et al., 2013).

Apricot (*Prunus armeniaca* L.) is one of the most economically important fruit species in which Turkey maintains a leading position globally in both production and export (FAO, 2022; Asma, 2000). In Turkish apricot cultivation, seedling rootstocks are predominantly used. These rootstocks generally induce vigorous tree growth, which leads to the establishment of orchards at wide planting distances

such as 8×8 m, 10×10 m, or even 12×12 m. Consequently, the tree density in such orchards varies between 7 and 15 trees per decare (Asma & Ozturk, 2005). However, cultivation on seedling rootstocks requires a relatively long juvenile period, with trees reaching full production only after 7–8 years (Layne et al., 1996).

The excessive vigor of seedling-based trees increases orchard management costs, particularly in pruning, pest and disease control, and harvesting (Webster, 2004). In table apricot production, where hand harvesting is required to maintain fruit quality, this issue is especially critical. Mechanical shaking methods often result in the simultaneous collection of ripe and unripe fruits, leading to physical injuries, reduced postharvest quality, and shortened shelf life (Bassi and Audergon, 2001). Furthermore, physical damage on branches and fruits provides entry points for pathogens, thereby increasing the risk of infection (Gülcan, 2010). These challenges highlight the necessity of using dwarf and semi-dwarf rootstocks compatible with apricot in order to improve orchard efficiency and fruit quality.

The choice of rootstock in apricot cultivation varies significantly depending on geographical region. In Europe, plum-based rootstocks (*Prunus cerasifera*, *Prunus domestica*, and their hybrids) are widely utilized due to their adaptability to diverse soil and

climatic conditions (Gogorcena et al., 2004; Jiménez et al., 2013). In contrast, in North America, peach rootstocks and various interspecific hybrids are preferred (Layne et al., 1996; Reighard & Loreti, 2008). Reports indicate that, across apricot-growing countries, rootstock breeding programs have primarily focused on developing genotypes derived from wild plum species due to their broad adaptability (Gürçan et al., 2018). Nevertheless, a universal rootstock capable of adapting to all ecological conditions has not yet been developed (Bassi & Audergon, 2006; Reighard & Loreti, 2008; Monastrá and De Salvador, 1993). Over the past three to four decades, extensive selection and hybridization programs have been conducted within the *Prunus* genus to improve traits related to dwarfing, productivity, and adaptability. However, compared to cultivar breeding, research efforts dedicated to apricot rootstock breeding have received considerably less attention, and studies focusing on the identification and development of suitable rootstocks remain relatively limited (Kırca, 2025; Asma 2005)

This study was designed in three phases, the first of which encompassed selection activities carried out between 2020 and 2024. Wild plum populations naturally distributed in the provinces of Malatya and Elazığ were evaluated during this phase. From these populations, dwarf and semi-dwarf clonal rootstock candidates with potential compatibility for apricot were selected. The research was conducted utilizing the field and laboratory facilities of the Apricot Research Institute Directorate.

2. MATERIAL AND METHOD

Material

The plant material of this study consisted of 74 wild plum genotypes representing clonal rootstock candidates. These genotypes were identified through systematic selection methods. Analysis of their taxonomic distribution revealed that 37 genotypes belonged to *Prunus cerasifera*, 16 to *Prunus spinosa*, 9 to *Prunus divaricata*, and 12 to *Prunus domestica*.

Table 1. List of promising rootstock candidates with their respective codes and origins identified during the selection process.

