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## Biodiversity in morpho-physiological characteristics of indigenous plum germplasm from Azad Jammu and Kashmir, Pakistan

Hajra NISAR<sup>1</sup>, Maqsood AHMED<sup>2</sup>, Sajjad HUSSAIN<sup>3</sup>, Muhammad Akbar ANJUM<sup>3</sup>

<sup>1</sup>University of Poonch  
Rawalakot, Azad Jammu and Kashmir, Pakistan

<sup>2</sup>Mirpur University of Science and Technology  
Mirpur, Azad Jammu and Kashmir, Pakistan

<sup>3</sup>Bahauddin Zakariya University  
Multan 60000, Pakistan  
E-mail: sajjad.hussain@bzu.edu.pk

### Abstract

Plum (*Prunus domestica* L.) and its wild relatives are found at different locations in Pakistan, existing in naturalized form, which have not been characterized yet. In the present work, genetic diversity in morpho-physiological characteristics of sixteen plum genotypes growing in the area of Rawalakot, district Poonch, Azad Jammu and Kashmir, Pakistan were studied. Various parameters like tree size, number of branches per plant, leaf area, number of flowers per plant, blooming period, number and percentage of fruits set per plant, number and percentage of fruits matured per plant, fruit size and fruit weight were taken into count and variation observed in these characteristics was discussed. The results suggested that the plum genotypes differed in their morpho-physiological traits, and this ultimately provides important information on how to make the best use of these plum genotypes in future breeding programmes. The differences were probably due to their genetic make-up as well as prevailing climatic factors in the region.

Key words: biodiversity, morphological characteristics, Pakistan, plum genotypes, principle component analysis, *Prunus* sp.

### Introduction

Plum (*Prunus domestica* L.) is a temperate zone fruit crop, which belongs to the genus *Prunus* of subfamily *Amygdaloideae* (syn. *Prunoideae*), family *Roseaceae* (Potter et al., 2007). Its basic chromosome number is 8. Plum originated from five centres; these include Western Asia for *Prunus insititia* (Damson plum), Europe for *Prunus domestica* (European plum), Western and Central Asia for *Prunus cerasifera* (cherry plum), North America for *Prunus americana* (American plum) and China for *Prunus salicina* (Japanese plum) (Watkins, 1976). Plum is grown all over temperate zones of the world and top ten plum producing countries are China, Serbia, USA, Romania, Turkey, Spain, Italy, Bosnia and Herzegovina, France and Ukraine. In Pakistan, plum is commercially grown on an area of about 6781 hectares and with a total annual production of 56223 tonnes (Aslam, Amin, 2013). Almost one-half of the plums production in the world is used fresh whereas the rest consumed as processed. The most important processed plum food stuffs are prunes, canned plums, prune juice, sauce, paste, prune bits and juice concentrates (Chang et al., 1994; Siddiq, 2006). The wild plum (*Prunus* spp.) having distinct fruits is also

found widely in some areas of the world and mostly used in the industry for drying, jam making and for its juice. Growing and utilization of particular local cultivars including wild plums as food and for medication has been a usual practice for centuries (Ahmed et al., 2009; Nisar et al., 2015). Commercial cultivars and wild species have been evaluated against distinctive local cultivars originating from the same vicinity (Rop et al., 2009).

The state of Azad Jammu and Kashmir, Pakistan is situated between the two foremost centres of origin: the Caucasus Mountains and China. The area is mountainous and possesses a distinctive environment with diverse climatic conditions ranging from temperate to subtropical. Several temperate fruit crops, e.g., pear, apple, peaches, apricot, plum, almond and walnut are grown in the area. A large amount of genetic diversity subsists in these fruit crops that accumulated through mutation, hybridization and naturally seed based proliferation (Ahmed et al., 2009; Paganova, 2009). Plum and their wild relatives are found in the area, existing in naturalized form, which have not been characterized yet. Further, no efforts have been made for enhancement and exploitation of indigenous

plum species for food and other uses. Therefore, systematic characterization of local plum germplasm for sustainable use is necessary. The proposed study was envisaged to characterize various genotypes of plum (cultivated and wild), existing in the area on the basis of their physiological and morphological traits and assess biodiversity among the diverse population. The study will contribute to the knowledge about the genus *Prunus* and will be helpful in broadening the plum gene pool, which can be utilized in future plant breeding programs for the improvement of existing plum cultivars.

## Materials and methods

The study on biodiversity in indigenous germplasm of plum (*Prunus domestica* L.) was conducted during the year 2011 to 2012. This study included a survey of Rawalakot region of district Poonch of Azad Jammu and Kashmir, northern Pakistan to select diverse plum genotypes and assess variability in their physiological and morphological characteristics.

*Ecological characteristics of the location.* The study area in Rawalakot is situated between an altitude of 1800–2100 m above sea level and latitude of 33–73 in the north-east of Pakistan. The area lies under the foothills of the great Himalayas in Rawalakot. The area is mainly hilly and mountainous with valleys and stretches of plains. The climate is moist subtropical to cold temperate with an average rainfall varying from 800 to 1600 mm. Some parts of this region are extremely rugged, precipitous and highly unstable (Nisar et al., 2015).

