

The morphological variability in populations of *Chondrilla* was subject to the numerical analysis using the unweighted pair group method with arithmetic mean (UPGMA). The study showed that out of the seven species of the genus found in European Russia, it is only *C. ambigua* that has the status of undoubted species. A distinct difference is observed between the two groups of populations: the first group comprising *C. juncea*, *C. latifolia*, *C. brevirostris*, and the mixed population of *C. juncea* / *graminea*; and the second group comprising the populations of *C. graminea* and *C. acantholepis*. In general, all the species are poorly isolated. The factor analysis using principal coordinate analysis (PCO) yielded similar results. It is assumed that a complex pattern of interspecific variability in *Chondrilla* is due to the hybridization by facultative apomixis and / or the selection impacted by the ecotopic factors.

The genetic diversity of twenty-one populations of *Chondrilla* found in European part of Russia was subject to the analysis using the inter-sequence simple repeat method (ISSR). The cluster analysis (UPGMA) and the unrooted tree built using the neighbour joining method yielded similar results according to which the samples were subdivided into the two following groups: the first group comprising *C. ambigua* and *C. brevirostris* as the two stable sub-clusters; and the second group containing the other samples.