No	Rootstock Codes	Origin	No	Rootstock Codes	Origin
1	23 AĞ 04	<i>P. cerasifera</i>	38	44 AK 17	<i>P. divaricata</i>
2	23 KK 06	<i>P. cerasifera</i>	39	23 KK 16	<i>P. divaricata</i>
3	44 DR 08	<i>P. cerasifera</i>	40	44 YY 21	<i>P. divaricata</i>
4	44 AK 10	<i>P. cerasifera</i>	41	44 YY 20	<i>P. divaricata</i>
5	44 DŞ 12	<i>P. cerasifera</i>	42	23 AĞ 01	<i>P. divaricata</i>
6	23 MR 02	<i>P. cerasifera</i>	43	23 AĞ 02	<i>P. divaricata</i>
7	44 YY 11	<i>P. cerasifera</i>	44	23 KK 13	<i>P. divaricata</i>
8	23 AĞ 03	<i>P. cerasifera</i>	45	23 KK 03	<i>P. domestica</i>
9	44 KL 01	<i>P. cerasifera</i>	46	44 AK 13	<i>P. domestica</i>
10	44 HK 11	<i>P. cerasifera</i>	47	44 DŞ 05	<i>P. domestica</i>
11	44 HK 17	<i>P. cerasifera</i>	48	44 YY 05	<i>P. domestica</i>
12	44 YY 24	<i>P. cerasifera</i>	49	44 YY 18	<i>P. domestica</i>
13	23 AR 01	<i>P. cerasifera</i>	50	44 YY 07	<i>P. domestica</i>
14	23 KK 17	<i>P. cerasifera</i>	51	23 KK 03	<i>P. domestica</i>
15	23 SV 10	<i>P. cerasifera</i>	52	44 YY 17	<i>P. domestica</i>
16	23 KK 05	<i>P. cerasifera</i>	53	44 AK 08	<i>P. domestica</i>
17	44 PT 06	<i>P. cerasifera</i>	54	44 PT 13	<i>P. domestica</i>
18	44 HK 04	<i>P. cerasifera</i>	55	44 DŞ 10	<i>P. domestica</i>
19	44 AK 04	<i>P. cerasifera</i>	56	44 PT 10	<i>P. domestica</i>
20	44 YY 19	<i>P. cerasifera</i>	57	23 KK 07	<i>P. munsoniana</i>
21	44 PT 04	<i>P. cerasifera</i>	58	23 KK 09	<i>P. munsoniana</i>
22	44 HK 07	<i>P. cerasifera</i>	59	23 AR 11	<i>P. spinosa</i>
23	44 DŞ 15	<i>P. cerasifera</i>	60	23 AK 01	<i>P. spinosa</i>
24	44 HK 02	<i>P. cerasifera</i>	61	23 AR 08	<i>P. spinosa</i>
25	44 YY 09	<i>P. cerasifera</i>	62	23 AR 06	<i>P. spinosa</i>
26	44 PT 03	<i>P. cerasifera</i>	63	23 KK 16	<i>P. spinosa</i>
27	44 DR 05	<i>P. cerasifera</i>	64	23 AR 09	<i>P. spinosa</i>
28	44 AK 03	<i>P. cerasifera</i>	65	23 KV 03	<i>P. spinosa</i>
29	44 DŞ 16	<i>P. cerasifera</i>	66	23 AR 13	<i>P. spinosa</i>
30	44 HK 15	<i>P. cerasifera</i>	67	23 KV 04	<i>P. spinosa</i>
31	44 DŞ 11	<i>P. cerasifera</i>	68	23 AR 03	<i>P. spinosa</i>
32	44 YY 04	<i>P. cerasifera</i>	69	23 AR 05	<i>P. spinosa</i>
33	Myrobolan 29C	<i>P. cerasifera</i>	70	23 AR 02	<i>P. spinosa</i>
34	23 BA 01	<i>P. cerasifera</i>	71	23 AR 15	<i>P. spinosa</i>
35	44 YY 08	<i>P. cerasifera</i>	72	23 SV 12	<i>P. spinosa</i>
36	44 DŞ 03	<i>P. divaricata</i>	73	23 PA 02	<i>P. spinosa</i>
37	44 AK 14	<i>P. divaricata</i>	74	23 AR 04	<i>P. spinosa</i>

Method

Within the scope of the project, survey studies were conducted in the provinces of Malatya and Elazığ at different time intervals. During these surveys, approximately 3,000 wild plum individuals belonging to various species were observed in their natural habitats. The surveys were carried out between July and October during the 2020–2021 period, covering an overall duration of about four months. Following species identification of the observed trees, observation forms were completed for the promising genotypes.

