

Research Article

<https://doi.org/10.31489/2026FEB3/192-200>

UDC 911:338.48 (574.1)

Received: 12.12.2025 | Accepted: 18.02.2026 | Published online: 30.09.2026

E.E. Andronov¹, T.E. Darbaeva², S.S. Bakiyev^{2*}, M.G. Kakishev², T.S. Ermekkaliev²

¹All-Russian Research Institute of Agricultural Microbiology, Saint-Petersburg, Russia;

²Makhambet Utemisov West Kazakhstan University, Uralsk, Kazakhstan

*Corresponding author: bakiyevserik@gmail.com

Study of the genus Rosehip (*Rosa*) using molecular biological methods

This study presents a molecular genetic analysis of a rosehip sample using DNA barcoding and phylogenetic approaches. The aim of the study was to identify the species based on a comparative analysis of nucleotide sequences of nuclear and chloroplast marker genes, including ITS, matK, rbcL, and trn. Genomic DNA was extracted from rosehip leaves using a modified CTAB method optimized for plant material rich in polyphenolic compounds. Target DNA fragments were amplified by polymerase chain reaction (PCR) using specific primer pairs. PCR products were visualized by agarose gel electrophoresis, purified, and sequenced using the Sanger method on an automated genetic analyzer. The resulting nucleotide sequences were edited, assembled into consensus sequences, and analyzed using SeqScape and MEGA software. Species identification was performed by comparing the sequences with those available in the GenBank database using the BLAST algorithm and by constructing phylogenetic trees. The results demonstrated 100% sequence identity for all studied genetic markers with reference sequences of *Rosa majalis*. Phylogenetic analysis confirmed that the investigated sample clustered with other representatives of this species within the genus *Rosa*. These findings indicate the high diagnostic value of the selected DNA markers for reliable molecular identification of the studied rosehip species. The integrated approach combining PCR amplification, sequencing, and phylogenetic analysis proved effective for taxonomic verification. The results may be applied in plant systematics, pharmacognosy, biodiversity studies, and quality control of medicinal plant raw materials.

Keywords: rosehip, *Rosa majalis*, DNA barcoding, PCR, sequencing, phylogenetic analysis.

Introduction

The genus *Rosa* L. (family Rosaceae) includes more than 100 species widely distributed across the temperate regions of the Northern Hemisphere. Representatives of this genus, particularly rosehips, are of significant economic and pharmacological importance due to their high content of biologically active compounds, including ascorbic acid, flavonoids, and organic acids. In this regard, accurate species identification of rosehips is of great importance for botany, pharmacognosy, and quality control of medicinal plant raw materials [1–5].

Traditional morphological methods for species identification within the genus *Rosa* are often complicated by high phenotypic variability, hybridization, and polyploidy. In recent decades, molecular genetic methods—particularly DNA barcoding—have become reliable tools for taxonomic identification of plants. The use of standard marker genes such as ITS, matK, rbcL, and trn enables accurate comparison of studied samples with reference sequences available in international databases.

The aim of this study was to perform molecular genetic identification of a rosehip sample using PCR amplification, sequencing, and phylogenetic analysis of nucleotide sequences of key marker genes. The obtained results make it possible to refine the systematic position of the studied sample, confirm its affiliation with the species *Rosa majalis*, and demonstrate the effectiveness of an integrated molecular approach in plant systematics.

Experimental

DNA Extraction from Plant Material

At the beginning of the experiment, clean rosehip leaves were dried on kraft paper at 50 °C for 60 minutes. DNA extraction was performed using a sorbitol washing buffer with 1 % DTT containing 100 mM Tris-HCl (pH 8), 0.35 M sorbitol, 5 mM EDTA (pH 8), and 1 % PVP-40. A total volume of 150 mL

of the buffer was prepared from 15 mL of 100 mM Tris-HCl, 3 mL of 5 mM EDTA, 3 g of PVP-40, 19 g of sorbitol, and 5 mL of DTT.

For cell lysis, a CTAB buffer (100 mM Tris-HCl, 3 M NaCl, 3 % CTAB, 20 mM EDTA, 1 % PVP-40, 1 % β -mercaptoethanol), preheated to 65 °C, was used [6, 7].

The extraction protocol included the following steps: grinding of rosehip leaves; washing with a DTT-containing buffer; centrifugation and removal of the supernatant; repeated washing with a buffer containing β -mercaptoethanol; addition of CTAB buffer; incubation at 65 °C; extraction with a chloroform–isoamyl alcohol mixture; DNA precipitation with isopropanol and sodium acetate; washing of the DNA pellet with ethanol; and dissolution of the DNA in TE buffer.

