

POPULATION AND EVOLUTIONARY GENETICS OF SPRUCES OF THE PALAEARCTIC

Population and evolutionary genetics of spruces of the Palaeartic. Grigorij G. Goncharenko, Vladimir E. Padutov. National Academy of Sciences of Belarus, Forest Institute, Gomel 2001, 196 pp. [In Russian].

The book offers a novel insight on the evolutionary relationships between spruces of the Palaeartic region based on population genetic parameters of individual species in the region. Geographically, the Palaeartic region is defined as the area encompassing the European continent, the Mediterranean fragment of North Africa and northwestern part of the Asian continent.

The authors made a successful attempt to elucidate the degree of intraspecific differentiation, intensity of gene flow within investigated populations, phylogenetic and evolutionary relationships within and between species inhabiting this huge territory. The above aspects of spruce genetics have not been investigated yet despite of enormous ecological and economic significance of all the six species compared which occur as the main components of forests between Baltic sea and Pacific ocean. Of the 7–12 *Picea* species distributed naturally in the Palaeartic region, the authors undertook analysis of *P. abies* (L.) Karst., *P. obovata* Ledeb., *P. orientalis* (L.) Link., *P. schrenkiana* Fisch et Mey, *P. ajanensis* (Lindl. Et Gord) Fisch. ex Carr. and *P. glehnii* Mast. only. The botanic and geographic treatments of individual species are given with regard to their distribution, relationships with other species and taxonomy. A broadly discussed problem is in this context the taxonomic status of *P. abies* and *P. obovata* with emphasis on a zone of introgression between them which extends from the Belarus to the foot of the Ural Mountain Ridge. The pertinance of *P. orientalis* to the section *Eupicea* or *Omorica* is another aspect which stands in the very center of the authors' attention when treating this species from Caucasus. A role of *P. ajanensis* as an intermediate form between spruces of southern China and *Picea* species from the north-western part of North America is discussed in case of this representative of the Far East of Russia, Northern China, Korea and Japan.

After introductory chapter, the two separate parts follow dealing with methodical approaches in population and evolutionary studies and with commonly used isoenzyme starch gel electrophoresis. The most frequently used population genetic characteristics are in this context defined as well as the basic principles and methods of enzyme extraction, electrophoretic separation and histochemical detection. A core of the study is obviously represented by the chapter four containing the results of population genetic studies of individual species of spruces. Altogether 23 natural populations of *P. abies* from Eastern Europe, Belarus, Latvia and Russia are analyzed along with 4 populations of *P. obovata* from Asian side of the Ural Mountain Ridge, 7 populations of *P. schrenkiana* from the Tjan-Shan region, 5 populations of *P. ajanensis* from the Far East of Russia, 3 populations of *P. glehnii* from the island Sachalin and 4 populations of *P. orientalis* from Caucasus, respectively. The corresponding number of sampled trees of individual species ranged from 46 of *P. glehnii*, 80 trees of *P. orientalis*, 94 trees of *P. ajanensis*, 130 trees of *P. obovata* and 184 trees of *P. schrenkiana* to 822 trees of *P. abies*. Fifteen enzyme systems analyzed so far were

found to be encoded by 25 loci in all the six species investigated. Except for the basic genetic characteristics, the most polymorphic loci are given for each species along with a schematic illustration of the results of cluster analysis of their populations based on Nei's coefficient of genetic distance. A detailed genetic analysis revealed more than 90 % of genetic variation to be concentrated within populations as compared with only 3 % of genetic variation detected between populations of *P. abies*, *P. glehnii* and *P. orientalis*. The analysis resulted in delineation of 2 zones of introgression between *P. abies* and *P. obovata* as well as in finding considerable resources of genetic variation in *P. abies*, *P. obovata*, *P. ajanensis* and *P. glehnii*. A narrowed genetic variation has on the other hand been reported for *P. schrenkiana*, whereas the genetic resources of *P. orientalis* are estimated by the authors as very limited.

There was observed a close correlation between the extent of genetic variation of investigated species and size of their habitats. Based on the results of isoenzyme analysis, the generally postulated western border of *P. obovata* distribution on the Ural Mountain Ridge was shown by the authors to be shifted much more to the East, e. g. to the area of the rivers Ob and Irtisch. Accordingly, the hybrid form between *P. abies* and *P. obovata* was reported to exhibit a high degree of similarity to *P. abies* deviating profoundly from the typical populations of *P. obovata* in central Siberia. Owing to the very broad zone of introgression, the authors recommend the name of *P.x medioxima* for the hybrid form instead of *P.x fennica* used until now, mainly because of its occurrence beyond the area typical for the latter.

Evaluating evolutionary and phylogenetic relationships between investigated species in the closing section of the book, the authors present 3–12 diagnostic genes discriminating between individual species. The species *P. abies* and *P. obovata* were shown to exhibit the highest degree of genetic affinity. *P. orientalis* differs from both the above species by 5 loci, whereas *P. schrenkiana* by 10 loci. Considerable divergence has also been revealed between the pair of species *P. glehnii* – *P. ajanensis* (5 loci) and *P. schrenkiana* – *P. orientalis* (6 loci). The relationships derived in this way are broadly discussed with the classical taxonomic accounts of *Picea* species, preferentially with those proposed by the Russian and Soviet authors who have been concerned with spruces on the respective area in the past. The contribution of the book in the field of spruce taxonomy including population genetics of selected group of species is obvious. Its most remarkable feature is a deep insight into genetic variation of the spruces across a huge territory of the Euro-Asia. Involving into comparison the species with large habitats along with those with scattered occurrence gives an idea of diversity within the genus *Picea* as well as of the contribution of its representatives in maintaining diversity of the world's forests.

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