

SPECIES DIVERSITY OF THE *CHENOPODIACEAE* VENT. FAMILY IN THE FLORA OF THE AKTOBE FLORISTIC DISTRICT (KAZAKHSTAN)

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Abstract

Ecosystem preservation and rational use are possible only under the condition of the species diversity of its components. The *Chenopodiaceae* Vent. family is a necessary research area. Due to the abundance of species, it is actively used in agriculture, ecology, medicine, pharmacology, and public health (in many countries, including Kazakhstan), which increases the value of the research results. This work aims to identify the species diversity of the *Chenopodiaceae* Vent. in the flora of the Aktobe floristic district (Kazakhstan). The data were collected from 2017 to 2022 using the methods of route survey, analysis of herbarium collections, and literature review. In the course of the study, classical botanical, ecological, and geographical methods were applied. 78 species belonging to 25 genera were identified. Of them, seven main genera made up the bulk (67.9%) of the *Chenopodiaceae* whereas 12 genera accounted for 48.0% of the total number of genera. Among the main genera were *Salsola*, *Chenopodium*, and *Atriplex*. The study analyzes the ecological strategy of species, spectra of life forms, and habitats. Understanding the *Chenopodiaceae* Vent. Biodiversity makes it possible to develop rational methods for using natural resources of the region, in particular, for developing forage crops and understanding the mechanisms of salt and drought resistance.

Key words: Habitat, Life form, Amaranthaceae, Chenopodiaceae, Biodiversity.

Introduction

The study and conservation of bio and floral diversity are global problems (Zanina & Smirnova, 2020). The preservation of the entire global ecosystem is impossible without preserving the species diversity of its components (Kashina *et al.*, 2022).

The focus of our study was the species diversity of the *Chenopodiaceae* Vent. family. The *Chenopodiaceae* Vent. family includes halophilic floral complex, plants of disturbed habitats, weeds of crops, and synanthropic species. The *Chenopodiaceae* are characterized by significant polymorphism, ontogenetic variability, and complex systematics (Sukhorukov *et al.*, 2014; Uotila, 2013; Flowers & Colmer, 2015).

The choice of the *Chenopodiaceae* Vent. family, on one hand, is related to the fact that it is an angiosperm, and it is widely distributed throughout the globe, mainly in areas with arid climates and saline soils, typical for many countries, including Kazakhstan, Azerbaijan, Russia, and Iran (Keshavarzi & Zare, 2006). On the other hand, representatives of the family are important for understanding the evolutionary orientation of their traits and florogenesis and are of considerable scientific interest (Toderich *et al.*, 2023). Due to the external monotony, the identification of representatives of this family presents a considerable difficulty (Osmonali *et al.*, 2021). In addition, they have significant polymorphism and age variability. Therefore, many genera remain insufficiently studied.

The agricultural significance of the *Chenopodiaceae* Vent. is explained by the fact that some species are grown as food crops. For example, quinoa (*Chenopodium quinoa*)

is a highly nutritious plant that has gained worldwide popularity due to its high protein content and balance of essential amino acids (Markova & Sidorova, 2022). Understanding the genetics of these plants can lead to improved cultivation methods and increased yields. Black saxaul (*Haloxylon aphyllum*) is one of the few desert plants growing on saline soils and able to survive in a sharply continental arid climate. It survives because the density of its trunk is 2 times greater than the density of deciduous and coniferous trees of the temperate climatic zone, which increases the amount of carbon retained by managed saxaul forests compared to deciduous and coniferous forests in Russia and Europe (Akhmetov *et al.*, 2023).

As the *Chenopodiaceae* Vent. grow in harsh conditions, including salty, alkaline, and arid environments, the study of these plants provides an idea of the mechanisms of salt and drought resistance, which is becoming increasingly important in the context of climate change and sustainable agriculture in harsh conditions. The study of the *Chenopodiaceae* Vent. influences (Yessimbek *et al.*, 2022) the creation of sustainable and long-lasting protective forest plantations in the arid conditions of Kazakhstan, which remains a difficult task due to the continental climate, the great complexity of the forest-growing properties of soils, low agrotechnical quality of cultivation, and the lack of maintenance and protection measures.