The obtained extracts were used for subsequent purification procedures and PCR analyses. DNA concentration was assessed by a fluorometric method and ranged from 50 to 100 ng/ μ L. Primers used for PCR amplification are presented in Table 1.

Table 1

Primer pairs used

GEN	Primer_name	Primer_seq	Size (bp)	Primer annealing temperature
MatK	MatK_390-F	CGATCTATTCATTCAATATTC	801	53°C
	MatK_1326-R	TCTAGCACACGAAAGTCGAAGT		
TRN	trnHF_05-F	CGCGCATGGTGGATTACAATCC	220	58°C
	psbA3f-R	GTTATGCATGAACGTAATGCTC		
ITS	ITS-Bel3-F	GACGCTTCTCCAGACTACAAT	757	60°C
	ITS-p5-R	CCTTATCACTTAGAGGAAGGAG		
RbcL	rbclLa-F	ATGTCACCACAAACAGAGACTAAAGC	551	62°C
	rbclr590	AGTCCACCGCGTAGACATTCAT		

The PCR reaction mixture consisted of the following components: forward primer — 1 μ L, reverse primer — 1 μ L (20 pmol/ μ L), 2 $\times$ BioMaster UDG HS-qPCR reaction mix — 12.5 μ L, nuclease-free water — 7.5 μ L, and DNA template — 3 μ L (250–500 ng). The obtained DNA samples were stored in a freezer at –20 °C [8, 9].

The PCR program was as follows: initial denaturation at 95 °C for 2 min; 30 cycles of denaturation at 95 °C for 30 s, primer annealing at 53 °C for 40 s, extension at 72 °C for 40 s; and a final extension at 72 °C for 5 min [10].

Electrophoresis of Amplification Products

Analysis of the amplified DNA fragments was performed by horizontal electrophoresis in a 1.5 % agarose gel containing an intercalating agent, ethidium bromide, used for DNA visualization. Electrophoresis was carried out in a horizontal PowerPac chamber using a Bio-Rad Electrophoretic Bath power supply. A 1 $\times$ TAE buffer was used as the running (electrode) buffer [11].

PCR Product Purification and Nucleotide Sequencing

Prior to sequencing, PCR products were purified from residual primers and deoxynucleotide triphosphates using magnetic bead-based purification with silica-coated paramagnetic particles [12]. To prepare the binding buffer, 2.00 g of PEG and 1.46 g of NaCl were dissolved in 7 mL of deionized water, mixed thoroughly, and the volume was adjusted to 10 mL. The solution was stored at room temperature.

As the elution solution, 1 $\times$ TE buffer (10 mM Tris-HCl, pH 8) or deionized water was used. For purification, 15 μ L of PCR product (1 ng/ μ L) was mixed with 15 μ L of a 0.1 % suspension of magnetic particles (1–3 μ m) in the binding buffer (20 % PEG, 2.5 M NaCl). The particles were pre-washed with 3 % HCl. The mixture was incubated for 10 minutes at room temperature with shaking (1800 rpm, 2 min).

Next, the supernatant was removed on a magnetic stand, the particles were washed twice with 70 % ethanol (100 μ L each), and DNA was eluted with the selected buffer at 60 °C for 10 minutes. After removing the particles, the purified PCR product was collected for further analysis [13].

Sequencing Reaction

The sequencing reaction was performed using the BigDye Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems) according to the manufacturer's instructions. Fragment separation was carried out on an automated genetic analyzer (3730xl DNA Analyzer (Applied Biosystems)) [12]. The read length was

900–1000 bp. Leaf samples were collected from a single plant (one bush), and no analysis of variability between different individuals or populations was performed.

Detection of PCR Products and Nucleotide Sequence Analysis

Separation of the sequenced fragments was performed on an automated genetic analyzer, 3730xl DNA Analyzer (Applied Biosystems). The obtained nucleotide sequences, amplified using forward and reverse primers, were analyzed using SeqScape 2.6.0 (Applied Biosystems) and MEGA 11 software [14–16].

Results and Discussion

Molecular Genetic Analysis of Rosehip

The analysis of amplified target DNA fragments was performed by separating the DNA fragments in a 1.5 % agarose gel in the presence of the intercalating agent ethidium bromide, which was used for subsequent DNA visualization (Fig. 1, 2).