*A survey of the plum growing areas and selection of plum genotypes.* During the survey to get the first hand information local inhabitants were consulted about production, uses and present status of different plum genotypes grown in the region at various places. The location was selected with respect to the availability of diversity in plum genotypes. Regular visits were made during the period of flowering, fruit setting, fruit maturity and ripening stages during the year of 2011–2012. Finally, plants of sixteen plum genotypes with divergent characters were selected at fruit maturity stage. Codes were allotted to each genotype on the basis of their skin colour and/or fruit size, i.e. dark red (DR), small yellow (SY), reddish brown (RB) and large yellow (LY), and permanent tagging was done on the selected plants. Three bearing plants were selected for each plum genotype per study site for the elaborative investigation of morpho-physiological characteristics. All three plants of each plum genotype were the same in age, vigour and health. A short description of all plum genotypes/accessions was recorded in the form of passport data for tree growth habit and fruit and seed morphology with the help of *Prunus* descriptor developed by International Board of Plant Genetic Resources (Cobianchi, Watkins, 1984). Growth habit of the plum genotypes was noted as upright, semi-upright or spreading. Fruit morphology, fruit shape, fruit skin and flesh colour were recorded according to the RHS Colour Chart (2001). Seeds were examined for their colour, shape and weight.

*Characterization of plum genotypes.* The selected plum genotypes were characterized on the basis of the following morpho-physiological characteristics: tree height, number of branches per plant, leaf area, number of flowers per plant, blooming period, number and percentage of fruits set, number and percentage of fruits matured, fruit size (length and width) and fruit (flesh and stone) weight. Leaf area was estimated from fully developed leaves with the help of a leaf area meter AM 100 (Analytical Development Company Ltd., England). For the number of flowers per plant, three major limbs from the main trunk to remote branches at the central point of the canopy were selected at random. The number of flowers for each limb was counted at full blooming as described by Durgac et al. (2006), and the total number of flowers per tree was estimated by multiplying with the total number of limbs. Blooming period was counted from initiation of flower opening to wilting of most of the flowers on a tree. The percentage of fruit matured was estimated by the following formula: (number of fruit matured/number of fruit set) × 100.

*Statistical analysis.* The data on quantitative morpho-physiological characteristics were subjected to basic statistics (Gomez, Gomez, 1984). Cluster analysis based on Ward's method using squared Euclidian distance was performed using the statistical software package SPSS, version 12.0. Principal component analysis (PCA) was performed using statistical software programme STATISTICA, version 5.0. PCA was used to identify the components causing maximum genetic variation (Khodadadi et al., 2011; Aremu, Ibirinde, 2012; Siahbidi et al., 2013). For grouping of plum genotypes a variety of procedures were used (Bauer et al., 2007), including unweighted paired group method using arithmetic average (UPGMA) (Ahmed et al., 2009; Aremu, Ibirinde, 2012) and squared Euclidean distance and Ward's method (Khodadadi et al., 2011; Siahbidi et al., 2013).

## Results and discussion

*Passport data.* A short description of tree growth habit, fruit shape, fruit skin and flesh colour, seed colour and shape was developed in the form of passport data (Table 1).

*Tree growth habit.* Tree growth habit was recorded on the basis of visual inspection. Seven plum genotypes (43.75%) had upright growth habit, while three (18.75%) had extremely upright, three had semi-upright, and other three had spreading growth habit (Table 2). For characterization of plum genotypes, growth habit of plants is a very important feature. Climatic conditions, soil and locality influence the growth habit of tree. Tree shape, size, number and arrangement of leaves and branches depend upon light penetration into the tree canopy (Ahmed et al., 2013; 2014). In the present study, the trees of most of the plum genotypes were upright and only three accessions had spreading growth habit.

*Fruit shape, skin and flesh colour.* Among the sixteen plum genotypes, nine genotypes (56.25%) had round fruits and remaining seven (43.75%) had oval shaped fruits (Table 2).

**Table 1.** Passport data of sixteen selected genotypes of plum

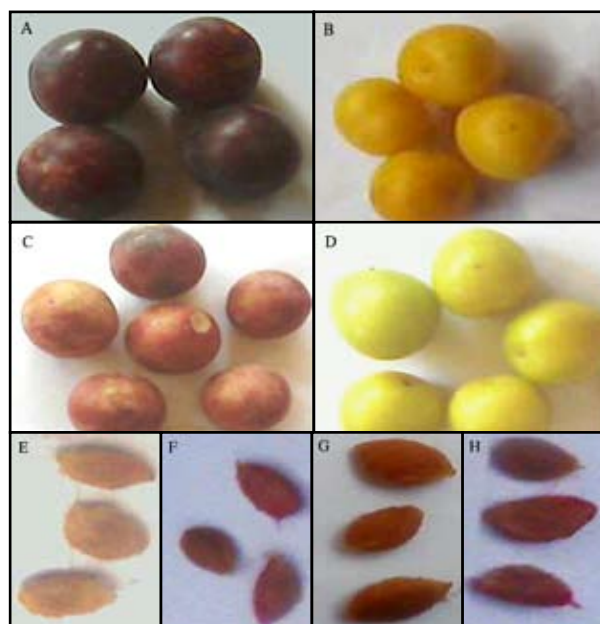
Genotype	Local name	Growth habit	Fruit shape	Fruit skin colour	Flesh colour	Seed colour	Seed shape
DR1*	Alu bukhara	upright	round	dark red	yellow	white	oval
DR2	Alu bukhara	extremely upright	oval	dark red	yellow	light brown	oval
DR3	Alu bukhara	extremely upright	oval	dark red	yellow	dark brown	elliptical
DR4	Alu bukhara	upright	oval	dark red	dark yellow	brown	round
SY1	Aluchi	upright	round	yellow	dark yellow	off white	elliptical
SY2	Aluchi	semi-upright	round	yellow	yellow	off white	round
SY3	Aluchi	spreading	round	yellow	yellow	brown	round
SY4	Aluchi	upright	oval	yellow	light yellow	brown	elliptical
RB1	Alucha	spreading	round	reddish brown	red	brown	elliptical
RB2	Alucha	semi-upright	round	reddish brown	red	dark brown	oval
RB3	Alucha	upright	round	reddish brown	red	dark brown	round
RB4	Alucha	spreading	round	reddish brown	yellow	off white	oval
LY1	Alu bukhara	extremely upright	oval	yellow	yellow	dark brown	oval
LY2	Alu bukhara	upright	oval	yellow	light yellow	brown	elliptical
LY3	Alu bukhara	upright	round	yellow	light yellow	off white	round
LY4	Alu bukhara	semi-upright	oval	yellow	yellow	dark brown	oval

Note. \* – plum genotypes were denoted on the basis of skin colour and/or fruit size, i.e. DR – dark red, SY – small yellow, RB – reddish brown and LY – large yellow.

