Original Article

Morphological Traits Evaluation of Rumex L. (Polygonaceae Juss.: Rumicoideae Leurss.) Using Principal Component Analysis

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Abstract

Problem Statement: The purpose of the present work is to use Principal Component Analysis (PCA) and phenetic clustering to examine and understand the patterns of morphological variation among taxa within the genus Rumex subfamily Rumicoideae (Polygonaceae).

Material & Methods (Approach): Morphological variation was assessed in ten Rumex taxa using Principal Component Analysis (PCA). Fourteen morphological features, which include 29 character states were examined.

Results: According to PCA, the first two factors explained 53.6% of the total variance, with inflorescence type making the most contribution. R. pictus was the most divergent, but *R. pulcher, R. vesicarius, R. roseus,* and *R. simpliciflorus* were closely related, according to UPGMA clustering. Both positive and negative relationships between attributes were found using correlation analysis.

Conclusions/Recommendations: The findings support the use of morphological features in improving classifications within Rumicoideae and demonstrate their taxonomic significance.

Keywords: Morphological correlation, PAST, PCA, Phenogram.

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1 INTRODUCTION

The goal of the current study is to determine the main axes of morphological variation and evaluate the taxonomic significance of each within genus *Rumex* L. this study seeks to provide a more comprehensive and resilient categorization of the subfamily.

One of the main subfamilies of the Polygonaceae is Rumicoideae, which includes genera like *Rheum*, *Oxyria*, and *Rumex* that are significant both ecologically and commercially. Morphological evidence is still crucial for resolving taxonomic uncertainties despite breakthroughs in molecular phylogenetics, particularly in cases where DNA evidence is sparse or inconsistent [1,2]. The vegetative and reproductive characteristics of these genera, such as achene morphology, inflorescence architecture, and leaf form, vary greatly [3,4]. Morphological variation in the subfamily Rumicoideae Leurss. is both taxonomically informative and diverse, which makes it a perfect fit for these kinds of analysis [5,6].

The progress in the taxonomic and cytological study of *Rumex* was largely accomplished by many researchers [7], they proposed that *Rumex* is composed of several smaller genera corresponding to cytological study.

Principal Component Analysis (PCA) and other multivariate statistical techniques have been widely used to analyze complicated morphological datasets, allowing researchers to identify patterns of variation among species [8,9]. PCA makes it easier to visualize and comprehend trait patterns by reducing multidimensional morphological datasets into principle components that capture the most variance [10,11].

2 Materials and Methods

The present study was carried out on eight species and two subspecies of *Rumex* *Viz.* *Rumex bucephalophorus* L., Sp. Pl. 1: 336 (1753), *Rumex crispus* L., Sp. Pl. [Linnaeus] 1: 335 (1753), *Rumex cyprius* Murb., Acta Univ. Lund. n.s., ii. No. 14, 20 (1907), *Rumex dentatus* L. subsp. *dentatus*, Mant. Pl. Altera 226 (1771), *Rumex dentatus* subsp. *mesopotamicus* Rech.f., Beih. Bot. Centralbl. 49(2): 16 (1932), *Rumex pictus* Forssk., Fl. Aegypt.-Arab. 77 (1775), *Rumex pulcher* L., Sp. Pl. 1: 336 (1753), *Rumex roseus* L., Sp. Pl. 1: 337 (1753), *Rumex simpliciflorus* Murb., Acta Univ. Lund. xxxv. Afd. II. no. 3 11 (1899), *Rumex vesicarius* L., Sp. Pl. 1: 336 (1753). The easily observable (29) character states of (14) morphological characters were summarized in table (1). These characters were investigated from herbarium specimens deposited at the Herbaria of Ain Shams University, Faculty of Science (CAIA), Cairo University, Faculty of Science (CAI), Flora and Phytotaxonomy Research Department (CAIM) and Orman Botanical Garden, Giza. Published descriptions also were consulted [12]. The identification and nomenclature were authenticated using [13,14] and International Plant Name Index [15].