The *Chenopodiaceae* family demonstrates a wide range of morphological diversity. This makes it an interesting object for evolutionary biology research, which can help to understand the evolutionary processes and genetic mechanisms that lead to such diversity. For example, the features of the anatomical structure of plant vegetative

organs adequately reflect their adaptation to growing conditions. *Haloxylon persicum* is a genetic derivative of *H. aphyllum*, which explains the mechanism of adaptation to hot and dry climates (Zhaglovskaia et al., 2015).

Some *Chenopodiaceae* species are known for their medicinal properties. For example, beetroot (*Beta vulgaris*) was studied for its beneficial effect on blood pressure and heart health (Bachheti & Bachheti, 2023). The results of published works, despite their focus on experimental studies on animals, allows us to conclude that amaranth, quinoa, and buckwheat grain, as well as grain fractions of pseudo-cereals, such as proteins and polysaccharides, can have a positive effect on the microbiota, including against the background of a high-fat diet, preventing the development of dysbiotic disorders (Markova & Sidorova, 2022). The study of these species can contribute to the development of natural health products and alternative medicines (Zayachkovskaya et al., 2021).

The *Chenopodiaceae* family is studied to determine the phytoremediation potential, since some species effectively accumulate and tolerate high levels of heavy metals. This makes them suitable for phytoremediation, i.e., the use of plants for cleaning soil, air, and water contaminated with hazardous substances (Phang et al., 2023).

Knowledge of the resistance of the *Chenopodiaceae* to recreational loads allows determining the nature and scope of their recreational use and landscaping (Ospangaliyev et al., 2023), organizing its rational use, and reducing the damage caused to nature in recreational areas. Zhamurina (2013) experimentally found that city goosefoot (*Chenopodium urbicum* L.) was resistant to trampling in recreational areas.

Botanical studies show changes in the *Chenopodiaceae* Vent., especially because they are closely related to the *Amaranthaceae* family. Since the APG II classification (Anon., 2016), the *Chenopodiaceae* has been considered a subfamily of the *Amaranthaceae*. However, not all researchers agree with separating the *Chenopodioideae* subfamily into an independent family (Fuentes-Bazan et al., 2012). Ongoing research is needed to understand plant taxonomy and the relationships between different plant families.

The review of research fields highlights the importance of the *Chenopodiaceae* family and explains why we believe that further research on the species diversity of the *Chenopodiaceae* Vent. is necessary.

This work aims to identify the species diversity of the *Chenopodiaceae* Vent. family in the flora of the Aktobe floristic district (AFD) (Kazakhstan).

Material and Methods

The object of the study is the *Chenopodiaceae* Vent. family in the AFD.

The work was based on the 2017-2022 data collected using the route method, analysis of herbarium collections, and generalization of literary data.

Classical botanical, ecological, and geographical methods were used in the study (Osmonali et al., 2021). The analysis of flora was based on a program of floristic studies of varying degrees of detail (Aipeisova et al., 2023).

A chorionomic approach was used to identify the types of flora habitats (Aipeisova et al., 2023). The types of

habitats were determined by the fact that the entire area or most of it was confined to phytochorions, established by E.M. Lavrenko and A.A. Takhtajyan (Aipeisova, 2009).

The analysis of life forms was carried out according to I.G. Serebryakov. During the analysis, types and groups of life forms and species and their number were determined (Aipeisova, 2009).

The name of the plant species was given following the summary made by S.K. Cherepanov (Agafonov & Tulsy, 2018).

Species conservation is particularly important for the steppe zone of Kazakhstan, which is an example of anthropogenic pressure on the ecosystem of an entire landscape zone, the root cause of which is the plowing of land during the development of virgin lands (Kamp et al., 2016).