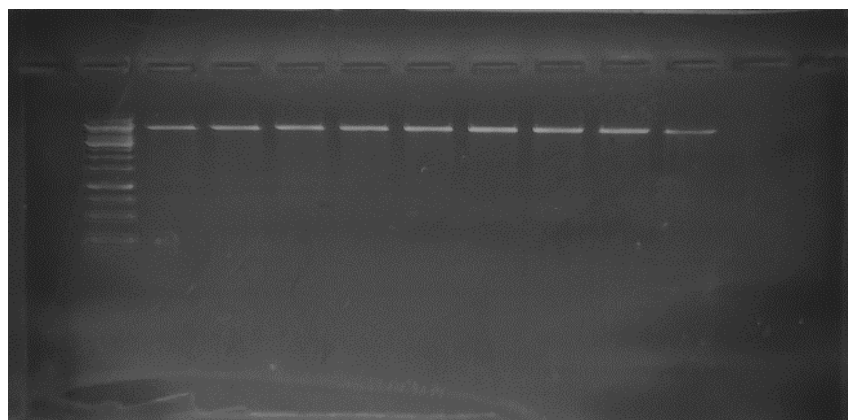


Figure 1. DNA Gel Electrophoresis

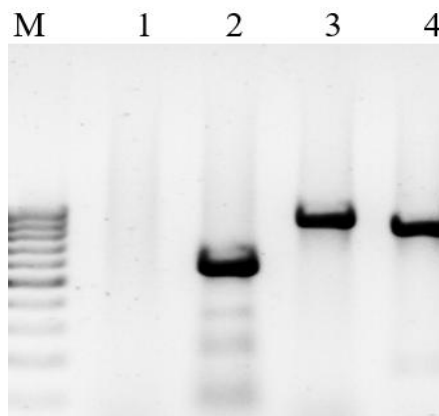


Figure 2. Gel Electrophoresis of PCR-Amplified Gene Fragments:
M — molecular weight marker (Fermentas, 100–1000 bp, 100 bp increments);
1 — negative control; 2 — *rbcL* (551 bp); 3 — *matK* (801 bp); 4 — ITS (757 bp)

The electrophoresis results confirmed that a specific fragment was amplified in all samples. No PCR products were observed in the negative control sample, indicating the absence of contamination in the reaction. Figure 2 shows the electrophoresis of the rosehip PCR products.

Figure 2 shows the amplification results, confirming the successful generation of specific fragments for the three target genes, corresponding to the expected molecular sizes.

The obtained nucleotide sequences were analyzed and assembled into a single consensus sequence using SeqMan software (DNASTAR). During processing, terminal regions—including primer sequences and low-quality fragments—were removed. Identification of the obtained sequences was carried out using the BLAST algorithm on the GenBank platform (<https://blast.ncbi.nlm.nih.gov/Blast>).

1) Nucleotide sequence of the ITS gene:

5' TGC GGAGGATCATTGTCGAAACCTGCCTAGCAGAACGACCCGAG

AACATGTTTCAACGCTTGGGGGCGGAGGGTCTTGCGGCTCTGCGCCCCCTTATCCTAGGAG
 GCAAGTGTCTTGCGCGTTGCATTTTCGGTGCTTGCGCTTGACCGACCCTCCCGGGCGTACTGAAC
 ACCGGCGTGAATTGCGCCAAGGAACCTTGAATGAAAGAGCGTTTCCCCCGCCGTCCCGGAGACG
 GTGCTCGTGCGGGTGGTTTCGTCTGCTTCAATATGTCTAAACGACTCTCGGCAACGGATATCTC
 GGCTCTCGCATCGATGAAGAACGTAGCGAAATGCGATACTTGGTGTGAATTGCAGAATCCCGT
 GAACCATCGAGTCTTTGAACGCAAGTTGCGCCCCGAAGCCATTAGGCCGAGGGCACGTCTGCCT
 GGGCGTCACACGTCTGTTGCCCCCCCCAACCCCTCGGGAGTTGGATGGGACGGATGATGGCCTC
 CCGTGTGCTCAGTCACGCGGTTGGCATAAATACCAAGTCCTCGGCGACCAACGCCACGACAATC
 GGTGGTTGTCAAACCTCGGTTTCCTGTCTGCGCGCGTGTGATCGAGTGCTTTCTTAAACAATG
 CGTGTCTGATCCGTCTGATGCTTCAACGCGACCCAGGTCAGGCGGGGTTACCCGCTGAATTTAA
 GCATATCAATAAGCGGAGGAAAAGAACTTACAAGGATTCCCTTAGTAACGGCGAGCGAACCG
 GGAATAGCCCAGCTG — 3'.

