Assessment of Fruit and Some Biochemical Characteristics of Almond Genotypes Selected From Natural Populations of Kayseri Province

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Abstract

Almond (*Prunus amygdalus* L.) can grow under dry climate and harsh soil conditions. The fruits are drupe. Seed-propagated almond populations exist in various parts of Turkey. Several studies have been performed to select the promising genotypes among these populations with regard to fruit quality, yield, late foliations and etc. characteristics. Rich almond populations are shown around the foothills of Erciyes Mountain in Kayseri province of Central Anatolia. In this study, some fruit and biochemical characteristics of 34 almond genotypes selected as promising genotypes with regard to late foliation and yield were determined. Significant variations ($P < 0.05$) were observed in investigated traits of the genotypes. Of selected genotypes, fruit weights varied between 1.5±0.4- 7.6±0.5 g, fruit lengths between 40.7±0.7 - 19.9±2.9 mm, fruit heights between 17.4±0.8 – 10.3±2.1 mm and fruit widths between 27.6±0.7 – 11.8±0.7 mm. With regard to fruit shape of genotypes, 13 were identified as long oval, 12 as elliptical, 5 hearth-shaped and 4 as round. Considering the biochemical characteristics, crude oil contents varied between 54.9 - 42.1% and protein contents varied between 24.6 – 17.7%.

1. INTRODUCTION

Almond culture was said to be initiated four thousand years ago in Iran, Turkey, Syria and Palestine regions and spread throughout the world from these regions [1]. Almond is native to Western and Central Asia [2]. It is quite resistant to droughts and can grow in poor soils and under various ecological conditions ([3], [4], [5]). As compared to native countries, productions have grown quite more rapidly in the USA and Spain ([4], [5]). The reasons for such slow growths in productions of native countries may be related to early-blooming of almond species and thus much more prone nature to spring late freezes, large portions of production sites are composed of wild populations, yields are not consistent and socio-economic states of the countries may influence the productions ([6], [5]).

The world almond production is around 1.9 million tons and the USA, Spain and Australia are the leading producers. With 85% increase during the last decade, Turkish almond production reached to 75 thousand tons [7]. Although almond is cultured in several regions of Turkey, Mersin (9400 tons), Antalya (5700 tons), Muğla (5700 tons), Çanakkale (5300 tons) and Denizli (4600 tons) are the prominent provinces [8].

Selection breeding is the oldest breeding method and breeder selects proper plants from natural populations without creating a genetic variation and using the natural variation (Gulsoy and Balta, 2014). There are rich almond genetic resources in various parts of Anatolia. Seed-propagated trees with different genetic characteristics play a significant role in this richness. There is a need to assess the current gene sources and to get promising genotypes with regard to fruit quality attributes and yields. Almond species are quite prone to late spring freezes and thus identification of late-blooming genotypes will only be possible with selections to be made from these large populations. Since the almond is the first blooming tree in spring, culture is quite restricted in regions with late-spring freeze risks. Therefore, development of late-blooming cultivars has become the primary target of almond breeding programs ([6], [9]). The cultivars of Avalon, Solana, Sonora, Price Texas, Ne Plus Ultra, Peerles, Rosetta and Thomson used in leading almond producer country, the USA, were obtained through selections as chance seedlings ([10], [1]). The almond trees in current local populations are lost either with natural means or with anthropogenic reasons. Therefore, these populations should urgently be searched through for promising genotypes. In this way, it will be possible to identify chance seedlings with desired fruit and tree characteristics among the genetic resources spread over regions with different climates and ecological conditions [1].

Seed-propagated almond trees are quite common over the rough terrains around the northern foothills of Erciyes Mountain of Kayseri Province. In this study, naturally-growing almond populations of the region were investigated and fruit quality attributes, protein and crude oil contents of promising genotypes were identified.

