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Genetic characterization of *Rosa* species using morphological markers

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ABSTRACT

Genetic diversity in roses is unparalleled to any other flower crops. A large number of rose species is grown all around the world. There is a rich wealth of indigenous rose species such as *Rosa brunonii, R. macrophylla, R. moschata, R. spinossisima, R. rubiginosa, R. wichuraiana* etc. are grown wild in India. They are the important source of genes responsible for various traits, viz. both biotic and abiotic stress tolerance, fragrance, perpetual flowering, hardiness which need to be protected for further use in breeding programs. Morphological markers or traits based species identification are best for visualization, reproducibility and easy to use, besides serving as a reality check for molecular studies. In this study, 31 rose species were characterized for 18 vegetative characters as per PPV FRA guidelines for DUS testing of rose. Genetic diversity of rose species was done based on dissimilarity calculation, hierarchical cluster analysis, linear discriminant analysis and principal component analysis using R software. *R. banksiae* - *R. chinensis* 'Viridiflora' and *R. banksiae* - *R. rubiginosa* showed the highest diversity while *R. brunonii* and *R. dumalis* shows least diversity. Species were divided into five major clusters using hierarchical cluster analysis which was validated by linear discriminant analysis. Here, both Indian originating species *R. brunonii* and *R. moschata* fell into the same cluster while significant diversity noticed in *R. damascena* and *R. wichuraiana.* Results of principal component analysis follow a similar pattern as of dendrogram. *R. banksiae* was most distinctly placed which is well supported as only thornless species used in the study. Although no single morphological traits can be used to differentiate species, it is necessary to create a passport data for further studies.

Key words: Characterization, Cluster analysis, Diversity, Morphological markers, *Rosa* species, Thornless

The genus *Rosa* (Family: Rosaceae) is one of the most important genera of ornamental plants with respect to the economic and cultural history of humankind. This includes approximately 120 species distributed in the northern hemisphere (Wissemann 2003) and Asia is one of the important gene centers where the majority of the species are found (Broertjes and van Harten 1978). Conventional taxonomy (Wissemann 2003) divides the genus into four subgenera, three of which are monotypic: *Hulthemia* (Dumort.) Focke, *Platyrhodon* (Hurst) Rehder, and *Hesperhodos* Cockerell.

The fourth sub genus, *Rosa*, includes about 95% of all species and is subdivided into 10 sections namely, Banksiae (Sps: *R. banksiae* Ait. f.), Bracteatae, Caninae (Sps: *R. canina* L.; *R. rubiginosa* Brotero), Carolinae, Indicae/Chinensis (Sps: *R. chinensis* Jacq.; *R. gigantea* Collett.; *R. indica* Hook. f.), Cinnamomeae (Sps: *R.rugosa* Thunb.), Gallicae (Sps: *R. gallica* L.; *R. damascena* Mill.; *R. centifolia* (L.) Regel), Levigatae, Pimpinellifoliae (Sps: *R. sericea* Lindl.; *R. foetida* Herrm.) and Synstylae (Sps: *R. moschata* Herrm.; *R. multiflora* Thunb.; *R. wichuraiana* Crep ex Desegl.).

Numerous taxonomic studies have been done in this genus (Cre´pin 1889, Rehder 1940, Wissemann 2003), however, species relationships within *Rosa* remain difficult because of intraspecific variability, polyploidy, interspecific hybridization and multiple names was given to morphological variants and hybrids. Approx. 14 to 4,000 species of *Rosa* have been reported (Linnaeus 1753, Gandoger 1881, Cre´pin 1889, Rehder 1940, Wissemann 2003). Of the 120 species (Most accepted) in the subgenus *Rosa*, only eight species, viz. *R. chinensis, R. damascena, R. foetida, R. gallica, R. gigantea, R. moschata, R. multiflora* and *R. wichuraiana* are said to have played an important role in the development of modern garden roses (Gudin