The Aktobe region is of undoubted interest from a botanical and geographical point of view. Its significant part lies in the steppe zone within the junction of the Eurasian continent. The Aktobe region is one of the most significant industrial regions in Kazakhstan, characterized by an increase in the anthropogenic factor, including man-made vegetation disturbances due to intensive exploitation of oil and gas fields and an increase in the volume of quarry developments that require the activation of biodiversity conservation and the creation of a monitoring system for the flora. "Interestingly, in Kazakhstan, no more than 2% of accumulating waste is processed and utilized today" (Safarov et al., 2023).

The AFD is characterized by the complexity of the vegetation cover and soils, which determines the diversity of its floral elements. "The flora of the territories adjacent to 40 springs within the boundaries of four regions of Western Kazakhstan is represented by 252 species, 167 genera, and 55 families" (Idrissova et al., 2019).

Results and Discussion

In the spectrum of the leading families of the AFD, the *Chenopodiaceae* rank 5th (Aipeisova, 2012).

The place of the *Chenopodiaceae* in the AFD can be explained by the proximity to Northern Turan, saline habitats, the degradation of soils and vegetation due to anthropogenic influence, and, above all, the plowing of virgin lands and their current partial abandonment.

Some representatives of the family are edificers and sub-edificers of plant communities: *Anabasis salsa*, *Anabasis aphylla*, *Camphorosma monspeliaca*, *Atriplex sap*, *Salsola orientalis*, and *Kochia prostrata*.

The *Chenopodiaceae* family in the AFD is represented by 78 species belonging to 25 genera (*Agriophyllum squarrosum* (L.) Moq.; *Anabasis aphylla* L., *A. cretacea* Pall., *A. salsa* (C. A. Mey.) Benth. ex Volkens, *A. truncata* (Schrenk.) Bunge; *Arthrophyllum pulvinatum* Litv., *Atriplex calotheca* (Rafn) Fries, *A. cana* C. A. Mey., *A. crassifolia* C.A. Mey., *A. littoralis* L., *A. nitens* Schkuhr, *A. patula* L., *A. prostrata* Boucher, *A. pungens* Trautv., *A. tatarica* L.; *Axyris amaranthoides* L.; *Bassia hyssopifolia* (Pall.) O. Kuntze., *B. sedoides* (Pall.) Aschers.; *Camphorosma lessingii* Litv., *C. monspeliaca* L.; *Ceratocarpus arenarius* L., *C. utriculosus* Bluk.; *Ceratoides papposa* Botsch. et Ikonn.; *Chenopodium album* L., *C. botryodes* Smith, *C. foliosum* Aschers., *C. glaucum* L., *C. hybridum* L., *C. opulifolium* Schrad. Ex Koch et Ziz, *C.*

polyspermum L., *C. rubrum* L., *C. strictum* Roth., *C. urbicum* L.; *Climacoptera brachiata* (Pall.) Botsch.; *Corispermum declinatum* Steph. ex Iljin, *C. hyssopifolium* L., *C. orientale* Lam.; *Girgensohnia oppositiflora* (Pall.) Fenzl; *Halimione pedunculata* (L.) Aell., *H. verrucifera* (Bieb.) Aell.; *Halimocnemis sclerosperma* (Pall.) C.A. Mey.; *Halocnemum strobilaceum* (Pall.) Bieb.; *Kalidium caspicum* (L.) Ung.-Sternb., *K. foliatum* (Pall.) Moq.; *Kochia iranica* Bornm., *K. laniflora* (S. G. Gmel.) Borb., *K. prostrata* (L.) Schrad., *K. scoparia* (L.) Schrad.; *Nanophyton erinaceum* (Pall.) Bunge; *Ofaiston monandrum* (Pall.) Moq.; *Petrosimonia brachiata* (Pall.) Bunge, *P. brachyphylla* (Bunge) Iljin, *P. glaucescens* (Bunge) Iljin, *P. litwinowii* Korsh., *P. monandra* (Pall.) Bunge, *P. sibirica* (Pall.) Bunge, *P. triandra* (Pall.) Simonk.; *Polycnemum arvense* L., *Salicornia europaea* L.; *Salsola acutifolia* (Bunge.) Botsch., *S. australis* R. Br., *S. collina* Pall., *S. foliosa* (L.) Schrad., *S. laricina* Pall., *S. larisifolia* Turcz. et Litv., *S. nitraria* Pall., *S. orientalis* S.G.Gmel., *S. paulsenii* Litv., *S. soda* L., *S. tamariscina* Pall.; *Suaeda acuminata* (C.A. Mey) Moq., *S. altissima* (L.) Pall., *S. confusa* Iljin, *S. corniculata* (C. A. Mey.) Bunge, *S. dendroides* (C.A. Mey) Moq., *S. linifolia* Pall., *S. physophora* Pall., *S. prostrata* Pall.) (Aipeisova, 2012).