Morphological characters states by taxon matrix was subjected to phenetic analysis by use of PAleontological STatistics Version 3.23 [16]. Principal component analysis (PCA) ordination and similarity matrix were performed using the same software, based on the investigated morphological characters of the studied taxa.

Table 1. The extracted morphological characters, their states and codes of the studied taxa.

No.	Character	Character state and its (code)
1.	Stem strength	Erect (0) Prostrate (1)
2.	Stem branching	From base (0) Lateral (1)
3.	External appearance	Terrete (0) Angled (1)
4.	Lamina composition	Simple (0) Lobed (1)
5.	Lamina base	Symmetric (0) Asymmetric (1)
6.	Lamina shape	Sagittate (0) Orbicular (1)
7.	Lamina margin	Entire (0) Undulate (1)
8.	Lamina apex	Acute (0) Acuminate (1)
9.	Ochrea union	Connate (0) Bifid (1)
10.	Inflorescence type	Raceme (0) Spike (1) cluster (2)
11.	Flower	Pedicelled (0) Sessile (1)
12.	Nutlet shape	Lenticular (0) Trigonous (1)
13.	Nutlet surface	Smooth (0) stiff bristles (1)
14.	Nutlet wings	Absent (0) Present(1)

3 Results

The phenetics depending on the coded morphological data matrix of the studied taxa generated a dendrogram (figure 1). The phenogram was revealed that at 0.6 taxonomic distance there was a close relationship among four studied species *Viz.* *R. pulcher*, *R. roseus*, *R. simpliciflorus*, *R. vesicarius* where *R. pulcher* and *R. vesicarius* more related to each other as the same degree as *R. roseus* and *R. simpliciflorus* at 0.8 taxonomic distance. The nearest taxon to this group was *R. cyprius* at taxonomic distance 0.5. *R. crispus* and *R. bucephalophorus* were separated at basal level (about 0.45 taxonomic distance). The two studied subspecies were tied together while *R. pictus* was the earliest taxon that separated from the entire group at 0.2 taxonomic distance.

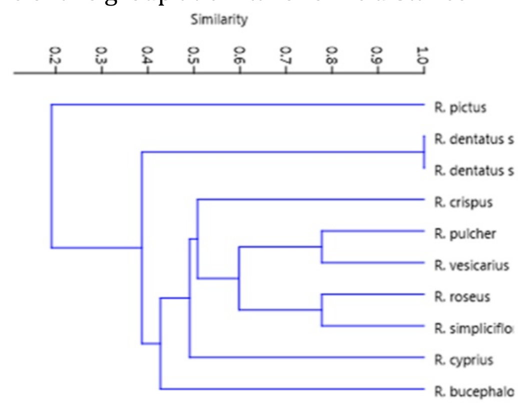

Figure 1. UPGMA clustering of the studied taxa based on morphological characters

The present study tried to find a correlation among the investigated morphological characters, it has been found that as indicated in Figure 2, there are positive correlations between some of the morphological characters such as stem strength *Vs.* flower sex, inflorescence *Vs.* stem branching, while there are negative correlations between some of the morphological characters such as strength *Vs.* leaf composition and flower sex.

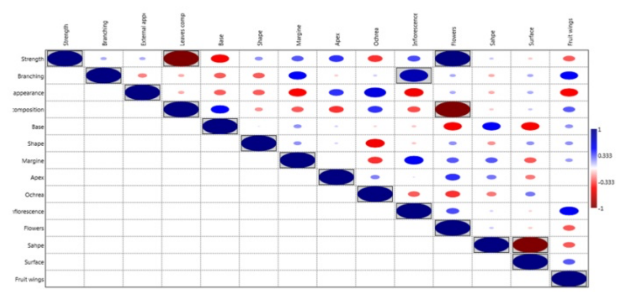

Figure 2. Correlation among the investigated morphological characters of the studied taxa.