2. MATERIAL AND METHODS

Almond tree populations located around Alidaği mountain, north of Erciyes mountain and south of Kayseri city center, (Haymana Bağları, Hisarcık Valley, Talas Tablakaya, Beğendik Bagları, Sakar Çiftliği, mountainous districts around Kayseri Organized Industrial Region and Yılanlıdağ regions) were used as the plant material of the present study. A total of 480 almond trees were evaluated and 34 of them were selected with regard to blooming, yield and fruit characteristics. Yield levels were assessed through a scale (1: low yield; 2: medium yield; 3: high yield). Fruit weight, fruit length, fruit width, fruit height, kernel taste, double kernel and fruit shape of selected genotypes were analyzed. Among the biochemical characteristics, crude oil and protein contents were determined in accordance with reference [11]. For investigated fruit characters, data were analyzed using JMP trial version (SAS Institute Inc.) and means were separated and grouped using Tukey's test ($P < 0.05$). Differences among selected genotypes were put forth and ultimately superior ones were identified.

3. RESULTS AND DISCUSSION

Variations were observed among genotypes with regard to investigated traits. Of the selected almond genotypes, 19 were identified as high yield, 11 as medium yield and 4 as low yield. Fruit weights varied between 1.5 – 7.6 g and significant variations were observed in fruit weights of the genotypes. Genotype 34 (7.6±0.5 g) and genotype 33 (6.9 ±0.5 g) had the highest fruit weights (Figure 1). Reference [12] in a study carried out in Kahramanmaras province, reported fruit weights of selected genotypes as between 1.31 - 7.58 g. Reference [13] in a study carried out in Isparta province, reported fruit weights of promising genotypes as between 3.51 - 5.43 g. Reference [14] in a selection study carried out in Mardin-Derik, reported fruit weights of investigated genotypes as between 1.75 - 4.77 g. Reference [15] in a selection work carried out in Aydın province, reported almond fruit weights as between 2.44 - 7.57 g. Current findings on fruit weights were generally complying with those earlier findings.

Significant differences ($P < 0.05$) were also observed in fruit dimensions of the genotypes. Fruit lengths varied between 40.7 - 19.9 mm, fruit heights between 17.4 – 10.3 mm and fruit widths between 27.6 – 11.8 mm (Table 1). In an earlier study, fruit lengths of almond genotypes were reported as between 24.00-42.88 mm, fruit heights between 16.56-29.50 mm and fruit widths between 10.60-19.18 mm [1]. On the other hand, reference [14] reported these attributes respectively as between 27.81-35.69 mm, 17.11-24.90 and 11.84-16.77 mm. Reference [15] reported fruit lengths as between 29.06-39.15.

Figure 1. Fruit and kernel images of the genotypes 34 (above) and 33 (below) with the greatest fruit weights

With regard to fruit shape of the genotypes, 13 were identified as long oval, 12 were elliptical, 5 were hearth-shaped and 4 were round shaped. With regard to kernel color, 4 had light, 8 medium and 22 had dark color kernels. On the other hand in a previous study, kernel color was mostly reported as medium. In that study, 12 genotypes had very light, 55 light, 62 medium and 28 genotypes had dark color kernels [1]. Again, reference [14] indicated kernel color of 13 selected almond genotypes as medium. Considering the taste of kernels, 9 had bitter taste and 25 had sweet taste. Reference [11] found 114 of 120 genotypes as sweet taste. On the other hand, reference [1] in a study carried out in Tunceli province, indicated taste of 82 genotypes as sweet, 8 genotypes as medium and 67 genotypes as bitter. Double kernel was not seen in almond genotypes of the present study. Although double kernel ratios vary with cultivars, it is not desired since it reduces commercial value [15].