In the first year of the project, preliminary consultations were held with District Agricultural Directorates in Malatya and Elazığ, where wild plum populations are particularly widespread. Through these consultations, survey areas were identified, baseline data were collected, and necessary planning was completed. Additional information was also obtained from local inhabitants, which allowed for on-site adjustments to the survey schedules. Based on these plans, surveys were conducted twice annually, in May and September, throughout 2020 and 2021.

During the field surveys, wild plum genotypes with potential suitability as apricot rootstocks were identified, and their geographical coordinates were

recorded using GPS (Global Positioning System). Morphological traits such as tree vigor, growth habit, suckering tendency, branch angle, and branching pattern were systematically assessed and documented in selection forms. Based on these preliminary evaluations, approximately 159 wild plum genotypes representing different species were selected. Scions collected from the selected genotypes were grafted onto the Myrobalan 29C clonal rootstock under controlled conditions at the Institute.

The grafted plants were grown in nursery conditions, and after one year, the resulting rootstocks were transplanted into experimental plots at a spacing of 1.5×1 m for subsequent evaluations. Between 2023 and 2024, growth and development of the 2–3 year-old plants were monitored. Particular emphasis was placed on shoot growth parameters, and data regarding vigor and development potential were systematically recorded.

Evaluations of data

The obtained data were evaluated using a weighted ranking method (Table 2). Based on this assessment, the candidates were ranked in descending order according to their total scores. In the evaluation process, growth vigor was considered the primary criterion.

Table 2. Weighted evaluation table used to assess the growth vigor of promising dwarf and semi-dwarf rootstock candidates.

Criteria	Relatives	Classification	Points
Internode length	20	Short	7
		Medium	5
		Long	3
Shoot length	20	Short	7
		Medium	5
		Long	3
Shoot diameter	15	Thin	7
		Medium	5
		Thick	3
First branch height	15	Shorter	9
		Short	7
		Moderate	5
		High	3
		Higher	1
Branch angle	20	Narrow	3
		Medium	5
		Wide	7
Number of lateral branches	10	Low	3
		Moderate	5
		High	7

3. RESULTS

The evaluation of internode length, also referred to as the distance between successive nodes, provided

valuable insights into plant elongation and canopy architecture. In this study, internode length varied considerably, ranging from 9.69 cm in 23 AĞ 04 to the minimum value observed in 44 YY 05. As internode elongation directly influences shoot growth, the

observed results confirmed a close association between these two parameters. Indeed, the longest shoot was recorded in 23 KK 06, while the shortest was measured in 44 YY 07. These findings are in line with previous studies that identified internode length as a determinant of plant vigor and growth habit in *Prunus* spp. (Westwood, 1993; Hartmann & Kester, 2011; Tworkoski & Fazio, 2016). Shoot diameter, considered an integrative trait reflecting elongation and vegetative robustness, also exhibited wide variability. The highest value was measured in 44 AK 13 (6.13 mm), whereas the lowest was observed in 23 KV 03 (2.54 mm). Such variation highlights genotypic differences in growth vigor and is consistent with Webster (2004) and Basak (2011), who emphasized shoot thickness as a reliable indicator of plant strength. Similar findings in peach and apricot rootstock studies further support the relevance of shoot diameter as an indicator of graft compatibility and orchard performance. The height of the first branching point, ranging from 38 cm in 23 KK 17 to 6 cm in 44 YY 18, provided additional insights into canopy development and management suitability. Higher branching positions generally promote an open crown architecture, which facilitates mechanization and enhances light distribution, while lower branching contributes to denser tree forms. Similar observations have been documented in apple and peach rootstocks, where higher branching correlated with improved orchard efficiency (Loreti & Massai, 2002). Branch angle, a critical morphological parameter influencing canopy structure, varied from 89° in 44 HK 11 to narrower angles in 44 YY 24. Wide branch angles are associated with spreading growth forms, greater light interception, and increased fruit bud initiation (Costes