**Table 2.** Summary for frequency of qualitative traits (passport data) of plum germplasm

Trait	Category	No. of accessions	Percentage
Tree growth	extremely upright	3	18.75
	upright	7	43.75
	semi-upright	3	18.75
	spreading	3	18.75
Fruit shape	round	9	56.25
	oval	7	43.75
Fruit skin colour	dark red	4	25.00
	yellow	8	50.00
	reddish brown	4	25.00
Flesh colour	yellow	8	50.00
	dark yellow	2	12.50
	light yellow	3	18.75
	red	3	18.75
Seed colour	white	1	6.25
	light brown	1	6.25
	brown	5	31.25
	dark brown	5	31.25
	off white	4	25.00
Seed shape	oval	6	37.50
	elliptical	5	31.25
	round	5	31.25

On the basis of skin colour, the plum genotypes were divided into three groups – dark red, yellow and reddish brown. Observations illustrated that four plum genotypes (25%) had dark red, other four (25%) had reddish brown and remaining eight (50%) had yellow coloured fruits (Table 2, Fig. 1). Peel colour is one of the most important qualitative parameters for determining quality as it increases the aesthetic value of fruits to the consumers. However, peel colour depends upon plant location, temperature of location, tree growth habit, microclimate of the tree canopy and light distribution (Erez, Flore, 1986) and is significantly affected by the prevailing environmental conditions of the growing area.



**Figure 1.** Variability in fruit and seed characteristics of plum genotypes: fruits – A = DR1, B = SY4, C = RB3, D = LY4 and seeds – E = DR2, F = RB1, G = LY1, H = DR4

Vursavus et al. (2006) also recorded significant difference in fruit colour of three sweet cherry varieties and reported that the variation was due to varietal characters as well as due to environmental and growth conditions. Observations on flesh colour indicated that only three plum genotypes (18.75%) had red coloured pulp, eight (50%) had yellow, two (12.50%) had dark yellow and remaining three (18.75%) had light yellow coloured flesh (Table 2). Flesh colour is a genetic character; however, it may vary depending upon the fruit maturity stage and is strongly influenced by prevailing environmental conditions at the time of maturity.

**Seed colour and shape.** Eleven plum genotypes (68.75%) had light brown to dark brown colour, while

four (25.00%) had off-white and only one (6.25%) had white coloured seed (Table 2). Data related to seed shape exhibited that the plum genotypes had three shaped seeds, i.e. oval, round and elliptical (Table 1). Six plum genotypes (37.50%) had oval shaped seed, five (31.25%) had round shaped and remaining five (31.25%) had elliptical seeds (Table 2). Seed colour and shape are also genetic characters. In the present study, the plum genotypes studied differed in their seed colour and shape, indicating genetic variability (Fig. 1).

**Morpho-physiological characteristics of plum genotypes. Tree height.** The mean values for tree height varied from 3.29 to 7.50 m among the plum genotypes.

The maximum height (7.50 m) was measured in trees of RB4 and the minimum (3.29 m) was recorded in DR1 (Table 3). Tree height depends upon growth habit and many other factors including nature of rootstock (if used), topography, soil texture, structure, fertility status, prevailing climatic conditions (temperature, sunlight, rainfall, etc.) and cultural practices (nutrient application, pruning, training, etc.) adopted. Ahmed et al. (2014) also reported that location, soil and climatic factors greatly influence the tree height.

**Number of branches per plant.** The plum genotypes studied differed in their number of branches per plant. The branch number varied from 3 to 10 among