Significant differences were observed in chemical composition of selected genotypes. Crude oil contents varied between 42.1 (Genotype 14) – 54.9% (Genotype 31) and protein contents varied between 17.7 (Genotype 3) – 24.6% (Genotype 19). The crude oil and protein of almond are quite significant for human health. In a previous study, it was noticed that edible seeds and nuts had high contents of lipids, proteins, dietary fiber and ash (minerals) and they had a good essential amino acids profile, usually with a slight lysine deficiency [16]. The genotypes with high crude oil and protein contents identified in these studies may constitute a significant source for human nutrition. Current findings on crude oil and protein contents were generally complying with the findings of previous studies on almonds. Reference [17] reported average protein content of almonds as 19% and crude oil content as 54%; reference [18]) in a study carried out in Spain, reported average crude oil content as 66.40% and protein content as 15.80%.

Table 1. Some fruit and biochemical characteristics of almond genotypes studied

G. No	F.W. (g)			F.L. (mm)			F.H. (mm)			F.W. (mm)			F.S.	Seed color	O.C. (%)	P.L. (%)
1	3,4	± 0,5	l-n	37,5	± 1,9	bc	12,6	± 0,9	m-o	18,4	± 0,6	kl	LO	Dark	47,8	18,3
2	2,3	± 0,5	op	25,7	± 1,5	p	10,7	± 0,7	p	18,4	± 1,4	kl	E	Dark	50,0	19,3
3	3,5	± 0,3	l-n	29,6	± 0,5	l-o	12,8	± 0,6	l-o	20,4	± 0,8	f-j	LO	Dark	47,1	17,7
4	4,9	± 0,3	f-ı	32,8	± 0,5	e-k	14,5	± 0,7	f-l	22,3	± 0,4	b-d	LO	Dark	52,4	18,9
5	3,7	± 0,6	j-n	31,5	± 2,0	h-l	13,7	± 0,9	ı-m	20,9	± 1,0	d-ı	E	Medium	52,0	19,0
6	3,0	± 0,1	no	31,9	± 0,2	g-l	11,6	± 0,4	n-p	17,8	± 0,2	l	H	Dark	50,0	19,3
7	3,3	± 0,2	mn	26,9	± 1,7	op	14,9	± 0,4	d-k	18,8	± 0,4	j-l	E	Medium	47,8	19,6
8	1,9	± 0,4	p	26,0	± 0,8	p	11,1	± 1,2	op	15,1	± 0,4	m	LO	Dark	49,4	18,1
9	3,2	± 0,5	mn	27,9	± 1,9	n-p	13,5	± 1,2	j-m	19,2	± 1,5	ı-l	LO	Dark	47,3	18,9
10	3,9	± 0,8	j-m	32,3	± 1,7	f-l	14,1	± 0,9	h-m	19,9	± 1,2	g-k	E	Light	47,4	18,4
11	3,3	± 0,3	l-n	30,9	± 0,8	ı-m	14,0	± 0,7	ı-m	21,5	± 1,0	c-g	LO	Dark	47,3	18,5
12	4,4	± 0,2	h-j	35,2	± 1,0	c-f	13,8	± 0,4	ı-m	22,2	± 0,6	b-f	E	Light	52,5	18,3
13	4,5	± 0,8	g-j	33,6	± 3,4	d-ı	17,4	± 0,8	a	21,4	± 4,0	c-h	E	Dark	48,1	19,9
14	3,6	± 0,3	j-n	30,1	± 0,4	k-n	12,8	± 0,7	l-o	20,4	± 0,7	e-j	LO	Dark	45,6	19,1
15	4,2	± 0,2	ı-l	30,5	± 1,2	j-n	16,9	± 0,4	a-c	23,4	± 0,4	b	H	Dark	46,6	19,1
16	2,0	± 0,4	p	26,1	± 0,7	p	11,1	± 1,9	op	15,4	± 0,5	m	LO	Dark	49,6	18,2
17	5,2	± 0,6	e-h	33,1	± 1,2	e-j	14,7	± 1,0	m-o	22,3	± 0,5	b-e	E	Dark	51,0	18,0
18	4,4	± 0,5	h-k	35,2	± 1,9	c-e	15,2	± 0,8	d-j	20,8	± 0,7	d-ı	LO	Dark	53,5	18,3