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2000). The study of phylogeny is of utmost importance as to use them in various breeding programs. The phylogenetic relationships within genus *Rosa* have remained obscure till today due to the difficulty of grouping species and a complex taxonomy. There is a vast wealth of indigenous rose varieties and species in India which ought to be protected and can be further utilized for rose breeding. As many as 16 species and four hybrid species were found growing wild in different phytogeographical zones of India (Rathore and Umesh 1992). Out of that, six wild species were found to be grown only in western Himalaya (*R. brunonii, R. moschata, R. multiflora* and *R. cathayensis R. macrophylla* and *R. webbiana,* Singh *et al.* 2017). Many wild species have been evolved to survive under abiotic stresses such as droughts, extreme heat and cold and biotic stresses such as insects, pests, and diseases. Hence, these are suitable to use in different breeding programs in order to develop varieties suitable for local agro-ecological conditions. The species, viz. *Rosa brunonii, R. macrophylla, R. moschata, R. spinossisima, R. rubiginosa, R. wichuraiana, etc.* provide genes for both biotic and abiotic stresses along with other traits such as fragrance, perpetual flowering, hardiness and some unknown traits which may become important in further breeding programs. The study of phylogeny that relies on morphological markers of any plant is the oldest one and is most classical. Morphological markers are the phenotypic markers of any plants and are the earliest markers used to describe the observable characters of the plant. Morphology-based species identification is a very important source of information due to its visualization and reproducibility besides being cheaper and hence anyone can use anywhere. Although these are rigorous, morphology-based phylogenies act as a "reality check" for molecular studies till we do not have error proof molecular techniques (Jenner 2004). Quick and accurate identification of species in the field/forest/laboratory based on morphological traits is critical to many other areas like ecological and behavioural adaptation, physiology, besides systematics (Maddison 1996).

Keeping these considerations into view the present investigation was carried out to study the genetic relationship among *Rosa* species on the basis of morphological markers.

MATERIALS AND METHODS

The present study was carried out at the Research Farm of the Division of Floriculture and Landscaping, IARI, New Delhi during 2015-17. Thirty-one species of rose were collected from ICAR-Indian Agricultural Research Institute, New Delhi, ICAR-National Bureau of Plant Genetic Resources, Regional Station, Shimla, Himachal Pradesh and ICAR-IARI, Regional Station Katrain, Himachal Pradesh (Table 1). Few species with unknown grouping were also collected from wild sources in Katrain, Himachal Pradesh. The observations were recorded for 18 vegetative characters, viz. plant growth habit, young shoot anthocyanin colouration, young shoot hue of anthocyanin colouration, prickles characteristics (Predominant colour, shape of lower side, curvature), leaf characteristics (Leaf colour, glossiness of adaxial surface, leaf pubescence, leaflet serration of margin, terminal leaflet: length and breadth, terminal leaflet: shape of the blade, tip, and base) and type of stipule (Supplement Table). As most of the work was done at ICAR-IARI, New Delhi where most of the species do not flower, hence, flowering data were not recorded. For vegetative traits, scoring was done as per N-DUS guidelines of Rose given by PPVFRA, New Delhi (Authority, PPVFR, 2012). For the characters which were not included in PPVFRA rose DUS guidelines, such as presence or absence of prickles on the shoot, the shape of terminal leaflet blade and type of stipule, a scoring pattern was created similar to DUS guidelines and further analysis was done.

14 sets of the variable were used for the further analysis of 31 genotypes. As some variables were uniform throughout the genotypes, they were not considered during dissimilarity calculation, hierarchical cluster analysis, linear discriminant analysis and Principal Component Analysis. "Pairwise dissimilarity (distances) matrix" was calculated between observations using "Daisy function of R" as it can use mixed types variables for analysis. Hierarchical Clustering of *Rosa* species was done using the same data by "Ward D clustering". *Ward's* minimum variance method is suitable for finding compact clusters in R (Maechler *et al.* 2017). Linear Discriminant Analysis was also done for validating cluster analysis output (Venables and Ripley 2002). Principal components analysis (PCA) was used to identify multidimensional relationships among various morphological traits used for dividing the genotypes into various groups (Revelle 2017).