**Table 3.** Mean values for morpho-physiological characteristics (vegetative and flowering) of plum genotypes

Genotype	Tree height m	No. of branches plant <sup>1</sup>	Leaf area cm <sup>2</sup>	No. of flowers plant <sup>1</sup>	Blooming period, days	No. of fruits set plant <sup>1</sup>	Fruit set %
DR1*	3.294 ± 0.017**	5.00 ± 0.75	12.96 ± 1.34	2700 ± 54	7.67 ± 0.97	621 ± 68	23.00 ± 0.66
DR2	4.596 ± 0.007	4.00 ± 1.20	10.66 ± 1.85	1500 ± 139	7.33 ± 1.10	270 ± 19	18.00 ± 1.24
DR3	5.197 ± 0.003	7.00 ± 0.14	16.23 ± 0.63	3400 ± 24	15.00 ± 1.93	918 ± 26	27.00 ± 0.18
DR4	3.497 ± 0.015	4.00 ± 1.20	17.92 ± 0.26	2400 ± 75	9.00 ± 0.44	456 ± 32	19.00 ± 1.13
SY1	4.298 ± 0.009	8.00 ± 0.59	23.54 ± 0.98	3700 ± 17	14.00 ± 1.53	1073 ± 54	29.00 ± 0.05
SY2	4.196 ± 0.010	5.00 ± 0.75	26.37 ± 1.60	1800 ± 118	8.33 ± 0.71	378 ± 23	21.00 ± 0.89
SY3	4.793 ± 0.006	6.00 ± 0.31	15.23 ± 0.84	3000 ± 33	13.00 ± 1.14	750 ± 50	25.00 ± 0.42
SY4	5.495 ± 0.001	9.00 ± 1.03	19.13 ± 0.10	5000 ± 109	9.00 ± 0.44	1850 ± 107	37.00 ± 0.99
RB1	6.998 ± 0.010	10.00 ± 1.48	20.45 ± 0.30	5500 ± 145	7.33 ± 1.10	2310 ± 173	42.00 ± 1.58
RB2	6.198 ± 0.004	8.00 ± 0.59	17.83 ± 0.27	4000 ± 38	8.00 ± 0.84	1240 ± 20	31.00 ± 0.29
RB3	5.896 ± 0.002	4.00 ± 1.20	22.85 ± 0.83	2100 ± 97	12.00 ± 0.74	483 ± 48	23.00 ± 0.66
RB4	7.497 ± 0.014	3.00 ± 1.64	23.57 ± 0.98	1200 ± 160	11.00 ± 0.35	180 ± 32	15.00 ± 1.60
LY1	7.195 ± 0.012	9.00 ± 1.03	25.73 ± 1.46	5300 ± 130	8.33 ± 0.71	2067 ± 139	39.00 ± 1.23
LY2	7.195 ± 0.012	8.00 ± 0.59	21.04 ± 0.43	4300 ± 59	10.00 ± 0.05	1419 ± 46	33.00 ± 0.52
LY3	6.998 ± 0.010	8.00 ± 0.59	15.47 ± 0.79	4600 ± 81	9.00 ± 0.44	1610 ± 73	35.00 ± 0.76
LY4	5.994 ± 0.003	9.00 ± 1.03	16.35 ± 0.60	4900 ± 102	13.00 ± 1.14	1960 ± 123	40.00 ± 1.35

Note. \* – plum genotypes were denoted on the basis of skin colour and/or fruit size, i.e. DR – dark red, SY – small yellow, RB – reddish brown and LY – large yellow; \*\* – standard error.

the plum genotypes, being the maximum in RB1 and the minimum in RB4 (Table 3). Number of branches in tree depends upon tree's growth habit, prevailing environmental conditions and cultural operations especially pruning and training of the trees. Ahmed et al. (2014) also observed that number of branches in a tree is greatly affected by location, soil and climatic factors.

**Leaf area.** Mean values for average leaf area of the plum genotypes indicated that the genotypes studied differed for the parameter under study (Table 3). The maximum leaf area (26.37 cm<sup>2</sup>) was recorded in SY2 and the minimum (10.66 cm<sup>2</sup>) in DR2. Although leaf size is a genetic character and varies from genotype to genotype, growing conditions, i.e. soil and climatic conditions and plant nutrition applied also affect the leaf size.

**Number of flowers per plant.** The plum genotypes studied differed in their flower number per plant. The maximum number of flowers per plant (5500) was counted in RB1 and the minimum (1200) in RB4 (Table 3). Blooming depends upon tree health and environmental conditions of the area especially the chilling hours. However, the plum genotypes also differ in their chilling requirements.

**Blooming period.** The data showed that the blooming period ranged from 7.33 to 15.00 days among the plum genotypes, being the maximum in DR3 and

the minimum in RB1 (Table 3). Blooming period usually depends upon the genotypes, locality aspect and prevailing temperatures. The genotypes growing on northern aspects have longer blooming period. Further, if prevailing temperature is low, duration of flowering may be extended.

**Number and percentage of fruits set per plant.** The mean values for the number of fruits set exhibited that number of fruit set varied from 180 to 2310 per tree (Table 3). The highest number of flowers was recorded for RB1 and the smallest for RB4. Interestingly, fruit set percentage followed almost the same pattern. Fruit set in the studied plum genotypes ranged from 15% to 42%. The maximum fruit set (%) was recorded in RB1 and the minimum in RB4. Fruit set depends on availability of compatible pollen, pollinating insects, prevailing temperature and humidity. Occurrence of rainfall at flowering may reduce the fruit set.

**Number and percentage of fruits matured per plant.** Fruit number matured per plant ranged from 24 to 900, being lowest in RB4 and the highest in RB1 (Table 4). Percentage of fruits matured per plant followed almost the same sequence, which varied from 13 to 39. The smallest value was recorded in RB4 and the highest value was noted in RB1. The productivity in different genotypes of a fruit crop varies due to variation in initial

