

**MOLECULAR TAXONOMY OF ASTERACEAE SPECIES IN THE NUROTA
PHYTOGEOGRAPHIC DISTRICT****Sindorov Abdumo‘min O‘rolbek o‘g‘li**

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Annotation: the study analyzed 85 species of the Asteraceae family distributed in the Nurota phytogeographic district to determine their molecular taxonomic position. The data were mainly downloaded from the NCBI GenBank database. At the same time, molecular markers for *Cousinia botschantzevii* Juz. ex *Tscherneva*, an endemic representative of the Nurota district, were sequenced and analyzed for the first time.

Keywords: genBank, phytogeographic, endemic, phylogenetic, internal transcribed spacer.

Annotatsiya: Tadqiqotda Nurota fitogeografik okrugida tarqalgan Asteraceae (Qoqio‘tlardoshlar) oilasiga mansub 85 ta tur molekulyar taksonomik o‘rnini aniqlash maqsadida tahlil qilindi. Ma‘lumotlar asosan NCBI GenBank ma‘lumotlar bazasidan yuklab olindi. Shu bilan birga, Nurota okrugining endemik vakili bo‘lgan *Cousinia botschantzevii* Juz. ex *Tscherneva* uchun molekulyar markerlar birinchi marta ketma-ketlikka olindi va tahlil qilindi.

Kalit so‘zlar: genBank, fitogeografik, endemik, filogenetik, internal transcribed spacer.

Аннотация: в ходе исследования было проанализировано 85 видов семейства Asteraceae, распространенных в Нуратинском фитогеографическом районе, с целью определения их молекулярно-таксономического положения. Данные были получены преимущественно из базы данных NCBI GenBank. При этом впервые были секвенированы и проанализированы молекулярные маркеры для эндемичного для Нуратинского района вида *Cousinia botschantzevii* Juz. ex *Tscherneva*.

Ключевые слова: генБанк, фитогеографический, эндемичный, филогенетический, внутренний транскрибируемый спейсер.

In this study, 85 species of the Asteraceae family distributed in the Nurota phytogeographic district were analyzed to determine their molecular taxonomic position. The data were mainly downloaded from the NCBI GenBank database. At the same time, molecular markers for *Cousinia botschantzevii* Juz. ex *Tscherneva*, an endemic representative of the Nurota district, were sequenced and analyzed for the first time. This allowed us to introduce new molecular data for this species into science.

For molecular phylogenetic analysis, widely used ribosomal DNA markers were selected. In particular, internal transcribed spacer 1 (ITS1, partial sequence), 5.8S ribosomal RNA gene, internal transcribed spacer 2 (ITS2, complete sequence), and large subunit gene (LSU rDNA) of ribosomal RNA sequences were used. These markers are effective in studying the phylogenetic relationships of the Asteraceae family due to their high resolution at the species level. One of the species *Menyanthes*

trifoliata L. (Menyanthaceae family) was used as an outgroup in constructing phylogenetic trees. This selection allowed us to determine the rooting of the tree and more accurately assess the branching within the ingroup.

The overall matrix alignment based on the obtained sequences consisted of 660 nucleotides. As a result of the analysis, the following were noted in this matrix: 201 conservative (unchanged) nucleotide positions, 51 parsimony informative sites, 62 singleton sites (see Figure 16).

The results serve to shed light on the molecular diversity of species of the Asteraceae family distributed in the Nurota phytogeographical district and their evolutionary relationships.