The principal component analysis (PCA) clarified that, the percentage of explained variances reached 35.7% in relation to the first component PC1 and 17.9% due to PC2 (Table 2, Figure 3). From the loadings plot of PC1 as the major shareholder (Figure 4), it has been positively correlated with some morphological characters that reached to its maximum value in inflorescence (0.70) while it has been negatively correlated with external appearence (-0.30) and ochrea (-0.24). PCA ordination that based on the investigated morphological characters of the studied taxa are presented in figure (5). Among the studied taxa, the most distant and the closest species are determined. *R pulcher*, *R. vesicarius* and *R. pictus* are the most distantly related species (percentage of dissimilarity: 3.3), *R. dentatus* subsp. *dentatus* and *R. dentatus* subsp. *mesobotamicus* are the completely closely related species while *R. vesicarius* and *R. pulcher* are closeley related at percentage of dissimilarity; 1.4 as the same as *R. roseus* and *R. simpliciflorus*. The length of the arrow is directly proportional to the variability included in the two components, the minimal vector length for example nutlet shape and surface indicates that the first two components contains almost no information about this element with loading score 0.03, while the loading score of the longest vector representing lamina margin reached 0.36. The angle between two arrows clarifies the correlation between them; the acute angle means positive correlation, the right angle means no correlation, while the obtuse angle means negative correlation.

Table 2. PCA variable loadings of a two-dimensions, eigenvalues, contributions and scores of the components for (14) morphological characters of the studied taxa of genus *Rumex*.

No.	Character	Axis 1	Axis 2
1.	Stem strength	0.11436	0.3907
2.	Stem branching	0.30346	-0.07759
3.	External appearance	-0.26769	0.24584
4.	Lamina composition	-0.11436	-0.3907
5.	Lamina base	-0.01687	-0.3063
6.	Lamina shape	0.049601	0.085883
7.	Lamina margin	0.36226	0.077262
8.	Lamina apex	-0.00476	0.34032
9.	Ochrea union	-0.24303	-0.16586
10.	Inflorescence type	0.7242	-0.00318
11.	Flower	0.11436	0.3907
12.	Nutlet shape	0.035623	0.10005
13.	Nutlet surface	-0.03562	-0.10005
14.	Nutlet wings	0.2774	-0.45286
Eigen-value		1.08284	0.544592
Contribution %		35.698	17.954

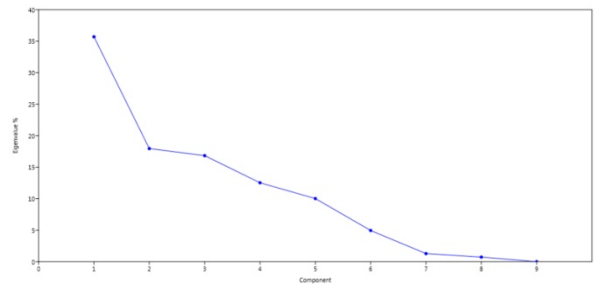

Figure 3. Scree plot indicating the percentage of explained variances *Vs.* principal components.

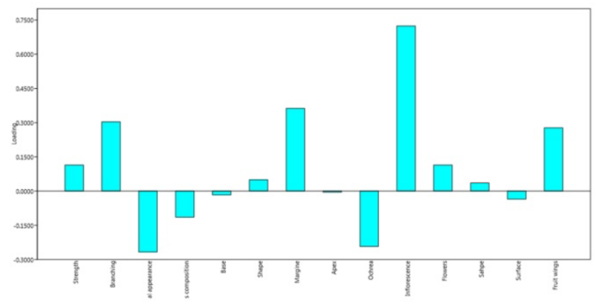

Figure 4. Loadings of morphological characters according to the first principal component (PC1).

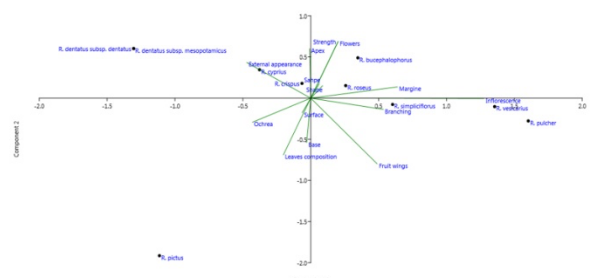

Figure 5. Principal component analysis of the studied taxa based on the morphological characters, indicating minimum spanning tree and biplot.

