A Numerical-Taxonomic Study of the *Juncus bufonius* Aggregate (*Juncaceae*) in Slovakia

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Abstract: Samples of 34 populations of the *Juncus bufonius* aggregate in Slovakia have been submitted to a numerical-taxonomic treatment. Three species corresponding to three known cytodesmes, i.e. *J. bufonius* L. s.str. (2n = c. 100-110), *J. ambiguus* Guss. (2n = 34) and *J. minutulus* (ALB. et JAHAN.) PAAIN et al. emend. SNOG. (2n = c. 72), have been confirmed for the study area. A survey of quantitative characters by various ordination and cluster techniques reveals that the length of capsules, seeds, inner tepals and anthers as well as the ratio of anther to filament length are significant for the segregation of the cytodesmes.

The karyotaxonomical investigations in the *Juncus bufonius* aggregate (*Juncaceae*) have revealed the existence of three cytodesmes, namely 2n = 34, 2n = c. 72 and 2n = c. 100-110 (SNOGERUP 1971, VAN LOENHOUD & STERK 1976, MIŠIETA 1980, see also HOLUB 1976). The diversity in chromosome number has promoted more intensive chorological and morphological studies of the aggregate. VAN LOENHOUD & STERK (1976) suggested the identification of the cytodesmes with three formerly described species: *J. ambiguus* Guss., *J. minutulus* (ALB. et JAHAN.) PAAIN et al. emend. SNOG. and *J. bufonius* L. s.str. respectively.

Only a small number of reliable quantitative characters are for available the segregation of the aggregate species. Furthermore, the taxonomical position of *J. minutulus* needs clarification, because of

The present study hopes to contribute to the elucidation of the taxonomical pattern of the *J. bufonius* aggregate in Slovakia, especially in regard to the position of *J. minutulus*, and to aid in the determination of its members on the basis of a set of quantitative characters selected by means of numerical-taxonomic methods.

**Methods**

Principal components analysis (PCA; see for example Sneath & Sokal 1973) and Reciprocal Averaging (RA; Hill 1973) have been adopted as ordination techniques to get an insight into the structure of the data and eventually to detect, taxonomic clusters in multidimensional character space. First, two ordination axes were examined.

Numerical-taxonomic techniques of cluster analysis have been used to bring the data into a hierarchical systems. To avoid a biased approach by adopting only one method, 7 of them have been used: Single Linkage Clustering (SLC), Complete Linkage Clustering (CLC), Average Linkage Clustering (ALC), McQuitty’s Similarity Analysis (MQSA; Weighted pair-group method using arithmetic averages sensu Sneath and Sokal l. c.), Ward’s Method (WM; Sum-of-squares clustering sensu Orloci 1967), Lance-Williams Beta-Flexible Method (LWBFM; Lance and Williams 1967), Gower’s Median Method (GMM; weighted pair-group methods using centroid). For further informations on the theoretical background and computational algorithms the works of Sneath & Sokal (l. c.), Clifford & Stephenson (1975) and Orloci (1978) should be consulted.

The computations have been executed by the programmes PCFLOR based on correlation matrix for R-type of PCA (Goldstein & Grigal 1972), DECORANA for RA (Hill 1979) and CLUSTAN package of Wishart (1978) for all the cluster analyses.

The one-way classification analysis of variance (anova) has been adopted to compare the variance within the selected sets (Sokal & Rohlf 1969). Within a set a priori tests have been performed. F-values are an aid to get information on the distribution abilities of particular characters. Nine samples (for numbers see Material), namely those 1, 18, 21 (*J. ambiguus*), 4, 24, 22 (*J. minutulus*) and 2, 10, 31 (*J. bufonius*) have been chosen arbitrary to be statistically tested by F-tests.

The methods of chromosomal countings are presented in Mičeta (1980, 1983).

**Material**

Samples of 34 populations of the *Juncus bufonius* aggregate have been chosen from various parts of Slovakia to represent all the polyploid levels within the aggregate. An atypical morphotype, viz. a sample of *J. bufonius* s. str. converging towards *J. minutulus*, some cultivated populations and a few samples from identical localities but from different collection periods have been added. The measurements were done on 15 to 25 specimens per sample at a rate