RESULTS AND DISCUSSION

Variability based on rose DUS guidelines of PPV FRA

Based on morphological traits, it is inferred that high variation is available in genus *Rosa*. Variations were noticed for almost all important vegetative characters. The morphological traits which were used to differentiated instinct species are plant growth habit, the shape of prickles, leaflet shape and size, leaf serration and shape of stipules. Plant growth ranges from upright to strongly spreading which can serve various purposes. The upright growing species like *R. glutinosa* and *R. hybrida* cv. Rose Sherbat can use for tall growing purposes while strongly spreading (Wild species 4) and moderately spreading species (*e.g. R. indica major, and R. banksiae*) can be used for breeding climber types of cultivars. The second important trait is anthocyanin colouration of young shoots and its hue. As it is a well-known fact that anthocyanin acts as an antioxidant and protects plants from various abiotic stresses and delaying leaf senescence (Landi *et al.* 2015). Hence, species having strong hue of anthocyanin colouration can be an effective source of resistance against abiotic stress. Various species such as *R. brunonii, R. moschata, R. dumalis, R. glutinosa*, Wild species 3 and Wild species 5 has been recorded to have strong anthocyanin colouration, and further these may be utilized for transferring the anthocyanin content trait.

Table 1 List of rose genotypes used for morphological characterization

Species name	Accession no./ Identification no	Source	Collected from (Lat_Lon)
Rosa nitida × *R. rugosa*	EC 035571	ICAR-IARI, New Delhi	28.64N_77.15E
R. slancensis	EC 037349	ICAR-IARI, New Delhi	28.64N_77.15E
R. indica major	EC 129073	ICAR-IARI, New Delhi	28.64N_77.15E
R. macrophylla	IC 564816	ICAR-IARI, New Delhi	28.64N_77.15E
R. brunonii	IC 564794	ICAR-IARI, New Delhi	28.64N_77.15E
R. wichuraiana	EC 033173	ICAR-IARI, New Delhi	28.64N_77.15E
R. moschata	EC 018586	ICAR-IARI, New Delhi	28.64N_77.15E
R. tomentosa	EC 032911	ICAR-IARI, New Delhi	28.64N_77.15E
R. dumalis	EC025995	ICAR-IARI, New Delhi	28.64N_77.15E
R. multiflora	EC032219	ICAR-IARI, New Delhi	28.64N_77.15E
R. glutinosa	EC 025999	ICAR-IARI, New Delhi	28.64N_77.15E
R. damascena	EC025987	ICAR-IARI, New Delhi	28.64N_77.15E
R. bourboniana	IC010649	ICAR-IARI, New Delhi	28.64N_77.15E
R. chinensis viridiflora	FLS-IARI/P10/B15-1	ICAR-IARI, New Delhi	28.64N_77.15E
R. indica var. *odorata*	FLS-IARI/MB10-A	ICAR-IARI, New Delhi	28.64N_77.15E
R. banksiae	IW004421	ICAR-IARI, R.S, Katrain	32.09N_77.13E
R. rubiginosa	EC026371	ICAR-NBPGR, R S, Shimla	31.09N_77.15E
Rosa sps	FLS-P8/B19-2	ICAR-NBPGR, R S, Shimla	31.09N_77.15E
R. inodora	EC025783	ICAR-NBPGR, R S, Shimla	31.09N_77.15E
R. spinossisima	EC032847	ICAR-NBPGR, R S, Shimla	31.09N_77.15E
R. rubrifolia	EC032417	ICAR-NBPGR, R S, Shimla	31.09N_77.15E
R. damascena cv. Jwala	FLS-P10/B19-1	ICAR-IARI, New Delhi	28.64N_77.15E
R. damascena cv. Himroz	FLS-P9/B19-1	ICAR-IARI, New Delhi	28.64N_77.15E
R. damascena cv. Rani Sahiba	FLS-P8/B19-1	ICAR-IARI, New Delhi	28.64N_77.15E
R. hybrida cv. Rose Sherbat	FLS-IARI/1B/R3-C4	ICAR-IARI, New Delhi	28.64N_77.15E
R. hybrida cv. Dr. Huey	FLS-P11/B19-3	ICAR-IARI, New Delhi	28.64N_77.15E
Wild Species 1	FLS/2016/RW1	ICAR-IARI, RS, Katrain	32.10N_77.13E
Wild Species 2	FLS/2016/RW2	ICAR-IARI, RS, Katrain	32.10N_77.13E
Wild Species 3	FLS/2016/RW3	ICAR-IARI, RS, Katrain	32.11N_77.16E
Wild Species 4	FLS/2016/RW4	ICAR-IARI, RS, Katrain	32.09N_77.13E
Wild Species 5	FLS/2016/RW5	ICAR-IARI, RS, Katrain	32.10N_77.13E