**Table 4.** Mean values for various morpho-physiological parameters of fruits of plum genotypes

Genotype	No. of fruits matured plant <sup>-1</sup>	% of fruits matured plant <sup>-1</sup>	Fruit length cm	Fruit diameter cm	Flesh weight g	Stone weight g	Total fruit weight g
DR1*	124.00 ± 7.50**	20.00 ± 2.69	3.98 ± 0.64	5.65 ± 0.30	54.43 ± 1.44	1.76 ± 0.14	56.17 ± 1.42
DR2	40.67 ± 10.40	15.00 ± 3.28	3.07 ± 0.06	4.19 ± 0.75	24.77 ± 0.06	1.58 ± 0.18	26.33 ± 0.09
DR3	230.00 ± 13.80	25.00 ± 3.10	2.84 ± 0.37	3.47 ± 0.22	15.47 ± 0.53	1.33 ± 0.32	16.80 ± 0.57
DR4	73.00 ± 9.20	16.00 ± 3.16	2.41 ± 0.94	2.41 ± 0.34	10.13 ± 0.80	1.20 ± 0.34	11.30 ± 0.85
SY1	279.00 ± 12.10	26.00 ± 2.01	3.64 ± 0.69	4.22 ± 0.78	51.17 ± 1.28	2.16 ± 0.35	53.33 ± 1.28
SY2	71.00 ± 9.30	18.00 ± 2.93	3.14 ± 0.03	3.75 ± 0.28	21.50 ± 0.23	1.89 ± 0.37	23.37 ± 0.24
SY3	173.00 ± 5.80	23.00 ± 2.34	2.42 ± 0.92	2.65 ± 0.39	3.93 ± 1.12	1.60 ± 0.14	11.60 ± 0.83
SY4	629.00 ± 10.00	34.00 ± 2.96	1.90 ± 0.61	2.44 ± 0.51	6.37 ± 0.99	1.21 ± 0.33	7.58 ± 1.03
RB1	900.00 ± 19.40	39.00 ± 3.55	4.32 ± 0.58	4.47 ± 0.65	53.73 ± 1.41	2.89 ± 0.63	56.63 ± 1.44
RB2	348.00 ± 13.00	28.00 ± 2.25	3.45 ± 0.44	3.09 ± 0.42	28.00 ± 0.10	1.95 ± 0.48	29.97 ± 0.10
RB3	97.00 ± 8.40	20.00 ± 2.69	2.66 ± 0.61	2.97 ± 0.55	15.23 ± 0.55	1.53 ± 0.26	16.73 ± 0.57
RB4	24.00 ± 10.90	13.00 ± 3.52	2.47 ± 0.86	2.55 ± 0.49	5.93 ± 1.02	1.11 ± 0.10	7.04 ± 1.06
LY1	744.00 ± 14.00	36.00 ± 3.19	4.43 ± 1.03	4.54 ± 0.62	64.00 ± 1.93	2.91 ± 0.67	66.90 ± 1.96
LY2	425.00 ± 13.00	30.00 ± 2.49	3.74 ± 0.82	3.76 ± 0.29	33.53 ± 0.38	1.22 ± 0.31	34.75 ± 0.34
LY3	531.00 ± 6.60	33.00 ± 2.84	3.18 ± 0.08	3.11 ± 0.40	18.33 ± 0.39	1.31 ± 0.25	19.63 ± 0.42
LY4	744.00 ± 14.00	38.00 ± 3.43	2.25 ± 0.15	2.50 ± 0.65	9.17 ± 0.85	1.22 ± 0.81	10.38 ± 0.89

Note. \* – plum genotypes were denoted on the basis of skin colour and/or fruit size, i.e. DR – dark red, SY – small yellow, RB – reddish brown and LY – large yellow; \*\* – standard error.

fruit set, its retention and subsequent fruit growth and development. However, the number and percentage of fruits matured depend upon plant health, its nutritional status and endogenous hormonal level, climatic factors, and insect-pests and diseases attack.

**Fruit size.** Fruit size was measured in terms of fruit length and fruit width. Fruit length varied from 1.90 to 4.43 cm among the cultivars studied (Table 4). LY1 had the longest fruits and SY4 had the shortest fruits. Fruit diameter ranged from 2.41 to 5.65 cm. Fruits of DR1 had the largest diameter and those of DR4 had the smallest diameter. Fruit size depends upon genotype, prevailing climatic conditions and cultural practices adopted to maintain the plant health. Similarly, closer spacing between plants of the same and other species affects the fruit size due to competition for light, nutrition and water (Nawaz et al., 2007). Variation in fruit size has already been reported among the genotypes of various temperate fruits, i.e. plum (Walkowiak-Tomczak et al., 2008), apricot (Haciseferogullari et al., 2007), apple (Kumar et al., 2006; Sousa et al., 2006), sweet cherry (Vursavus et al., 2006), etc.

**Fruit weight.** Flesh weight ranged from 3.93 to 64.00 g among the plum genotypes evaluated (Table 4). The maximum weight (64.00 g) of flesh was recorded in LY1 and the minimum (3.93 g) in SY3, indicating that the flesh content was highly variable among the plum genotypes reflecting great diversity in the existing plum germplasm. As far as stone weight is concerned, the genotype LY1 had the heaviest stone (2.91 g), followed by RB1 (2.89 g), and RB4 had the lightest stone weight (1.11 g). Overall, the maximum fruit weight (66.90 g) was recorded in LY1 and the minimum (7.04 g) was weighed in RB4, showing a great variability in fruit weight among the plum genotypes. Milošević and Milošević (2012) have also reported variability in fruit weight among the different plum hybrids studied. Similarly, variation in fruit weight among apple (Kumar et al., 2006), apricot

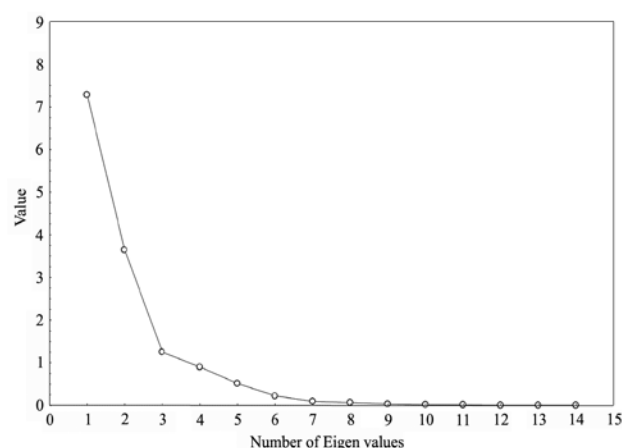
(Haciseferogullari et al., 2007) and cherry (Vursavus et al., 2006; Yilmaz et al., 2009; Sulusoglu, 2011) genotypes has also been reported.