& García-Villanueva, 2007). Narrower angles, on the other hand, may result in upright growth and excessive vegetative vigor, which is often undesirable in intensive orchard systems. The number of lateral branches, reflecting canopy density and yield potential, ranged from high values in 23 KK 17 to minimal branching in 23 KV 03. Such diversity underscores the genetic variation within the evaluated material and its potential to meet different orchard design requirements. While increased branching may enhance yield potential, it also implies greater pruning needs, thus requiring a balance between productivity and management efficiency. The weighted scoring system produced values ranging from 360 to 690, with 23 AR 11 achieving the highest score. Importantly, 54 genotypes scored above 600, while 16 genotypes exceeded 500, highlighting the strong overall performance of many candidates. Considering both field observations and scoring results, a total of 64 genotypes were selected as promising rootstock candidates. Notably, nearly 50 of these demonstrated dwarf or semi-dwarf growth, a highly desirable feature for high-density orchard systems. These findings are consistent with international breeding programs, where dwarfing rootstocks are preferred for maximizing yield efficiency in limited space (Tworkoski & Fazio, 2016). Taken together, these results confirm that morphological traits such as internode length, shoot diameter, branching point, branch angle, and lateral branching are decisive in determining rootstock suitability. The consistency of these findings with the literature reinforces the potential of wild plum genotypes as valuable resources for rootstock improvement.

Table 3 (a). List of wild plum (*Prunus* spp.) genotypes evaluated in the selection process.

No	Genotype	Internode Length (cm)	Shoot Length (cm)	Shoot Diameter (mm)	First Branch Height (cm)	Branch Angle (°)	Number of Lateral Branches	Weighted Score
1	23 AR 11	6,48	33,00	3,76	6,00	75,00	25,00	690,00
2	23 AK 01	5,45	29,00	2,68	8,00	78,00	9,00	690,00
3	23 AR 08	4,78	38,00	4,17	12,00	79,00	12,00	690,00
4	23 AG 04	9,69	39,00	4,29	11,00	73,00	19,00	690,00
5	23 AR 06	9,31	41,00	3,30	17,00	82,00	12,00	690,00
6	23 KK 06	5,43	45,00	4,07	8,00	72,00	12,00	690,00
7	23 KK 03	5,84	32,00	3,24	12,00	78,00	11,00	690,00
8	44 DR 08	3,30	32,00	3,98	11,00	79,00	9,00	690,00
9	44 AK 10	4,46	22,00	3,30	14,00	84,00	9,00	690,00

10	23 KK 07	3,43	22,00	4,19	15,00	78,00	8,00	690,00
11	44 DŞ 12	5,75	34,00	3,46	28,00	75,00	17,00	680,00
12	23 MR 02	4,25	28,50	3,82	21,00	73,00	13,00	680,00
13	44 AK 13	9,52	46,00	6,13	11,00	79,00	15,00	680,00
14	23 KK 16	6,52	33,00	4,03	28,00	74,50	15,00	680,00
15	44 YY 11	10,27	36,00	3,65	11,00	69,00	14,00	670,00
16	23 AĞ 03	5,56	19,00	3,47	12,00	67,00	16,00	670,00
17	23 AR 09	5,88	45,00	4,12	15,00	62,00	18,00	670,00
18	44 KL 01	5,46	39,00	3,18	21,00	72,00	19,00	660,00
19	44 DŞ 05	4,81	33,00	3,77	25,00	84,00	12,00	660,00
20	44 DŞ 03	4,85	41,00	4,13	18,00	84,00	12,00	660,00
21	44 HK 11	5,15	24,00	3,22	22,00	89,00	9,00	660,00
22	44 AK 14	5,19	24,00	4,57	18,00	79,00	8,00	660,00
23	23 KV 03	3,34	24,00	2,54	22,00	81,00	7,00	660,00
24	44 HK 17	5,93	32,00	4,01	19,00	78,00	11,00	660,00
25	44 YY 05	3,24	19,00	2,76	16,00	65,00	12,00	650,00
26	44 YY 24	6,55	35,00	4,08	12,00	56,00	8,00	650,00
27	44 YY 18	6,68	27,00	3,74	6,00	58,00	9,00	650,00
28	23 AR 01	6,34	32,00	3,47	35,00	72,00	13,00	650,00
29	44 YY 07	11,38	19,00	4,01	12,00	57,00	10,00	650,00
30	23 AR 13	5,25	26,00	3,43	9,00	67,00	8,00	650,00
31	23 KV 04	6,44	48,00	4,37	17,00	67,00	9,00	650,00
32	23 AR 03	5,62	26,00	2,96	16,00	57,00	8,00	650,00
33	44 AK 17	6,04	22,00	3,19	17,00	54,00	9,00	650,00
34	23 KK 16	6,26	23,00	3,41	28,00	58,00	15,00	640,00
35	23 KK 17	10,15	36,00	4,04	38,00	75,00	20,00	630,00