There are seven most prominent genera in the *Chenopodiaceae* family in the AFD (Fig. 1).

According to Fig. 1, the main part of the spectrum of the leading genera of the *Chenopodiaceae* includes *Salsola* (14.1% of the total number of species of the family), *Chenopodium* (12.8%), and *Atriplex* (11.5%). *Salsola* L. is a common genus, for example, for Armenia. It originated in South Africa no later than the Miocene, and the initial section for the genus is *Caroxylon* (Sonyan *et al.*, 2022). The number of species of the seven main genera of the *Chenopodiaceae* family in the flora of the AFD is 67.9%. The monotypic genera of the family are 12 genera that make up 48.0% of the total number of genera of the family (*Agriophyllum*, *Arthrophytum*, *Axyris*, *Ceratoides*, *Climacoptera*, *Girgensohnia*, *Halimocnemis*, *Halocnemum*, *Nanophyton*, *Ofaiston*, *Polycnemum*, *Salicornia*). Comparing the results obtained in a study conducted in the desert part of the Syrdarya River valley (Kazakhstan) (Osmonali *et al.*, 2021), we determined the species composition of the *Chenopodiaceae* family represented by 112 species belonging to 38 genera. The polymorphic genera include *Salsola* (17 species), *Atriplex* (15 species), and *Suaeda* (11 species). Genera represented by a small number of species predominate (26 genera with one or two species each). This shows that the *Chenopodiaceae* genera in Kazakhstan are characterized by general trends (for example, the leading genus *Salsola*) and distinctive characteristics (for example, the desert part of the Syrdarya River valley is characterized by a greater variety of genera, but about 67% of genera are represented by a small number of species). This highlights the need for species studies in various territories.

Representatives of the family show different ecological valence. *Atriplex littoralis* L., *Chenopodium botryodes*, *Chenopodium glaucum*, *Halimione pedunculata*, *Halimione verrucifera*, *Halimocnemis sclerosperma*, *Kalidium foliatum*, *Petrosimonia sibirica*, *Salsola nitraria*, *Salsola soda*, *Suaeda corniculata*, etc. grow on salt marshes. *Bassia sedoides*, *Petrosimonia brachyphylla*, *Petrosimonia glaucescens*, and *Salsola larisifolia* grow on alkaline salts.

Petro-calcefites include *Kochia prostrata*, *Nanophyton erinaceum*, and *Ceratoides papposa*. *Corispermum hyssopifolium* and *Corispermum orientale* grow only on sandy and sandy loam substrates, and *Anabasis cretacea* is noted in Kazakh flora only on Cretaceous massifs. In crops, deposits, vegetable gardens, and garbage places, *Axyris amaranthoides*, *Ceratocarpus utriculosus*, *Chenopodium album*, *Chenopodium glaucum*, *Chenopodium opulifolium*, *Chenopodium opulifolium*, *Chenopodium strictum*, *Corispermum declinatum*, etc. are common.

Analysis of life forms according to I.G. Serebryakov showed a clear predominance of annual plants (58 species, i.e., 74.4% of the total number of species of the family, which is 2.1% higher than the similar indicator of the flora of the desert part of the Syrdarya River valley) (Osmonali *et al.*, 2021). This is primarily a consequence of significant and prolonged anthropogenic pressure on the vegetation and soils of the AFD (Fig. 2).

According to Fig. 2, the smallest number of species was noted in shrubs (*Anabasis salsa*, *Suaeda dendroides*, *Suaeda physophora*) and semi-shrubs (*Anabasis aphylla*, *Atriplex sap*, *Athrophytum pulvinatum*, *Halimione verrucifera*, *Salsola orientalis*).