19	3,1	± 0,4	m-o	28,4	± 1,4	m-p	13,2	± 1,1	k-n	19,6	± 0,6	h-l	R	Dark	47,3	24,6
20	3,1	± 0,3	m-o	28,4	± 2,8	m-p	14,5	± 1,6	g-l	19,3	± 0,7	ı-l	LO	Medium	42,1	18,3
21	3,6	± 0,6	k-n	34,8	± 1,5	c-g	14,5	± 1,4	f-l	21,7	± 0,6	b-g	H	Medium	53,2	18,0
22	1,5	± 0,4	p	19,9	± 2,9	q	10,3	± 2,1	p	11,8	± 0,7	n	E	Dark	45,9	20,0
23	3,5	± 0,1	k-n	31,1	± 0,9	h-m	11,4	± 0,7	n-p	20,4	± 0,5	f-j	E	Medium	53,5	18,6
24	5,8	± 0,8	c-e	38,8	± 0,6	ab	15,4	± 0,8	b-ı	27,6	± 0,7	a	LO	Dark	52,8	19,3
25	3,7	± 0,6	j-n	31,1	± 1,5	h-m	14,6	± 1,1	e-k	21,2	± 1,0	c-h	E	Dark	49,7	18,0
26	6,8	± 0,4	b	40,7	± 0,7	a	15,9	± 1,0	a-g	27,1	± 0,6	a	LO	Dark	48,7	21,4
27	4,8	± 0,5	f-ı	33,9	± 3,2	d-h	15,2	± 1,9	c-j	21,4	± 1,1	c-h	H	Dark	46,9	21,6
28	5,6	± 0,2	d-f	34,6	± 0,7	c-g	16,5	± 0,6	a-d	23,0	± 0,3	bc	H	Light	52,0	21,3
29	5,3	± 0,7	e-g	30,9	± 1,7	ı-m	16,0	± 1,0	a-g	22,4	± 0,7	b-d	R	Medium	53,2	20,2
30	5,0	± 0,5	e-ı	30,0	± 2,3	k-n	15,8	± 0,9	a-h	22,6	± 0,7	b-d	R	Dark	47,7	21,2
31	6,3	± 0,8	b-d	37,2	± 2,2	bc	16,4	± 1,8	a-e	25,9	± 1,0	a	R	Light	54,9	20,2
32	6,5	± 0,4	bc	36,4	± 1,5	b-d	16,3	± 0,8	a-e	26,0	± 0,6	a	E	Medium	53,2	18,7
33	6,9	± 0,5	ab	38,4	± 1,9	ab	16,2	± 1,0	a-f	26,8	± 0,5	a	LO	Medium	50,6	19,8
34	7,6	± 0,5	a	37,1	± 1,3	bc	17,1	± 1,0	ab	27,4	± 0,5	a	E	Dark	48,1	18,5

G. No: Genotype No; FW: Fruit weight; FL: Fruit length; FH: Fruit height; FW: Fruit weight; FS: Fruit shape; LO: Long-oval; R: Round; E: Elliptic; OC: Oil content; PL: Protein level

Reference [19] reported crude oil contents of 21 almond cultivar and genotypes as between 36-5%. Reference [20] reported crude oil contents of 8 standard almond cultivars and 47 promising genotypes as between 48-67%. On the other hand, reference [21] reported crude oil contents of different almond genotypes as between 48.7–64.5% and protein contents as between 14.1-35.1%. Considering the statistical evaluation of

different fruit and biochemical characteristics together, it was observed that 7 out of 34 genotypes were prominent. These promising genotypes were identified as the genotypes 12, 13, 14, 17, 18, 26 and 28.

The genotypes identified in this study carried out in Kayseri province may be used in further breeding works and they may then be included among current standard varieties. These genotypes should be propagated through vegetative ways to assess the performance of these genotypes under different ecologies. Present outcomes may provide significant contribution in identification of quality genotypes among natural almond population of Turkey and prevention of extinction of genetic resources of the country.

ACKNOWLEDGEMENTS

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