Table 3 (b). List of wild plum (*Prunus* spp.) genotypes evaluated in the selection process.

No	Genotype	Internod Length (cm)	Shoot Length (cm)	Shoot Diameter (mm)	First Branch Height (cm)	Branch Angle (°)	Number of Lateral Branches	Weighted Score
36	23 KK 03	7,68	34,00	4,04	38,00	76,00	19,00	630,00
37	23 SV 10	5,75	32,00	3,79	38,00	72,00	12,00	630,00
38	44 YY 21	7,67	32,00	3,44	29,00	77,00	12,00	630,00
38	44 YY 20	10,57	28,00	4,77	18,00	78,00	9,00	630,00
39	23 AĞ 01	4,77	25,00	3,39	24,00	62,00	8,00	620,00
40	23 AĞ 02	4,19	28,00	4,11	25,00	59,00	8,00	620,00
41	23 KK 05	7,13	33,00	2,27	22,00	62,00	12,00	620,00
42	23 KK 13	5,73	36,00	3,91	48,00	82,00	13,00	620,00
43	44 YY 17	7,58	36,00	4,24	28,00	56,00	19,00	620,00

44	23 AR 05	6,51	23,00	3,22	22,00	62,00	11,00	620,00
45	44 PT 06	9,31	38,00	4,17	24,00	56,00	9,00	620,00
46	23 AR 02	4,30	16,00	2,90	22,00	68,00	9,00	620,00
47	44 AK 08	5,62	21,00	3,18	22,00	56,00	6,00	620,00
48	44 HK 04	7,98	41,00	4,32	27,00	55,00	11,00	620,00
49	44 AK 04	16,67	36,00	4,29	14,00	62,00	12,00	610,00
50	44 YY 19	7,57	37,00	4,07	16,00	44,00	8,00	610,00
51	23 KK 09	3,20	17,00	2,82	12,00	47,00	9,00	610,00
52	44 PT 04	6,51	41,00	3,48	9,00	49,00	9,00	610,00
53	44 HK 07	6,70	36,00	3,35	42,00	81,00	8,00	600,00
54	44 DŞ 15	7,88	43,00	3,82	34,00	55,00	8,00	590,00
55	44 HK 02	6,43	36,00	3,33	30,00	65,00	11,00	590,00
56	44 YY 09	3,63	17,00	2,57	32,00	67,00	12,00	590,00
57	44 PT 03	4,51	39,00	2,95	29,00	66,00	9,00	590,00
58	44 DR 05	4,77	28,00	3,21	27,00	47,00	10,00	580,00
59	44 AK 03	8,20	44,00	4,27	24,00	52,00	22,00	580,00
60	23 AR 15	6,50	18,00	3,56	28,00	47,00	8,00	580,00
61	44 PT 13	8,25	37,00	4,21	32,00	44,00	8,00	550,00
62	44 DŞ 16	4,98	22,00	4,19	32,00	49,00	11,00	550,00
63	44 HK 15	6,87	25,00	3,35	32,00	53,00	7,00	550,00
64	44 DŞ 11	7,94	87,00	5,56	44,00	81,00	8,00	530,00
65	44 YY 04	13,37	71,00	5,18	32,00	68,00	12,00	520,00
66	23 SV 12	11,32	72,00	7,12	34,00	56,00	12,00	520,00
67	44 DŞ 10	9,78	46,00	4,44	40,01	47,00	8,00	520,00
68	Myr. 29C	12,61	69,00	5,29	44,00	61,00	14,00	510,00
69	23 PA 02	19,49	101,00	7,39	32,00	56,00	16,00	470,00
70	44 PT 10	13,33	48,00	6,33	62,00	35,00	8,00	460,00
71	23 BA 01	16,81	92,00	9,67	38,00	57,00	12,00	450,00
72	23 AR 04	14,57	74,00	7,16	32,00	43,00	9,00	440,00
73	44 YY 08	34,07	174,00	8,04	45,00	67,00	15,00	360,00
Minimum		3,20	16,00	2,27	6,00	35,00	6,00	360,00
Maximum		34,07	174,00	9,67	62,00	89,00	25,00	690,00
Mean		7,64	38,34	4,08	23,97	65,55	11,58	617,03