RS, Regional station

Prickles are special structures associated with rose. They are different from the thorns and spines as vascular bundles are not present inside and are easily removable. They are present in various forms and densities among species and cultivars (Debener and Linde 2009). As prickles make commercial rose cultivation difficult mainly during cultural practices and harvesting, search for thornless cultivars have been a major breeding objective of almost all the breeding programs (Kanli and Kazaz 2009, Zlesak 2007).

Among the species studied, *R. banksiae* was found to be completely thornless. In both Wild species 1 and Dr Huey, prickles were not found on the shoots even though few prickles were present in the mature stem. The prickle density was very less in *R. spinossisima* whereas it was very high in species like *R. rubignosa, R. rubrifolia* and *R. damascena* cv. Himroz. Species having high prickle density can be used where there is a problem of herbivores as they get stuck in prickles, and eventually die due to immobilization and starvation (Yamazaki *et al.* 2014).

The relationship between leaf serration and climate has been widely studied and revealed in woody and herbaceous species, where it is hypothesized that leaves having serrated margins are more active than entire leaves in terms of photosynthesis and transpiration besides having a higher surface area (Royer and Wilf 2006, Semchenko and Zobel 2007). In general, most common serration found in rose is a serrate type but, few species having finer and denser serration was also noticed in the present study. *R. rubignosa* has a unique type of serration, i.e. crenate type while Wild species 4 has doubly serrate type depicting greater variation. Similarly, variation was also observed in leaf shape. It is said that the driver for evolution in leaf shape is thermos regulation, as maintenance of leaf temperature within a critical range is very critical for plant's growth and survival. Below a certain temperature range, there is irreversible damage occur to plant's photosynthetic apparatus (Nicotra *et al.* 2011). There is a vast range of variation within genus *Rosa*, the leaf shape varies from lanceolate to nearly round depicting range of adaptability to a wide range of climatic conditions. A great length of variation was also seen in the shape of the tip and base of terminal leaflets.

Rose leaves have the persistent type of stipules which are adnate in nature, i.e. it is fused together on part of the petiole length, but the anterior remains free. Rose stipule is an important character for rose species classification (Rathore and Umesh 1992). As per *Rosa* species (A bulletin) of ICAR-National Bureau of Plant Genetic Resources, New Delhi, stipules has been further classified as Clasped, Winged, Scaly/rudimentary and Fish tail. In our study, clasped and winged types of stipules were common among various species. Only *R. banksiae* and Wild species 4 had the scaly or rudimentary type of stipule.

Genetic distance among Rosa *species based on pairwise dissimilarity matrix*

Based on Pairwise dissimilarity (distances) matrix, the dissimilarity value between different species varies from 0.05 to 0.60. *R. banksiae -R. chinensis* 'Viridiflora' and *R. banksiae-R. rubiginosa* showed the highest diversity having maximum dissimilarity with a correlation coefficient of 0.60. It is clear from this that *R. banksiae* is the most unique and diverse among all the species used in the study. It is well supported by visual observations having thorn-less nature. It was in accordance with Rehder's classification where it was single species in Section 8 Banksianae of subgenus *Eurosa* (Rehder 1940). The karyotypic relationships among various *Rosa* species also reported *R. banksiae* as the most outgroup of subgenus *Eurosa* (Yan *et al.* 1997). Among all maximum similarity was observed between *R. brunonii* and *R. dumalis* with a coefficient value of 0.05 (Table 2).