2) Nucleotide sequence of the matK gene:

5' AATTATGCATCAGATTGTACTAATTACCCTACCCCATTCATCTGG

AAATCTTGTGTTCAAACCCCTTCGCTACTGCGTGAAAGATCCCTCTTCTTTGCATTTATTACG
 GCTCTTCTTTCACGAGTATTATAATTGGAATACTCTTATTACTCCAAAAAATCCATTTTGTCAA
 AAAGTAATCAAAGATTATTCTTGCTCCTATATAATTCTTATGTATGTGAATACGAATCCATTTTA
 CTTTTCTCCGTAACCAATCTAATCATTTACGATTAACCTCTTCTGGGATTCTTTTGTAGCGAAT
 ACGTTTTTATGAAAAAATAAAATATCCTGTTGAAGAAGTCTTTGCTAACGATTTTCCGGCCACC
 TTATGGTTCTTCAAGGATCCTTTTATACAGTATGTTAGATATCAAGGAAAATCGATTCTGGCATC
 AAAAGATACTCCTCTTCTGATGAATAAAGTGGAATATTATCTTGTCCATTTTGGCAATGTCAT
 TTTTATGTATGGTCTCAACCAGGAAGATCCATATAACCAATTATCCAAGCATTCCTTGATTTTGT
 GGTATCTTTCAAGCATCGACCGAATATTTCAAGTGGTCGGATCAATTGCTAGAAAATTCGTTTTT
 ATGGATAATGCTAGAAGAAGCTTGAACATTATTTCCAATTATTCCAATGATAGGATCGTTGGCT
 AAAGTGAAATTTTGTAAACACATCAGGGCATCCTATTAGTAAGTCCAGCTGGGCGGATTGTGCGG
 ATTCTGAAATTATCGACCGAAATTGTGGCGTTATAAGGGCCGAGGGA — 3'.

3) Nucleotide sequence of the rbcL gene:

5' — GCTGGTGTAAAGATTATAAATTGACTTATTATACTCCGGATTA

TGAAACCAAAGATACTAGATATCTTGGCAGCATTTTCGAGTAACTCCTCAACCTGGAGTCCG
 CCTGAGGAAGCAGGGGCAGCGGTAGCTGCGGAATCTTCTACTGGTACATGGACAACCTGTATGGA
 CTGATGGGCTTACCAGTCTTGATCGTTACAAAGGGCGATGCTACCACATTGAACCTGTTGCTGGA
 GAAGAAAGTCAATTTATTGCTTATGTAGCTTACCCTTTAGACCTTTTGAAGAGGGTTCCGTTACT
 AACATGTTTACTTCCATTGTAGGTAATGTGTTTGGGTTCAGGCCTTGCGCGCTCTACGTCTGGAG
 GATTTACGAATCCCTACTGCTTATGTTAAACCTTTCCAAGGCCCGCCTCACGGGATCCAAGTTGA
 AAGAGATAAATTGAACAAGTATGGCCGCCCCCTATTGGGATGTACTATTAAACCTAAATTGGGG
 TTATCCGCTAAGAATTACGGTAGAGCAGTTTATGAATGTCTACGCGGTGGACTAA — 3'.

4) Nucleotide sequence of the trn gene:

5' TCCGCCCTTGTAATTTTAAATAAAAATTTAAATAAAAATAGAA

ATTACAAATATTTCCACCATTATCATTACTTGTAAAAGAGAATACAACATAAATGGAAAC
 CCTTTTATTTTAATCTTTTAGTAAAAAAGAGTACTAAAATACTAATTTAATTGAAAATACT
 AATTTAATTATAGCACTAATTTTAATTAATAATTATAGTAATTAAATTTAA — 3'.

Phylogenetic trees constructed based on the analyzed nucleotide sequences are shown in Figure 3. Figures 4–6 present a comparative analysis of the obtained sequences with nucleotide data available in GenBank for representatives of the species *Rosa majalis*.