4. CONCLUSION

As a result of this research, wild plum (*Prunus* spp.) genotypes exhibiting different vigor levels and potentially suitable for use as rootstocks for major stone fruit species (particularly apricot, as well as plum, peach, and almond) were identified in the Malatya and Elazığ regions. The study was conducted within the framework of the fundamental principles of selection breeding, through which a systematic and carefully designed program was implemented. Based on the findings, a total of 64 genotypes were advanced to the Selection-II stage as rootstock candidates. Turkey possesses a remarkably wide genetic variation in wild plum species and their natural populations, representing an invaluable genetic reservoir for fruit production. This genetic diversity provides significant potential for the development of novel rootstocks that are capable of adapting to diverse ecological conditions, exhibiting resistance or tolerance to biotic factors (such as diseases and pests) and abiotic stresses (including drought, salinity, and low temperature), displaying dwarf or semi-dwarf growth habits, and being propagated clonally. Following the detailed characterization of the morphological, phenological, and physiological traits of these rootstock candidates, it is anticipated that such genotypes may also serve as parental material in future hybridization studies, thereby contributing to the advancement of rootstock breeding programs based on local germplasm. Developing alternatives to the widely used imported rootstocks through the utilization of indigenous genetic resources holds strategic importance for Turkish fruit cultivation. Such efforts would not only aid in the conservation of biodiversity but also reduce production costs. Furthermore, the development of rootstocks suited to modern high-density cultivation systems would enable higher productivity per unit area, representing a critical step toward the sustainability of fruit production in Turkey. In conclusion, the support and expansion of local rootstock breeding initiatives are of great importance, not only for reducing dependence on imported plant material but also for enhancing the competitiveness of Turkish fruit production in global markets.

RECOMMENDATIONS

Beyond scientific evaluation, practical and policy-oriented steps are necessary to maximize the value of these findings:

-Conservation of Local Germplasm – Establishing dedicated gene banks and in situ conservation sites to safeguard wild *Prunus* diversity.

-Integration into National Breeding Programs – Incorporating promising genotypes into ongoing breeding strategies to reduce dependency on imported rootstocks.

-Collaboration with Growers – Conducting participatory trials with farmers to assess the field performance, management needs, and economic feasibility of selected rootstocks.

-Investment in Research and Development – Supporting interdisciplinary research projects that combine classical breeding with modern biotechnological approaches.

-Policy Support and Incentives – Developing national strategies and providing financial incentives for the adoption of locally developed rootstocks in commercial orchards.

By integrating these scientific and practical approaches, the potential of wild plum genotypes can be fully harnessed, contributing to both the sustainability and the global competitiveness of Turkish fruit production.

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