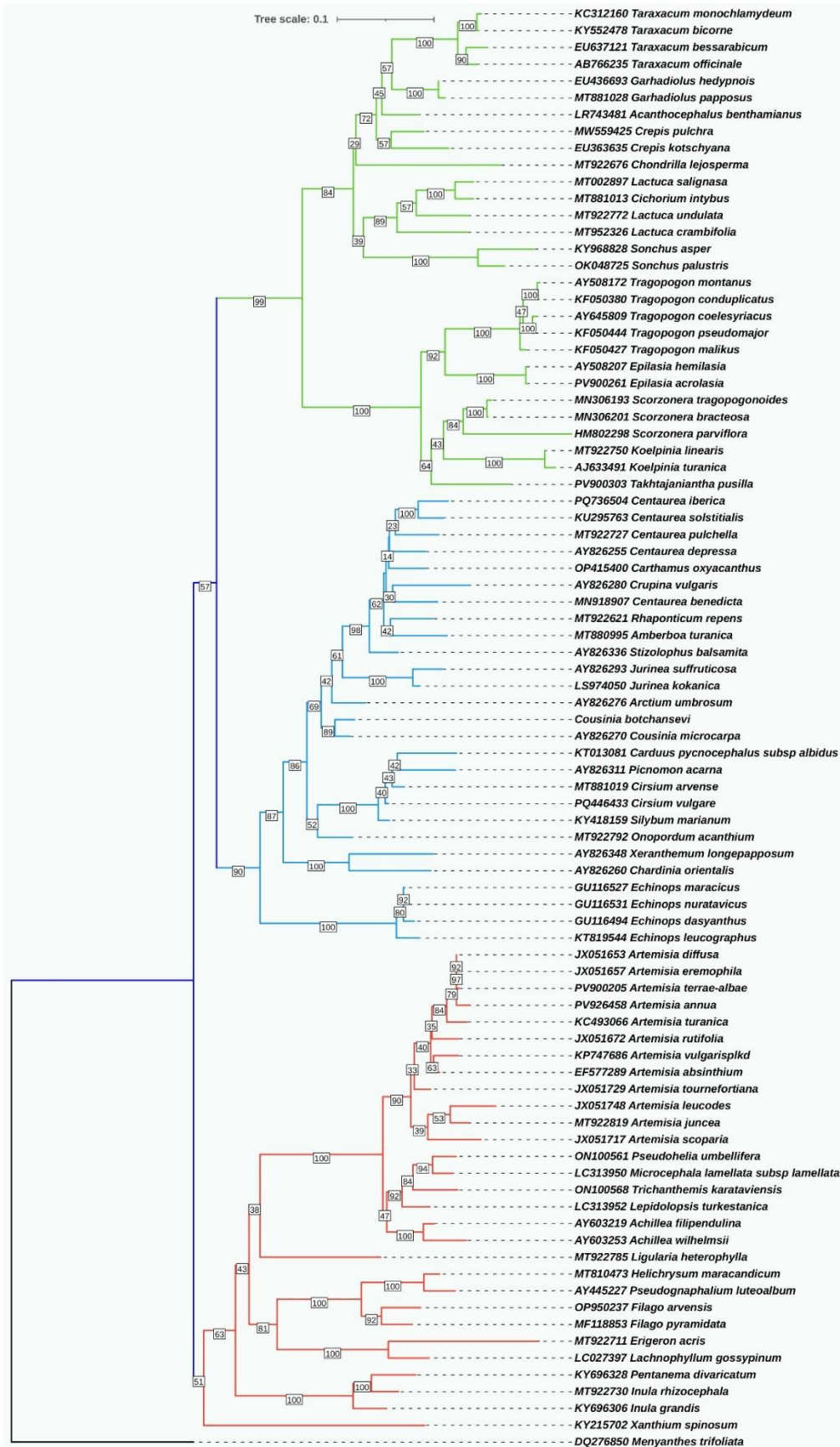
1-picture. General multiple alignment matrix of ITS nucleotide sequences of species of the Asteraceae family.

The tree shows three large, well-separated clades (see Figure 17), which correspond to the traditional subfamilies Asteroideae, Carduoideae, and Cichorioideae of the Asteraceae family. The trunk (main) branches are separated by high support, with the monophyly of Cichorioideae and Carduoideae confirmed by high/large bootstraps; the Asteroideae show extensive and diverse branching at the basal (bottom of the tree) part. Some internal nodes show moderate support (around 60–85), which may reflect rapid diversification within the tribes or the resolution limits of the ITS marker.

The basal part of the phylogenetic tree unites species belonging to the subfamily Asteroideae. This clade includes representatives of genera such as *Artemisia*, *Achillea*, *Inula*, *Filago*, *Xanthium*, *Helichrysum*. Most of them are medicinal and essential oil plants. Bootstrap values are in the range of 80–100%, and intergeneric relationships within the clade are well resolved.

The central part of the tree corresponds to the subfamily Carduoideae. This clade includes thorny plants such as *Centaurea*, *Carthamus*, *Cousinia*, *Jurinea*, *Echinops*, *Cirsium*, *Silybum*. An endemic species typical for the flora of Uzbekistan — *Cousinia bostchansévii* — was included in molecular analyses for the first time

The upper part of the phylogenetic tree corresponds to the subfamily Cichorioideae. This clade includes the genera *Taraxacum*, *Lactuca*, *Cichorium*, *Sonchus*, *Tragopogon*, *Crepis*, *Chondrilla*, *Scorzonera*. A distinctive feature of this group is the presence of milky juice in the leaves. In the tree, the species *Taraxacum officinale*, *Taraxacum bessarabicum* and *Taraxacum bicorne* were grouped together with 100% bootstrap, showing a high level of genetic similarity within the family.



2-picture. Phylogenetic tree constructed using Maximum Likelihood (ML) method based on ITS sequences of members of the Asteraceae family.

Foydalanilgan adabiyotlar ro‘yxati:

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