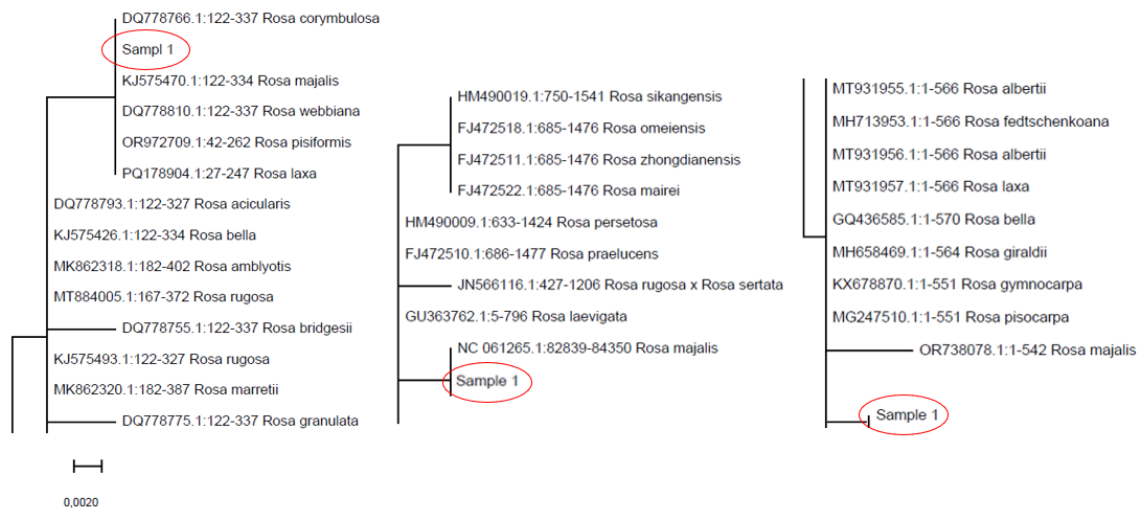


Figure 3. Phylogenetic trees constructed based on the nucleotide sequences of the genes (from left to right): trn, matK, rbcL

Analysis of the phylogenetic trees showed that the studied rosehip species clusters together with other species of the genus *Rosa*. The closest genetic relative, as demonstrated in Figure 3, is *Rosa majalis*, based on the analysis of all three investigated nucleotide gene sequences.



Figure 4. Comparative analysis of the nucleotide sequence of the ITS (internal transcribed spacer) gene region (434–504 bp)

As a result of the comparative analysis of the ITS gene nucleotide sequence of the studied rosehip sample, 100 % identity was found with the ITS gene sequences of previously identified *Rosa majalis* samples registered in the GenBank database under accession numbers MZ230091.1 and MZ230112.1.



Figure 5. Comparative analysis of the nucleotide sequence of the matK (maturase K) gene region (282–351 bp)

The comparative analysis of the matK gene nucleotide sequence of the studied rosehip sample revealed 100 % identity with the matK gene sequences of previously identified *Rosa majalis* samples registered in the GenBank database under accession numbers PQ421683.1 and NC_061265.1.

The comparative analysis of the *rbcl* gene nucleotide sequence of the studied rosehip sample revealed 100 % identity with the *rbcl* gene sequence of a previously identified *Rosa majalis* sample registered in the GenBank database under accession number OR738078.1.