The current geographical distribution of plants reflects the complex history of the formation and settlement of species and their complexes (Mukhambetov *et al.*, 2023). A comparative study of the areas, describing their types characterized by common features, is an important step towards establishing the historical reasons for their characteristic features (Mukhanov *et al.*, 2023).

The areal analysis of the species of the *Chenopodiaceae* in the AFD showed that the species of the family were represented by 24 types of ranges out of 53 types of ranges developed by us and divided into three groups (widespread, Eurasian steppe, and ancient Mediterranean).

Among the habitat groups, the ancient Mediterranean group prevails, represented by 35 species, which is 44.9% of the total number of species of the family in the flora. This group of habitats is dominated by the Turanian type of habitat consisting of 12 species (*Halimocnemis sclerosperma* (Pall.) C.A. Mey, *Nanophyton erinaceum* (Pall.) Vilde, *Salsola nitraria* Pall., *Salsola paulsenii* Litv. etc.). Second is the European-Eastern Mediterranean type of area with seven species, such as *Chenopodium opulifolium* Schrad. ex-Koch et Ziz, *Atriplex calotheca* (Rafn) Fries, *Halocnemum strobilaceum* (Pall.) Bieb. The next in the number of species is the Eastern Ancient Mediterranean type of area with six species (*Ceratoides papposa* Botsch. et Ikonn., *Ceratocarpus utriculosus* Bluk. and others) and the Iranian-Turanian type of area with five species (*Girgensohnia oppositiflora* (Pall.) Fenzl., *Anabasis aphylla* L., *Kochia iranica* Bornm. etc.).

The Eurasian steppe group of habitats includes 31 species, 40.7% of the total number of species of the family. In this group of habitats, six species are Black Sea-Kazakh-Turanian (*Bassia sedoides* (Pall.) Aschers., *Ceratocarpus arenarius* L.). Five species are Trans-Volga-Kazakh-Turanian (*Atriplex sapa* C.A. Mey., *Atriplex crassifolia* C.A. Mey). The Black Sea-Kazakhstan type of area is represented by four species; the remaining types include from one to three species.

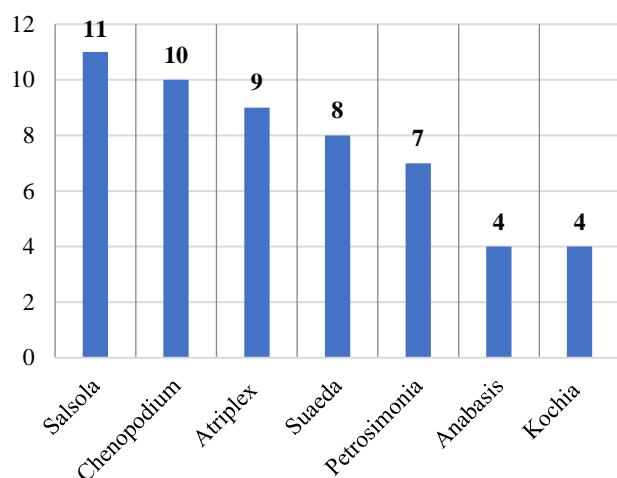


Fig. 1. Spectrum of the most prominent genera of the *Chenopodiaceae* family in the AFD.

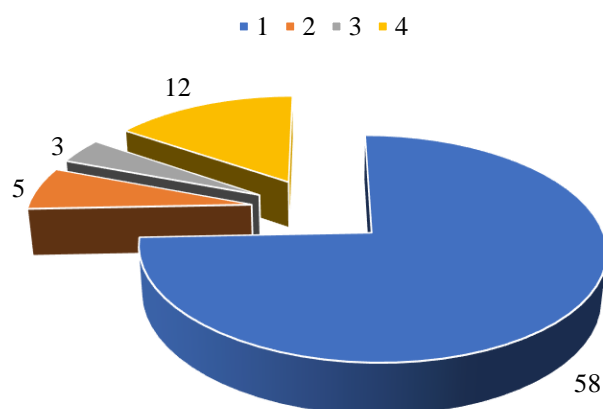


Fig. 2. The ratio of life forms according to I.G. Serebryakov.