Cluster analysis of Rosa *species*

Hierarchical cluster analysis of species was done by "Ward D clustering" and a dendrogram was constructed, where species were divided into five major clusters (Fig 1). Furthermore, the cluster analysis output was also validated by linear discriminant analysis using "MASS package of R, and the relationship between different clusters is given in the Table 3.

Cluster 1 includes five species, i.e. *R. rubiginosa, R. inodora, R. slancensis, R. bourboniana* and Wild species 4. Cluster 2 too includes five species namely *R. nitida* × *R. rugosa, R. wichuraiana, R. rubrifolia, R. multiflora* and Wild species 5. Cluster 3 includes six species such as *R. damascena* cv. *Jwala, R. chinensis* 'Viridiflora*', R. odorata, R. macrophylla, R. tomentosa* and *R. banksiae.* Clustering of *R. chinensis* 'Viridiflora*'* and *R. odorata* into the same cluster was in accordance with Rehder's classification in section Indicae, they are reported to be diploid in nature. Similar findings were also reported by Fernandez-Romero *et al.* (2011). *R. banksiae* was most diverse in the cluster which was also validated in dissimilarity index. Cluster 4 includes six species- *R. brunonii, R. dumalis, R. spinossisima, R. moschata,* Wild species 1 and Wild species 3. Here *R. brunonii,* and *R. dumalis* falls not only into same cluster but also in same sub cluster displaying their similarity. It is evident from the dissimilarity index too where coefficient value of 0.05 was obtained. Cluster 5 is the largest one which include nine species, viz. *R. damascena*, *R. damascena* cv. Himroz, *R. damascena* cv. Rani Sahiba, *R. glutinosa, Rosa sps, R. indica major*, Rose Sherbat, Dr Huey and Wild species 2. There is a significant diversity in the species *R. damascena*. The cultivar Jwala of *R. damascena* has fallen into a different cluster 3 whereas the *R. damascena,* Himroz and Rani Sahiba of *R. damascena* have fallen in the same clusters even in same sub cluster. Similar results were also found by Henuka *et al.* (2014).