**Principal component analysis.** Principle component analysis (PCA) for the morpho-physiological characteristics in various plum genotypes is given in Table 5.

**Table 5.** Principle component analysis (PCA) for some morpho-physiological traits of plum genotypes

Genotypes	Factor 1	Factor 2	Factor 3
Eigen value	7.28	3.64	1.25
Total variance %	51.98	26.02	8.91
Cumulative Eigen value	7.28	10.92	12.17
Cumulative variance %	51.98	78.01	86.92

In the present study, out of fourteen, three factors were extracted that have Eigen value more than 1 (Fig. 2).

**Figure 2.** Plot of Eigen values for 14 morpho-physiological traits of plum genotypes

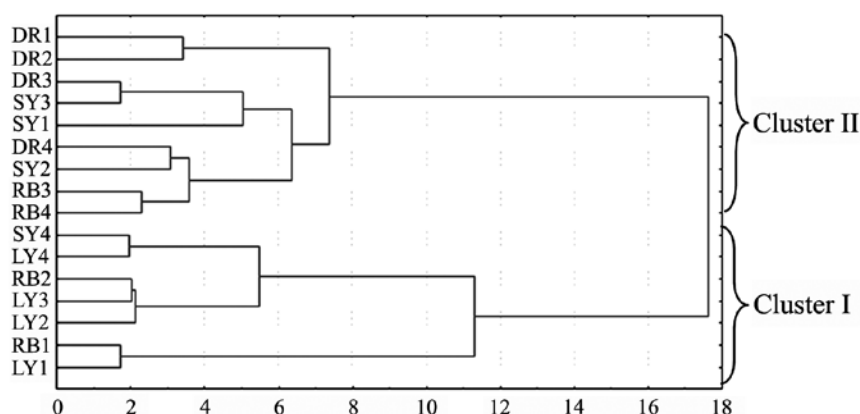
In the present study, factor 1 established maximum Eigen value of 7.28. The summation of the Eigen values is normally equivalent to the number of variables. Factor 1 showed maximum variability of 51.98%, followed by factor 2 (26.02%) and factor 3 (8.91%). These factors contributed 86.92% of the total variability among the plum genotypes which is very significant. According to Khodadadi et al. (2011), while evaluating the genetic diversity of wheat (*Triticum aestivum* L.) genotypes, PCA indicated that first five components explained over 97% of genetic variation. The first six principal components jointly explained 70.30% of the total variation among the African yam bean (*Sphenostylis stenocarpa* Hochst ex A.Rich) accessions (Aremu, Ibirinde, 2012). In another study, PCA revealed that in durum wheat (*Triticum durum* Desf.) lines, the first five components explained 73.76% of the total variation (Siahbidi et al., 2013).

**Factor loadings.** Factor 1 showed maximum positive loading of number of fruit set (0.92), percentage of fruit set (0.91), number of mature fruits (0.90) and percentage of mature fruits (0.90), while only one parameter showed negative factor loading (-0.23) that is duration of flowering (Table 6). It can be concluded that the total variability (51.98%) is residing in factor 1, hence it can be concluded that it is effectual factor for “fruit number”. As shown in Table 6, more than half of fruit traits contributed more than half to the total variability, which is of breeding significance. Factor 2 was connected to the maximum positive factor loadings of fruit diameter (0.83) and flesh and fruit weight (0.70) while the percentage of mature fruits (-0.42) and duration of flowering (-0.41) showed maximum negative loading. This factor can be called as “fruit size” factor. More than half of the parameters carry negative factor loadings in factor 2. Factor 3 was associated with the maximum number of parameters that have negative factor loadings. This variability can be exploited in improvement of the population. Large sized fruit is usually desired by local habitants as well as people of other regions of the country. In this study four plum genotypes showed large fruit size, i.e. DR1, SY1, RB1 and LY1 and these can be utilised in further breeding programmes.

**Table 6.** Factor loadings for morpho-physiological characters in sixteen plum genotypes

Parameters	Factor 1	Factor 2	Factor 3
Tree size, cm	0.47	-0.37	-0.49
Number of branches	0.90	-0.35	0.10
Number of flowers	0.90	-0.38	0.13
Duration of flowering	-0.23	-0.41	-0.21
Number of fruits set	0.92	-0.38	0.07
Percentage of fruit set	0.91	-0.39	0.09
Number of fruits matured	0.90	-0.38	0.05
Percentage of mature fruits	0.90	-0.42	0.09
Flesh weight, g	0.69	0.70	-0.01
Leaf area, cm <sup>2</sup>	0.21	0.09	-0.91
Fruit weight, g	0.69	0.70	-0.01
Fruit length, cm	0.66	0.69	-0.06
Fruit diameter, cm	0.42	0.83	0.21
Stone weight, g	0.69	0.53	-0.19

**Cluster analysis (hierarchical cluster).** The plum genotypes were divided into two main clusters cluster I and cluster II (Fig. 3). Cluster I was further sub-divided into two sub-clusters: a and b. Sub-cluster a contained only two plum genotypes LY1 and RB1. Sub-cluster b was further sub-divided into two sub-sub-clusters i and ii. Sub-sub clusters i showed that LY3 and RB2 were connected in same group while LY2 linked as outlier. Sub-sub-clusters ii contained only two plum genotypes SY4 and LY4. Major cluster II was further divided into two sub-clusters: a and b. Sub-cluster a was further sub-divided into sub-sub clusters i(a) and ii(a). In sub-sub-cluster i(a) RB3, RB4, SY2 and DR4 were closely linked whereas in sub-sub-cluster ii(a) DR3 and SY3 were connected in the same group, while SY1 was linked as outlier. Sub-cluster b contained only two plum genotypes DR1 and DR2 which are closely related. Culture analysis is widely used to study the relatedness among the genotypes (Khodadadi et al., 2011; Aremu, Ibirinde, 2012; Siahbidi et al., 2013). Sousa et al. (2006) distinguished 30 apple genotypes by main component analysis. They classified the genotypes into 10 divergent clusters. Pulp and rind mass and number of seeds were highly variable characters contributing to genetic diversity of the evaluated genotypes.