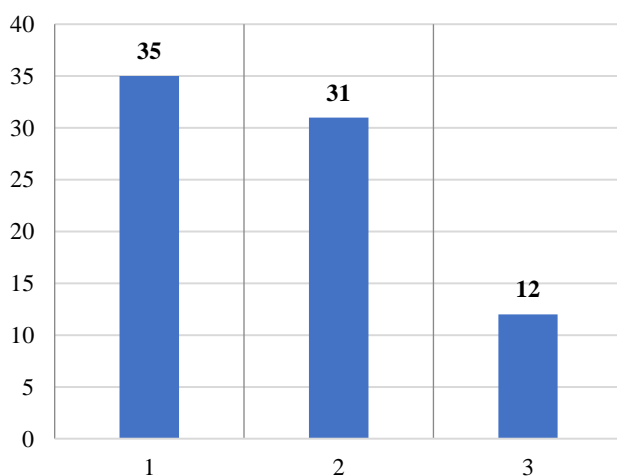


Fig. 3. Ratio of AFD area groups.

The smallest group is the widespread group of habitats with 12 species. These are species belonging to the multi-regional (*Chenopodium album* L., *Chenopodium glaucum* L.), Holarctic (*Chenopodium botryodes* Smith, *Salicornia europaea* L.), Palearctic (*Kochia scoparia* (L.) Schrad., *Chenopodium urbicum* L., *Atriplex patula* L.), Holarctic-

ancient Mediterranean (*Chenopodium rubrum* L., *Chenopodium hybridum* L.), and Eastern European-Asian types of habitats. These types of habitats include two or three species. *Arthrophytum pulvinatum* Litv. is an endemic relict species of flora. We classified this species as a part of desert-steppe Pliocene relics, along with *Anabasis cretacea* Pall., *Anabasis salsa* (C.A. Mey.) Benth. ex Volkens, and *Nanophyton erinaceum* (Pall.) Bunge. The ratio of AFD area groups is shown in (Fig. 3).

The ratio of groups and types of areas of the *Chenopodiaceae* in the AFD reflects their geographical position in the center of the continent of Eurasia in the steppe zone and the proximity to Northern Turan. This shows the heterogeneity and heterochronous character of the flora and is consistent with the history of the development of the studied area.

Economically (Shayakhmetova *et al.*, 2023), representatives of this family are fodder, medicinal, technical, food (Aslanov *et al.*, 2023), and ornamental plants, among which the group of fodder plants dominates (Karynbayev *et al.*, 2023), represented by 28 species (35.9%). These are such pasture plants as *Agriophyllum squarrosum*, *Anabasis aphylla*, *Anabasis cretacea*, *Anabasis salsa*, *Atriplex tatarica*, *Bassia sedoides*, *Climacoptera brachiata*, *Girgensohnia oppositiflora*, *Petrosimonia sibirica*, *Salsola soda*, *Nanophyton erinaceum*, and *Camphorosma monspeliaca*.

The largest number of species of the *Chenopodiaceae* Vent. family in the AFD is associated with a halophytic floral complex (61 species).

Conclusions

As a result of our study, the species composition of the *Chenopodiaceae* Vent. family was established, represented by 78 species belonging to 25 genera. The number of species of the seven leading genera of the family is 67.9% of the total number of species of the family. The head part of the spectrum of the family includes *Salsola* (11 species, 14.1%), *Chenopodium* (10 species, 12.8%), and *Atriplex* (9 species, 11.5%). Representatives of the family show different ecological valence. In the life forms determined according to I.G. Serebryakov, the annual species prevail (58 species, or 74.4% of the total number of species of the family), which is a consequence of significant and prolonged anthropogenic pressure on the vegetation and soils of the region. Chorological analysis shows the heterogeneity and heterochronicity of the flora, reflects its geographical location, and is consistent with the history of the development of the studied area.

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