Both the Indian originating species *R. brunonii*

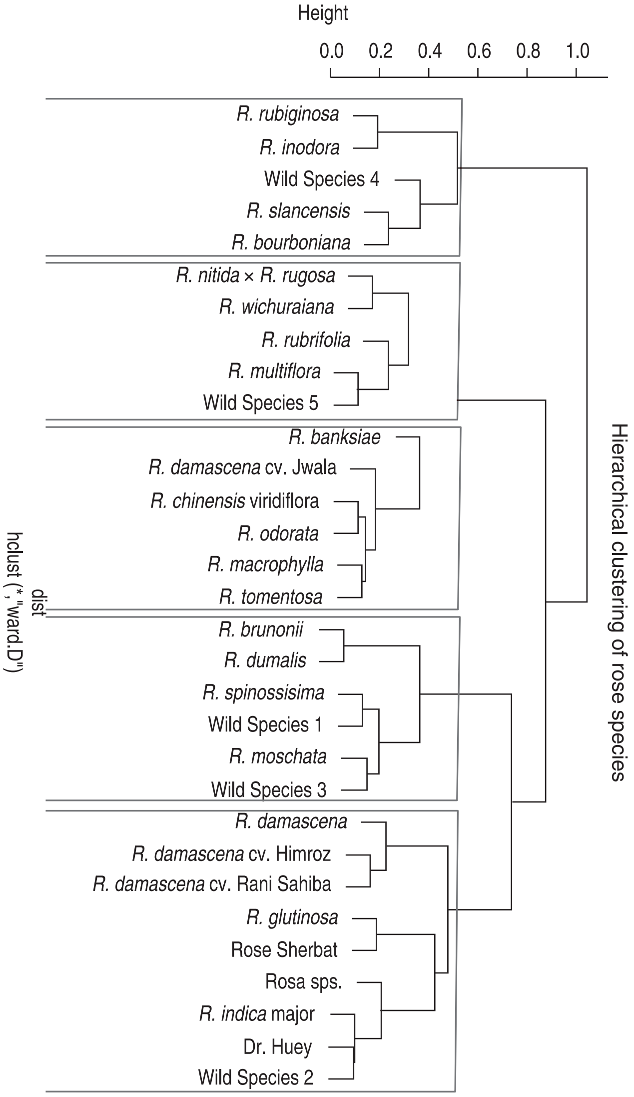

Fig 1 Dendrogram based on the hierarchical clustering of *Rosa* species

Table 2 Euclidean's pairwise dissimilarity (distances) matrix of rose species generated using morphological characters

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30
2	0.29																													
3	0.19	0.25																												
4	0.16	0.20	0.18																											
5	0.40	0.52	0.37	0.33																										
6	0.17	0.39	0.26	0.26	0.28																									
7	0.30	0.46	0.28	0.26	0.15	0.28																								
8	0.18	0.18	0.16	0.13	0.35	0.25	0.31																							
9	0.39	0.52	0.35	0.32	0.05	0.31	0.14	0.34																						
10	0.18	0.28	0.24	0.21	0.29	0.15	0.26	0.14	0.28																					
11	0.32	0.41	0.24	0.33	0.30	0.39	0.23	0.23	0.29	0.32																				
12	0.42	0.41	0.27	0.41	0.36	0.29	0.29	0.33	0.36	0.33	0.40																			
13	0.36	0.23	0.23	0.36	0.41	0.42	0.37	0.30	0.41	0.39	0.23	0.36																		
14	0.18	0.21	0.11	0.13	0.33	0.29	0.25	0.15	0.31	0.24	0.25	0.32	0.24																	
15	0.19	0.15	0.17	0.12	0.44	0.30	0.36	0.12	0.42	0.20	0.31	0.41	0.35	0.11																
16	0.22	0.39	0.33	0.19	0.45	0.39	0.35	0.32	0.43	0.33	0.44	0.60	0.53	0.29	0.29															
17	0.38	0.38	0.43	0.44	0.38	0.30	0.34	0.38	0.37	0.32	0.37	0.35	0.31	0.36	0.42	0.60														
18	0.19	0.31	0.18	0.28	0.41	0.22	0.35	0.21	0.40	0.26	0.24	0.31	0.32	0.25	0.21	0.39	0.42													
19	0.39	0.35	0.41	0.46	0.45	0.32	0.35	0.45	0.44	0.39	0.50	0.28	0.31	0.33	0.44	0.57	0.19	0.44												
20	0.24	0.44	0.30	0.25	0.27	0.23	0.15	0.26	0.26	0.16	0.34	0.36	0.39	0.30	0.34	0.31	0.40	0.35	0.35											
21	0.31	0.42	0.33	0.34	0.37	0.29	0.26	0.31	0.35	0.22	0.29	0.38	0.39	0.29	0.32	0.45	0.22	0.41	0.29	0.26										
22	0.17	0.33	0.16	0.13	0.26	0.25	0.21	0.15	0.24	0.24	0.25	0.32	0.29	0.12	0.23	0.29	0.35	0.25	0.37	0.23	0.33									
23	0.32	0.38	0.26	0.31	0.19	0.28	0.22	0.32	0.19	0.23	0.37	0.24	0.39	0.22	0.30	0.47	0.29	0.34	0.31	0.33	0.23	0.31								
24	0.27	0.40	0.19	0.32	0.22	0.20	0.18	0.30	0.22	0.21	0.25	0.18	0.28	0.23	0.31	0.49	0.34	0.19	0.31	0.25	0.28	0.24	0.16							
25	0.36	0.44	0.29	0.37	0.30	0.33	0.23	0.27	0.31	0.18	0.19	0.26	0.33	0.31	0.36	0.50	0.32	0.35	0.46	0.26	0.25	0.31	0.28	0.22						
26	0.17	0.33	0.09	0.26	0.35	0.29	0.30	0.24	0.35	0.24	0.23	0.34	0.20	0.17	0.25	0.34	0.46	0.19	0.43	0.27	0.35	0.23	0.29	0.18	0.28					
27	0.31	0.42	0.25	0.27	0.21	0.28	0.16	0.24	0.20	0.13	0.25	0.31	0.33	0.26	0.33	0.39	0.34	0.31	0.41	0.13	0.27	0.20	0.29	0.18	0.16	0.22				
281	0.19	0.34	0.10	0.22	0.27	0.26	0.23	0.20	0.26	0.25	0.16	0.31	0.22	0.18	0.26	0.35	0.43	0.15	0.46	0.30	0.33	0.18	0.25	0.14	0.26	0.09	0.23			
29	0.33	0.35	0.27	0.22	0.22	0.26	0.14	0.22	0.22	0.15	0.28	0.30	0.43	0.34	0.28	0.35	0.42	0.27	0.49	0.19	0.32	0.27	0.28	0.21	0.20	0.33	0.17	0.25		
30	0.46	0.37	0.40	0.50	0.51	0.38	0.47	0.48	0.51	0.40	0.47	0.36	0.29	0.50	0.49	0.57	0.41	0.36	0.41	0.47	0.50	0.50	0.44	0.29	0.39	0.42	0.46	0.39	0.38	
31	0.25	0.27	0.26	0.20	0.31	0.21	0.23	0.17	0.29	0.11	0.33	0.35	0.46	0.26	0.20	0.34	0.34	0.32	0.41	0.26	0.19	0.29	0.26	0.27	0.28	0.36	0.24	0.31	0.14	0.45