Conclusion

Funding

Conflict of Interest

Authors contribution

References

- 197

- 4 Аметов А.А. Характеристика растительных сообществ с участием *Lonicera iliensis* Pojark. в условиях среднего течения реки Или / А.А. Аметов, Н.М. Мухитдинов, К.Т. Абидулова, Л.Н. Карашолакова, А. Ыдырыс // Вестник КазНУ. Серия биологическая. — 2016. — Т. 4, № 69. — С. 12–21.
- 5 Семенютина А.В. Обоснование ассортимента шиповников для обогащения лесомелиоративных комплексов в засушливых условиях / А.В. Семенютина, А.С. Соломенцева // Известия Нижневолжского агроуниверситетского комплекса: наука и высшее профессиональное образование. — 2013. — № 3 (31). — С. 74–79.
- 6 Healey A. Protocol: a simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species / A. Healey, A. Furtado, T. Cooper et al. // Plant Methods. — 2014. — Vol. 10, No. 21. DOI: <https://doi.org/10.1186/1746-4811-10-21>.
- 7 Kim C.S. A simple and rapid method for isolation of high quality genomic DNA from fruit trees and conifers using PVP / C.S. Kim, C.H. Lee, J.S. Shin, Y.S. Chung, N.I. Hyung // Nucleic Acids Res. — 1997. — Vol. 25. — P. 1085–1086. DOI: [10.1093/nar/25.5.1085](https://doi.org/10.1093/nar/25.5.1085).
- 8 Johnsen K. Phenotypic and genotypic characterization of phenanthrene-degrading fluorescent *Pseudomonas* biotypes / K. Johnsen, S. Andersen, C.S. Jacobsen // Appl. Environ. Microbiol. — 1996. — Vol. 62, No. 10. — P. 3818–3825.
- 9 Scarpellini M. Development of PCR assay to identify *Pseudomonas fluorescens* and its biotype / M. Scarpellini, L. Franzetti, A. Galli // FEMS Microbiol. Lett. — 2004. — Vol. 236 (2). — P. 257–260. DOI: [10.1016/j.femsle.2004.05.043](https://doi.org/10.1016/j.femsle.2004.05.043).
- 10 Ramesh R. Polymerase chain reaction / R. Ramesh, A. Munshi, S.K. Panda // Natl Med J India. — 1992. — Vol. 5, No. 3. — P. 115–119.
- 11 Lee P.Y. Agarose gel electrophoresis for the separation of DNA fragments / P.Y. Lee, J. Costumbrado, C.Y. Hsu, Y.H. Kim // J. Vis. Exp. — 2012. — No. 62. — Article e3923. DOI: [10.3791/3923](https://doi.org/10.3791/3923).
- 12 Eren K. DNA sequencing methods: from past to present / K. Eren, N. Taktakoğlu, I. Pirim // Eurasian J. Med. — 2022. — Vol. 54. — P. 47–56. DOI: [10.5152/eurasianjmed.2022.22280](https://doi.org/10.5152/eurasianjmed.2022.22280).
- 13 Chen Y. Magnetic particles for integrated nucleic acid purification, amplification and detection without pipetting / Y. Chen, Y. Liu, Y. Shi, J. Ping, J. Wu, H. Chen // Trends Anal. Chem. — 2020. — No. 127. — P. 115912. DOI: [10.1016/j.trac.2020.115912](https://doi.org/10.1016/j.trac.2020.115912).
- 14 Liu G-Q. The molecular phylogeny of land plants: progress and future prospects / G-Q. Liu, L. Lian, W. Wang // Diversity. — 2022. — Vol. 14, No. 10. — P. 782. DOI: <https://doi.org/10.3390/d14100782>.
- 15 Edwards S.V. Natural selection and phylogenetic analysis / S.V. Edwards // Proc. Natl. Acad. Sci. U.S.A. — 2009. — Vol. 106, No. 22. — P. 8799–8800. DOI: <https://doi.org/10.1073/pnas.0904103106>.
- 16 Bakiyev S.S. Isolation, identification, and characterization of pathogenic *Aeromonas hydrophila* from critically endangered *Acipenser baerii* / S.S. Bakiyev, I. Smekenov, I. Zharkova, S. Kobegenova, N. Sergaliyev, G. Absatirov, A. Bissenbaev // Aquaculture Reports, 26, 101293. — 2022. — P. 1–11.

Е.Е. Андронов, Т.Е. Дарбаева, С.С. Бакиев, М.Г. Какишев, Т.С. Еремеккалиев

Молекулалық-биологиялық әдістерді қолдану арқылы *Rosa* (итмұрын) туысының түрін зерттеу

Зерттеу жұмысында итмұрын өсімдігінің үлгісіне молекулалық-генетикалық талдау жүргізіліп, ДНҚ-баркодтау және филогенетикалық әдістер қолданылды. Зерттеудің мақсаты — ITS, matK, rbcL және trn ядролық және хлоропластық маркерлік гендерінің нуклеотидтік тізбектерін салыстырмалы талдау арқылы өсімдіктің түрлік сәйкестігін анықтау. Геномдық ДНҚ итмұрын жапырақтарынан полифенолдарға бай өсімдік материалдарына бейімделген модификацияланған ЦТАБ-әдісімен бөлініп алынды. Мақсатты ДНҚ фрагменттері полимеразды тізбекті реакция әдісімен арнайы праймерлерді қолдана отырып амплификацияланды. ПТР өнімдері агарозды гель электрофорезі арқылы талданып, кейін тазартылып, автоматтандырылған генетикалық анализаторда Sanger секвенирлеу әдісімен секвенирленді. Алынған нуклеотидтік тізбектер өңделіп, консенсус-тізбектерге біріктірілді және SeqScape пен MEGA бағдарламалары арқылы талданды. Түрлік идентификация GenBank деректер базасымен BLAST алгоритмі көмегімен салыстыру және филогенетикалық ағаштар құру арқылы жүзеге асырылды. Зерттеу нәтижелері барлық зерттелген генетикалық маркерлердің *Rosa majalis* түрінің тізбектерімен 100 % сәйкестігін көрсетті. Филогенетикалық талдау зерттелген үлгінің *Rosa* туысына жататын *Rosa majalis* түрімен бір кластерде топтасатынын растады. Алынған нәтижелер итмұрын түрлерін молекулалық деңгейде дәл анықтауда қолданылған маркерлердің жоғары тиімділігін көрсетеді.