**Figure 3.** Cluster analysis based on morpho-physiological characters of plum genotypes



## Conclusion

Plums are profusely grown in district Rawalakot of Azad Jammu and Kashmir, northern Pakistan. Their wild relatives also exist in naturalized type in the area, which have not been explored yet. To assess the morpho-physiological diversity among the existing germplasm of plum, surveys were conducted during the years 2011 and 2012 and sixteen diverse plum genotypes were identified. The principle component analysis of morpho-physiological characters revealed that three factors each with the Eigen value greater than 1 showed 86.92% of the total variability among the plum genotypes. The cluster analysis for morpho-physiological characters exhibited that the plum genotypes fell into two major clusters on average Euclidean distances. Cluster II contained more genotypes than cluster I. There was only one genotype (SY1) in cluster II, which was the most diverse among the genotypes grouped in this cluster.

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## References

- Ahmed M., Anjum M. A., Rubbani M. A., Hassan L. 2009. Characterization of indigenous *Pyrus* germplasm of Azad Jammu and Kashmir revealed by SDS-PAGE analysis. *African Journal of Biotechnology*, 8: 6442–6452
- Ahmed M., Anjum M. A., Naz R. M. M., Khan M. R., Hussain S. 2013. Characterization of indigenous barberry germplasm in Pakistan: variability in morphological characteristics and nutritional composition. *Fruits*, 68: 409–422  
<http://dx.doi.org/10.1051/fruits/2013085>
- Ahmed M., Anjum M. A., Khaqan K., Hussain S. 2014. Biodiversity in morphological and physico-chemical characteristics of wild raspberry (*Rubus idaeus* L.) germplasm collected from temperate region of Azad Jammu and Kashmir (Pakistan). *Acta Scientiarum Polonorum: Hortorum Cultus*, 13 (4): 117–134
- Aremu C. O., Ibirinde D. B. 2012. Bio-diversity studies on accessions of African yam bean (*Sphenostylis stenocarpa*). *International Journal of Agricultural Research*, 7: 78–87  
<http://dx.doi.org/10.3923/ijar.2012.78.85>
- Aslam M., Amin S. 2013. Fruit, vegetables and condiments statistics of Pakistan 2011–2012. Government of Pakistan, Ministry of National Food Security and Research. Islamabad, Pakistan, <<https://docs.google.com/file/d/0B1wXTEitu71RRGpaODJMRfVlOWc/edit>>
- Bauer I., Drinic S. M., Drinic G., Micic D. I. 2007. Assessing temporal changes in genetic diversity of maize hybrids using RAPD markers. *Cereals Research Communications*, 35: 1563–1571  
<http://dx.doi.org/10.1556/CRC.35.2007.4.3>
- Chang T. S., Siddiq M., Sinha N. K., Cash J. N. 1994. Plum juice quality affected by enzyme treatment and fining. *Journal of Food Science*, 59: 1065–1069  
<http://dx.doi.org/10.1111/j.1365-2621.1994.tb08191.x>
- Cobianchi D., Watkins R. 1984. Plum descriptors: descriptor list for plum and allied species (*Prunus*). International Board of Plant Genetic Resources, p. 3–31
- Durgac C., Polat A., Kamiloglu O. 2006. Determining performances of some loquat (*Eriobotrya japonica*) cultivars under Mediterranean coastal conditions in Hatay, Turkey. *New Zealand Journal of Crop and Horticultural Sciences*, 34: 225–230  
<http://dx.doi.org/10.1080/01140671.2006.9514411>
- Erez A., Flore J. A. 1986. The quantitative effect of solar radiation on 'Red haven' peach fruit skin color. *HortScience*, 21: 1424–1426
- Gomez K. A., Gomez A. A. 1984. Statistical procedures for agricultural research (2<sup>nd</sup> ed.). New York, USA
- Haciseferogullari H., Gezer I., Ozcan M. M., Asma B. M. 2007. Post-harvest chemical and physical-mechanical properties of some apricot varieties cultivated in Turkey. *Journal of Food Engineering*, 79: 364–373  
<http://dx.doi.org/10.1016/j.jfoodeng.2006.02.003>
- Khodadadi M., Fotokian M. H., Miransari M. 2011. Genetic diversity of wheat (*Triticum aestivum* L.) genotypes based on cluster and principal component analyses for breeding strategies. *Australian Journal of Crop Science*, 5: 17–24
- Kumar P., Gangwar M. P., Dimri D. C. 2006. Evaluation of spur and colour mutant cultivars of apple (*Malus domestica* Borkh.) for their suitability under mid hill conditions of Uttaranchal. *Journal of Horticultural Sciences*, 1: 138–140
- Milošević T., Milošević N. 2012. Main physical and chemical traits of fresh fruits of promising plum hybrids (*Prunus domestica* L.) from Cačak (Western Serbia). *Romanian Biotechnological Letters*, 17 (3): 7358–7365
- Nawaz M. A., Ahmed W., Iqbal Z., Khan M. M. 2007. Evaluation of high density plantation on vigor and yield in Kinnow mandarin (*Citrus reticulata* Blanco). *International Symposium on Prospects of Horticultural Industry in Pakistan*, p. 87–92
- Nisar H., Ahmed M., Anjum M. A., Hussain S. 2015. Genetic diversity in fruit nutritional composition, anthocyanins, phenolics and antioxidant capacity of plum (*Prunus domestica*) genotypes. *Acta Scientiarum Polonorum, Hortorum Cultus*, 14 (1): 45–61
- Paganova V. 2009. The occurrence and morphological characteristics of the wild pear taxa in Slovakia. *HortScience*, 36: 1–13
- Potter D., Eriksson T., Evans R. C., Oh S., Smedmark J. E. E., Morgan D. R., Kerr M., Robertson K. R., Arsenault M., Dickinson T. A., Campbell C. S. 2007. Phylogeny and classification of Rosaceae. *Plant Systematics and Evolution*, 266: 5–43  
<http://dx.doi.org/10.1007/s00606-007-0539-9>
- RHS Colour Chart. 2001. Royal Horticultural Society <<http://www.rhododendron.org/colorcharts.htm>>
- Rop O., Jurikova T., Mlcek J., Kramarova D., Sengee Z. 2009. Antioxidant activity and selected nutritional values of plums (*Prunus domestica* L.) typical of the White Carpathian Mountains. *Scientia Horticulturae*, 122: 545–549  
<http://dx.doi.org/10.1016/j.scienta.2009.06.036>
- Siahbidi M. M. P., Aboughadareh A. R. P., Tahmasebi G. R., Teymoori M., Jasemi M. 2013. Evaluation of genetic diversity and interrelationships of agromorphological characters in durum wheat (*Triticum durum* Desf.) lines using multivariate analysis. *International Journal of Agriculture: Research and Review*, 3: 184–194
- Siddiq M. 2006. Plums and prunes. Hui Y. H. (ed.). *Handbook of fruits and fruit processing*, p. 553–564  
<http://dx.doi.org/10.1002/9780470277737.ch29>
- Sousa S. A., Dantas A. C. V. L., Silva S. A., Fonseca A. A. O., Machado M. S., de Almeida V. O. 2006. Fruit characterization of sugar apple genotypes in Presidente Dutra, Bahia. *Crop Breeding and Applied Biotechnology*, 6: 295–302  
<http://dx.doi.org/10.12702/1984-7033.v06n04a07>
- Sulusoglu M. 2011. The cherry laurel (*Prunus laurocerasus* L.) tree selection. *African Journal of Agricultural Research*, 6: 3574–3582