Note: 1-31 denotes species name enlisted in Table 1.

Table 3 Membership score of different clusters of dendrogram using linear discriminant analysis

	Cluster				
Cluster	1	2	3	4	5
1	**5**	0	0	0	0
2	0	**5**	0	0	0
3	0	0	**9**	0	0
4	0	0	0	**6**	0
5	0	0	0	0	6

(Himalayan Musk rose) and *R. moschata* (Musk rose) fell into the same cluster showing common lineage. This is in accordance with Rehder's classification where both species were grouped into section Synstylae. Wu *et al.* (2000) also reported similar observations using *matK* markers with both species grouping into the same sub clade. Two other species of same section *R. wichuraiana* and *R. multiflora* falls into another cluster showing great diversity in Synstylae section. Dr Huey (Hybrid *Wichuraiana*) shows a lot of variation from its parent *R. wichuraiana* and grouped into different clusters (Henuka *et al.* 2014).

Principal component analysis (PCA) of Rosa *species*

PCA was used to identify multi dimensional relationships among various traits for grouping species. It extracts all important variables in the form of different components from a large set of variables available in a data set and presents them in more interpretable form. Principle components altogether explained 100% of the accumulated variables. PCA was carried out on 14 traits of all the species, the first five principal components captured 70% of the variability. As shown in Fig 2, the Principal Component separated the *Rosa* species into five major clusters and *R. banksiae* was placed most distinctly from all other species. The results of PCA follows a similar pattern as of by hierarchical cluster analysis (Dendrogram). Species belonging to a common cluster in dendrogram have fallen nearer to each other (Fig 2).