4 Discussions

The dendrogram (Figure 1) that was produced by the phenetic analysis based on the coded morphological character matrix shows clear clustering tendencies among the *Rumex* species under study. With a taxonomic distance of 0.6, *R. pulcher*, *R. roseus*, *R. simpliciflorus*, and *R. vesicarius* cluster together, indicating a strong affinity among them according to the UPGMA-derived phenogram. This implies that these species have a comparatively high level of morphological resemblance. Despite having a larger taxonomic distance (0.8), two pairings within this group—*R. pulcher* and *R. vesicarius* and *R. roseus* and *R. simpliciflorus*—show even greater affinity, suggesting that they have convergent evolution as a result of comparable ecological stressors or shared derived physical characteristics [3,4].

R. cyprius is the next closest species to this cluster, branching out at a distance of 0.5. This intermediate position implies that *R. cyprius* retains unique features while sharing certain morphological traits with the core group [1]. Given that *R. crispus* and *R. bucephalophorus* are located near the base of the dendrogram (0.45), it is possible that they represent ancestral or evolutionarily different lineages and differ morphologically from the other species [17].

It's interesting to note that the two *R. dentatus* subspecies form a close cluster, suggesting that there is little physical difference between them, which supports their present subspecific categorization [5]. However, with a taxonomic distance of 0.2, *R. pictus* is the oldest diverging taxon, suggesting that it may be phenetically isolated from the other members of the group due to its significant morphological uniqueness [2].

Trait dependency is clarified by the correlation study between morphological characteristics (Figure 2). Co-evolution or developmental relationship of these features is suggested by positive correlations, such as those between stem strength and flower sex and between inflorescence type and stem branching. Conversely, negative correlations suggest potential trade-offs in morphological development or different adaptation strategies across species, especially between stem strength and leaf composition or flower sex [8].

Additional dimensional reduction and depiction of morphological variation are provided by the PCA findings (Figures 3–5). A total variation of 53.6% can be explained by the first two principal components (PC1: 35.7%, PC2: 17.9%), suggesting a modest level of morphological variety resolution [11]. Characteristics like inflorescence type (loading: 0.70) are favorably correlated with PC1, which captures the most variance, whereas external appearance (-0.30) and ochrea (-0.24) are negatively correlated. While external appearance and ochrea traits vary less or in opposite directions along this component, these contrasted loadings indicate that inflorescence structure is a major characteristic that distinguishes the taxa [18].

The spatial interactions between species are shown in Figure 5's biplot and minimal spanning tree. The most morphologically different species are *R. pulcher*, *R. vesicarius*, and *R. pictus* (dissimilarity: 3.3%), which supports the previous grouping results. The dendrogram results are supported by the fact that the two *R. dentatus* subspecies are morphologically identical in PCA space. Interestingly, although being closely related in the dendrogram, *R. vesicarius* and R. *pulcher* exhibit a 1.4% PCA dissimilarity, which is a considerable difference that is probably caused by trait combinations other than PC1 and PC2 [1].

Furthermore, the PCA biplot's arrow lengths show how each attribute contributed to the variance that was seen. While nutlet form and surface (loading: 0.03) contribute very little, suggesting their low taxonomic importance in this dataset, traits such as lamina margin (loading: 0.36) have a significant impact on the main components. Relationships seen in the matrix are validated by the angle between arrows, which reflect trait correlations. Positive trait correlations are shown by acute angles, negative correlations by obtuse angles, and independence by right angles [8].

Conclusion

Patterns of morphological similarity and divergence within the subfamily Rumicoideae have been effectively clarified using the combined application of PCA, correlation matrices, and UPGMA clustering. The results highlight the taxonomic similarity of certain species pairings and the differences of others, such as R. pictus. Furthermore, several physical traits—in particular, lamina edges and inflorescence structure—emerge as important taxonomic discriminators. In addition to validating current classifications, this integrated morphometric method may help guide future taxonomic changes within the group.

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