- Vursavus K., Kelebek H., Selli S. 2006. A study on some chemical and physico-mechanic properties of three sweet cherry varieties (*Prunus avium* L.) in Turkey. Journal of Food Engineering, 74: 568–575  
<http://dx.doi.org/10.1016/j.jfoodeng.2005.03.059>
- Walkowiak-Tomczak D., Reguła J., Łysiak G. 2008. Physico-chemical properties and antioxidant activity of selected plum cultivars fruit. Acta Scientiarum Polonorum: Technologia Alimentaria, 7: 15–22
- Watkins R. 1976. Cherry, plum, peach, apricot and almond. Simmonds N. W. (ed.). Evolution of crop plants, p. 242–247
- Yilmaz K. U., Ercisli S., Zengin Y., Sengul M., Kafkas E. Y. 2009. Preliminary characterisation of cornelian cherry (*Corunus mas* L.) genotypes for their physico-chemical properties. Food Chemistry, 114: 408–412  
<http://dx.doi.org/10.1016/j.foodchem.2008.09.055>

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## **Pakistano vietinių slyvų genetinių išteklių iš Azad Jammu ir Kashmir vietovių morfofiziologinės savybės**

H. Nisar<sup>1</sup>, M. Ahmed<sup>2</sup>, S. Hussain<sup>3</sup>, M. A. Anjum<sup>3</sup>

<sup>1</sup>Poonch universitetas, Pakistanas

<sup>2</sup>Mirpur mokslo ir technologijos universitetas, Pakistanas

<sup>3</sup>Bahauddin Zakariya universitetas, Pakistanas

### **Santrauka**

Naminė slyva (*Prunus domestica* L.) ir jos laukiniai giminaičiai, natūraliai augantys įvairiose Pakistano vietovėse, iki šiol nėra apibūdinti. Tirta šešiolikos genotipų slyvų, augančių Poonch rajone, Rawalakot regione, Azad Jammu ir Kashmir autonominėje respublikoje, Pakistane, morfofiziologinių savybių genetinė įvairovė. Vertinti šie rodikliai: medžių dydis, šakų skaičius medyje, lapų plotas, žiedų skaičius augale, žydėjimo periodas, augalo užmegztų vaisių skaičius ir procentas, subrendusių vaisių skaičius ir procentas, vaisių dydis ir masė. Straipsnyje aptariama šių rodiklių variacija. Tyrimo rezultatai parodė, kad slyvos genotipai skyrėsi morfofiziologinėmis savybėmis, ir suteikė svarbios informacijos, kaip šiuos genotipus būtų galima geriausiai panaudoti selekcinėse programose. Genotipų skirtumai gali būti nulemti jų genetinės sandaros ir šiame regione vyraujančių klimato veiksnių.

Reikšminiai žodžiai: bioįvairovė, morfoliginės savybės, Pakistanas, principinių komponentų analizė, *Prunus* sp., slyvos genotipai.