



DNA Bar-coding Technology in Belarus: Perspectives and Needs

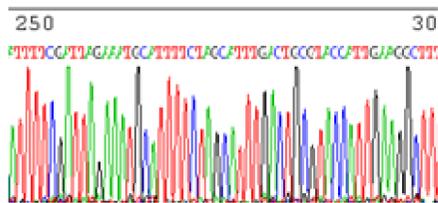
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- Biological diversity of the Republic of Belarus is represented by 500 animal species and 14 000 plant species, including 4100 of higher plants (1400 aboriginal species), 442 of bryophytes, 669 of lichens and more than 9 000 species of lower plants (algae and fungi). About 50 wild plants of aboriginal species have vanished over the last 100 years. 93,1% of Belarus territory is covered by flora, including 30% of the forest area;
- There are 50 unique protected areas in Belarus, including 5 National Parks and one Biosphere Preservation supported by UNESCO;
- Conservation of biological diversity is supported by the Belarus Government. The National Herbarium, the Bank of Plant Genetic Resources, the Republican DNA Bank and other collections are funded from the State budget;
- The Republican DNA Bank is recognized by the Council of Ministers of the Republic of Belarus as National Heritage;
- DNA-barcoding technique is taken as a basic approach to the species identification and genetic resources' inventory. In Belarus, access to genetic resources is regulated by the Nagoya Protocol to the Convention on Biological Diversity.

The Institute of Genetics and Cytology initiated use of a DNA-barcoding technique for taxonomy, including research in rare and endangered species. A plant DNA collection of 35 species (33 species among them belong to rare and endangered species) was first created at the Republican DNA Bank. The biological material was collected without removal of the whole plant from the places of its growing (two National Parks: Narochansky and Belovezhskaya Puscha). The list of those species is shown below.

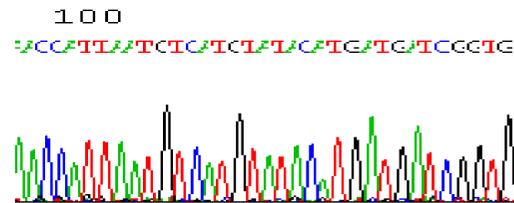
To conduct identification of plant genus, species and sub-species taxonomic categories the following plastid (*rbcl*, *matK* and *psbA-trnH*) and nuclear (ITS2) markers were used.

Anacamptis morio (ITS2)



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TCGACGCAAGTTGCGCCTGAGGCCAGCTGGCCAAGGGCAGTCCGCTGGGCGTC
AAGCATTGTGTCGCTCCATAGGACCTTCGCGGCCACGCGGCTGTCTCATCATGGAT
GCGGAGAATGGCCTGTCATGCGCTTATGTGTGGCTGGCTGAAGAGCGGGATGATAC
TCTCTTGGCAATGGCCGATTAATGGGTGGGATGGAAGCCCGTTGATTTCATCGTCC
GGTTGCTCTGAGAAATTATTGGATATTCCAGCTAACCCAATACAGTTGTCTATCGCAAG
ACAATTGACTGCGACCCCAGGATGGGCGGGATGACCCGCTGAGTTAAGCATATCA
ATAAGCGGAGGAGAAGAACTTACGAGGATTCCCCTAGTAACGGCGAGCGAACCGG
GATTTGCCAGCTTGGGAATCGGGCTGCTTWTGCGGCTCGAATTGTAGTCTGRAGA
AGCGTCA
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Dáphne cneórum (ITS2)

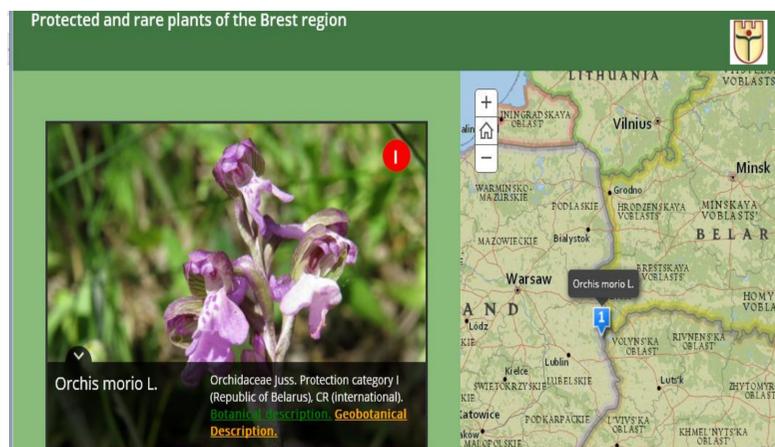


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ATYTGMAWTTTGTTRAGCATTACAACATTAGTTGGTGTAAAGGCTGGTAATGGCTCTC
CGTCCTCGTAGTAGTGCAGTTGGCTGAAATAGAGTAACCATTAATGTCATGTATACATG
ATGATCGGTGGTTTGTCTTGGCTTACCCTCGTTAAGTTATCATGTATAGCATGTCCATTGC
ACTTGGTTGCATTTTACTTCAAACTTTGTTTGAAGATAGTATGCATTGCGACCCCAG
GTCATACCCGCTGAGTTTAAAGCATATCAATAAGCGGAGGAGAAGAACTTACGGATTC
CCTTAKGAACGGCGAGCGAACCCGGAATAGCCCAGCTTAAAAATCGGTTGCCTTGGT
TTCCGAATTTGTAGTCKGGAGAARCGTCYACAA
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Orchys insectifera voucher NMW6053 5.8S ribosomal RNA gene, partial sequence; internal t	448	448	90%	1e-122	85%	KX166535.1
Orchys insectifera voucher NMW6052 5.8S ribosomal RNA gene, partial sequence; internal t	448	448	90%	1e-122	85%	KX166534.1
Anacamptis morio internal transcribed spacer 2 (ITS2)	433	433	49%	3e-118	100%	Z94092.1
Anacamptis cf. coriophora AG-2017 voucher AG 2773 small subunit ribosomal RNA gene, pa	418	418	68%	9e-114	90%	KU931737.1

Daphne mezereum voucher NMW4372 5.8S ribosomal RNA gene, partial sequence; internal transcribed sp	643	643	90%	0.0	99%	KX166606.1
Daphne mezereum voucher NMW269 5.8S ribosomal RNA gene, partial sequence; internal transcribed spa	643	643	90%	0.0	99%	KX166420.1
Daphne laureola voucher NMW4371 5.8S ribosomal RNA gene, partial sequence; internal transcribed spa	496	496	90%	3e-137	91%	KX166607.1

The DNA-barcoding technique used for the *Dáphne cneórum* plant genome analysis revealed the following mistake made by the taxonomist: the comparison of nucleotide sequences received for the *Dáphne cneórum* sample with the NCBI database resulted in the identification of that sample as *Daphne mezereum* (see the pictures shown above). We consider that result as evidence that a DNA-barcoding technique should be included in the list of taxonomic tools used for the taxonomic identification of biological objects. Training support in that area for our specialist is very welcome!



A cartographic map for rare and endangered plant species has been developed