The species of *Rosa* genus are highly variable, besides they hybridize easily and because of this, the conception of species varies greatly according to the views of different taxonomist starting from highly rated Rehder's classification. Even though no single morphological character can be used to distinguish one species from another, morphological characterization is must for supporting molecular data. Hence, we need to have a robust combined collaborative study including new advanced molecular markers along with the morphological database. *R. banksiae* has been

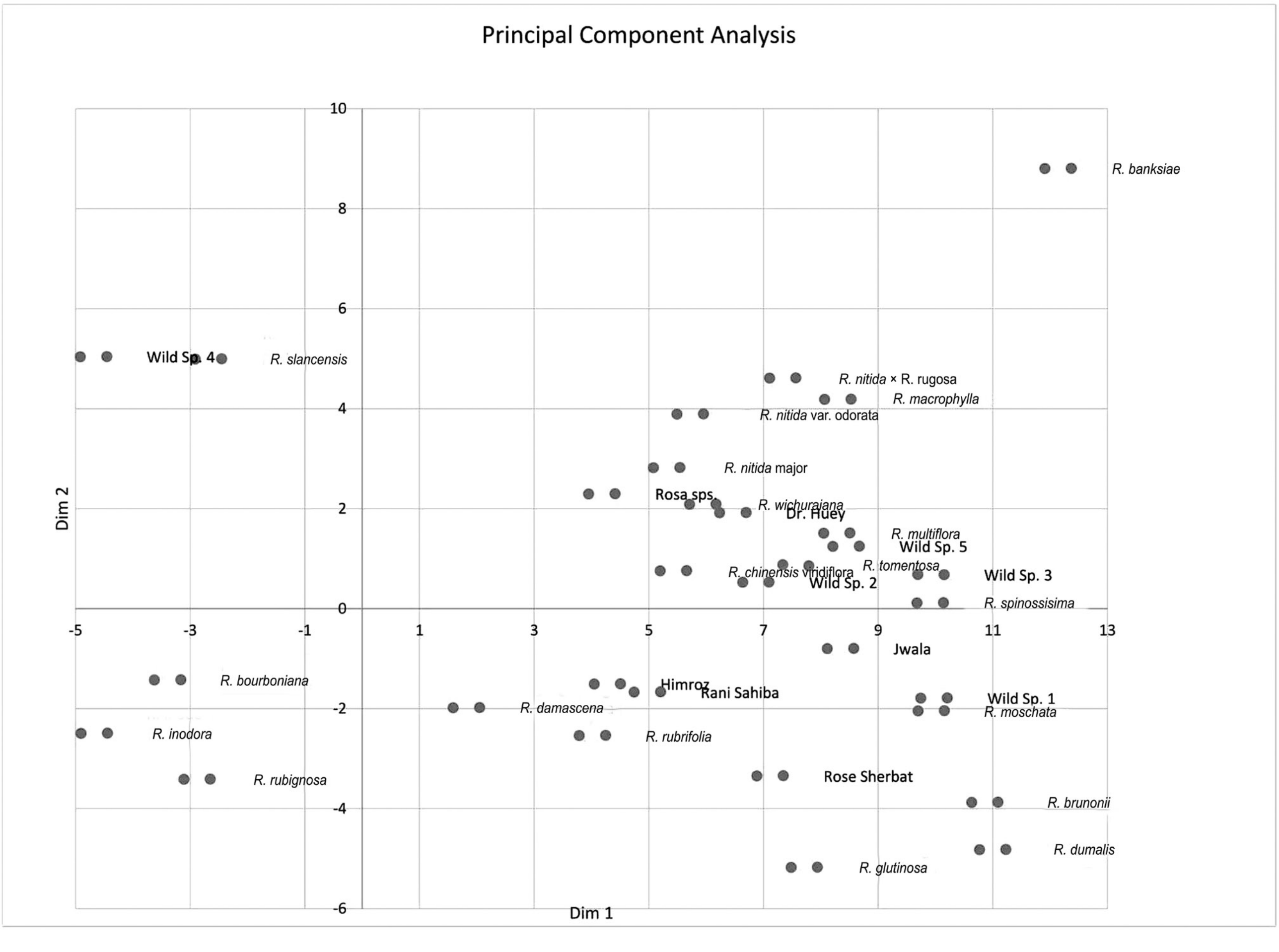

Fig 2 PCA (Dim 1 vs. Dim 2) based on the dissimilarity index of *Rosa* species

reported to be the only thornless species among the studied genotypes.

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