Кілт сөздер: итмұрын, *Rosa majalis*, ДНҚ-баркодтау, ПТР, секвенирлеу, филогенетикалық талдау.

Е.Е. Андронов, Т.Е. Дарбаева, С.С. Бакиев, М.Г. Какишев, Т.С. Еремеккалиев

Исследование вида рода *Rosa* (шиповник) с применением молекулярно-биологических методов

В работе представлен молекулярно-генетический анализ образца шиповника с использованием методов ДНК-баркодирования и филогенетического анализа. Целью исследования являлась видовая идентификация растения на основе сравнительного анализа нуклеотидных последовательностей ядерных и хлоропластных маркерных генов ITS, matK, rbcL и trn. Геномную ДНК выделяли из листьев шиповника с применением модифицированного ЦТАБ-метода, оптимизированного для растений с высоким содержанием полифенолов. Амплификация целевых фрагментов проводилась методом полимеразной цепной реакции с использованием специфических праймеров. Полученные ПЦР-продукты анализировали с помощью агарозного гель-электрофореза, после чего очищали и подвергали секвенированию методом Sanger на автоматическом генетическом анализаторе. Нуклеотидные последовательности были отредактированы, собраны в консенсус-последовательности и проанализированы с применением программных пакетов SeqScape и MEGA. Видовую принадлежность устанавливали на основе сравнительного анализа с базой данных GenBank с использованием алгоритма BLAST, а также посредством построения филогенетических деревьев. Результаты показали 100 % идентичность всех исследованных генетических маркеров с последовательностями вида *Rosa majalis*. Филогенетический анализ подтвердил кластеризацию исследуемого образца с представителями данного вида рода *Rosa*. Полученные данные свидетельствуют о высокой информативности использованных маркерных генов для молекулярной идентификации шиповника и подтверждают эффективность комплексного подхода, сочетающего ПЦР, секвенирование и филогенетический анализ. Результаты исследования могут быть использованы в систематике растений, фармакогнозии, а также при контроле подлинности лекарственного растительного сырья.

Ключевые слова: шиповник, *Rosa majalis*, ДНК-баркодирование, ПЦР, секвенирование, филогенетический анализ.

References

- 1 Ivashchenko, A.A. (2009). *Rastitelnyi mir Kazakhstana* [The flora of Kazakhstan]. Almaty: Almaty kitap baspasy [in Russian].
- 2 Pavlov, N.V. (1961). *Flora Kazakhstana* [Flora of Kazakhstan]. Nauka [in Russian].
- 3 Muranets, A.P., Yesimseitova, A.K., Dyusembekova, D.A., Nurtaza, A.S., Kalybaev, K.R., Kozhanov, K.Z., & Kakimzhanova, A. A. (2022). Izuchenie bioraznoobraziia dikorosov roda *Rosa* L. v Kazakhstane i ikh molekuliarno-geneticheskaia identifikatsiia [Study of the biodiversity of wild plants of the genus *Rosa* L. in Kazakhstan and their molecular genetic identification]. *Vestnik Evraziiskogo natsionalnogo universiteta imeni L.N. Gumileva. Seriya Biologicheskie nauki — Bulletin of L.N. Gumilyov Eurasian National University. Bioscience Series*, 139(2), 44–60. <https://doi.org/10.32523/2616-7034-2022-139-2-44-60> [in Russian].
- 4 Ametov, A.A., Muhitdinov, N.M., Abidkulova, K.T., Karasholakova, L.N., & Ydyrys, A. (2016). Kharakteristika rastitelnykh soobshchestv s uchastiem *Lonicera iliensis* Pojark. v usloviakh srednego techeniia reki Ili [Characteristics of plant communities with the participation of *Lonicera iliensis* Pojark. in the conditions of the middle course of the Ili River]. *Vestnik Kazakhskogo Natsionalnogo Universiteta. Seriya biologicheskaya — Bulletin of the Kazakh National University. Biology Series*, 4(69), 12–21 [in Russian].
- 5 Semenyutina, A.V., & Solomentseva, A.S. (2013). Obosnovanie assortimenta shipovnikov dlia obogashcheniia lesomeliorativnykh kompleksov v zasushlivykh usloviakh [Substantiation of the assortment of dog-rose for enrichment of forest reclamation complexes in arid conditions]. *Izvestiia Nizhnevolzhskogo agrouniversitetskogo kompleksa: nauka i vysshee professionalnoe obrazovanie — Proceedings of Lower Volga Agro-University Complex: Science and Higher Vocational Education*, 31(3), 74–79 [in Russian].
- 6 Healey, A., Furtado, A., Cooper, T., & Henry, R. J. (2014). Protocol: A simple method for extracting next-generation sequencing quality genomic DNA from recalcitrant plant species. *Plant Methods*, 10(21). <https://doi.org/10.1186/1746-4811-10-21>
- 7 Kim, C.S., Lee, C.H., Shin, J.S., Chung, Y.S., & Hyung, N.I. (1997). A simple and rapid method for isolation of high quality genomic DNA from fruit trees and conifers using PVP. *Nucleic Acids Research*, 25(5), 1085–1086. <https://doi.org/10.1093/nar/25.5.1085>
- 8 Johnsen, K., Andersen, S., & Jacobsen, C.S. (1996). Phenotypic and genotypic characterization of phenanthrene-degrading fluorescent *Pseudomonas* biotypes. *Applied and Environmental Microbiology*, 62(10), 3818–3825. <https://doi.org/10.1128/aem.62.10.3818-3825.1996>
- 9 Scarpellini, M., Franzetti, L., & Galli, A. (2004). Development of PCR assay to identify *Pseudomonas fluorescens* and its biotype. *FEMS Microbiology Letters*, 236(2), 257–260. <https://doi.org/10.1016/j.femsle.2004.05.043>

- 10 Ramesh, R., Munshi, A., & Panda, S.K. (1992). Polymerase chain reaction. *The National Medical Journal of India*, 5(3), 115–119.
- 11 Lee, P.Y., Costumbrado, J., Hsu, C.Y., & Kim, Y.H. (2012). Agarose gel electrophoresis for the separation of DNA fragments. *Journal of Visualized Experiments*, (62), Article e3923. <https://doi.org/10.3791/3923>
- 12 Eren, K., Taktakoğlu, N., & Pirim, I. (2022). DNA sequencing methods: From past to present. *The Eurasian Journal of Medicine*, 54, 47–56. <https://doi.org/10.5152/eurasianjmed.2022.22280>
- 13 Chen, Y., Liu, Y., Shi, Y., Ping, J., Wu, J., & Chen, H. (2020). Magnetic particles for integrated nucleic acid purification, amplification and detection without pipetting. *Trends in Analytical Chemistry*, 127, Article 115912. <https://doi.org/10.1016/j.trac.2020.115912>
- 14 Liu, G.Q., Lian, L., & Wang, W. (2022). The molecular phylogeny of land plants: Progress and future prospects. *Diversity*, 14(10), 782. <https://doi.org/10.3390/d14100782>
- 15 Edwards, S.V. (2009). Natural selection and phylogenetic analysis. *Proceedings of the National Academy of Sciences*, 106(22), 8799–8800. <https://doi.org/10.1073/pnas.0904103106>
- 16 Bakiyev, S.S., Smekenov, I., Zharkova, I., Kobegenova, S., Sergaliyev, N., Absatirov, G., & Bissenbaev, A. (2022). Isolation, identification, and characterization of pathogenic *Aeromonas hydrophila* from critically endangered *Acipenser baerii*. *Aquaculture Reports*, 26, Article 101293. <https://doi.org/10.1016/j.aqrep.2022.101293>

Information about the authors

Andronov Evgeny Evgenievich — Doctor of Biological Sciences, All-Russian Research Institute of Agricultural Microbiology, Saint-Petersburg, Russia; e-mail: andronovevgeney64@gmail.com, ORCID: <https://orcid.org/0000-0002-5204-262X>

Darbaeva Talshen Esenomanovna — Doctor of Biological Sciences, Professor at the Faculty of Natural Geography, Makhambet Utemisov West Kazakhstan University, Uralsk, Kazakhstan; e-mail: dtalshen@mail.ru; ORCID <https://orcid.org/0000-0003-2950-0423>

Bakiyev Serik Samigullovich (contact person) — PhD, Faculty of Natural Geography, Makhambet Utemisov West Kazakhstan University, Uralsk, Kazakhstan; e-mail: bakiyevserik@gmail.com; ORCID: <https://orcid.org/0000-0001-5095-6869>

Kakishev Murat Galikhanovich — PhD, Makhambet Utemisov West Kazakhstan University, Uralsk, Kazakhstan; e-mail: kakishev_murat@mail.ru, ORCID: <http://orcid.org/0000-0002-4601-4921>

Ermekkaliev Taras Serikkalievich — Master of Natural Sciences, Faculty of Natural Geography, Makhambet Utemisov West Kazakhstan University, Uralsk, Kazakhstan; e-mail: ermekkaliev_07@mail.ru; ORCID: <https://orcid.org/0000-0003-0831-1017>