Genetic Structure and Variation in *Pinus sylvestris* L. Populations Degrading Due to Pollution-induced Injury

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Abstract

The comparative study of genetic variation and differentiation of Ukraine's south-eastern five marginal *Pinus sylvestris* L. populations (which are differently damaged by emissions of large chemical enterprises producing mineral fertilizers, plastics and organic dyes and are degrading through it) was performed using the electrophoretic analysis of 9 gene-enzymous systems, encoded by 22 loci. About 82% of *P. sylvestris* genes have been found to be in a polymorphic state and each tree is on the average heterozygous in 22.3% of its genes. In the most degrading population which is 0.3 km from the main provenances of air pollutants mean indices of genetic polymorphism were lower, a number of alleles per a locus – by 18%, genotypes – by 13%, observed heterozygosity – by 12% and expected one – by 9% compared to the far removed population (more than 100 km). Those mean indices in two damaged-degrading populations were also by 7.9% to 16.7% lower than in three populations of the background and not polluted zone. The populations under consideration are weakly differentiated, NEI's genetic distance coefficient varied within 0.004 to 0.014, accounting at an average for 0.008. For the population degrading due to the untimely elimination of trees, damaged by pollutants, the values of these coefficients compared with the rest four populations did not exceed the average level.

Key words: Enzyme gene marker, heterozygosity, genetic diversity, genetic distance, *Pinus sylvestris* L.

Introduction

In the zones of dispersions from large steelworks, chemical plants and other industrial enterprises air pollution reaches the level, causing digression and quite often – degradation of forest ecosystems (SMITH, 1985; KORSHIKOV et al., 1995). In local regions damaging emissions, acting as a stress-selective factor, can change a population-and-genetic structure of species-edificators of these ecosystems at the expense of untimely death of the most susceptible individuals (KORSHIKOV, 1996; SCHOLZ, 1989; GEBUREK et al., 1987). Thus, the impoverishment of the gene pool was observed in populations of conifers, exposed to constant acute impact of emissions from large industrial enterprises, dealing with thermal treatment of mineral and organic raw materials (GEBUREK et al., 1987; PRUS-GLOWACKI and NOWAK-BZOWY, 1991; PRUS-GLOWACKI and GODZIK, 1991; BAKHTIYAROVA et al., 1995). It is considered that population systems of woody plants with high genetic diversity are more viable and have better adaptation capacities to unfavourable conditions of industrially polluted environment (SCHOLZ, 1989; SCHULTZE, 1990; PRUS-GLOWACKI and GODZIK, 1991). It is rather problematic to determine a degree of natural factors impact and stress-emission effects on the evolutionary-and-genetic processes in populations of arboreal plants (SCHOLZ, 1988). For this comparative assessment of genetic variation main parameters and of a structure of populations which differ significantly in the level of industrial air pollution impact should be performed in one ecological-and-geographical region (SCHULTZE, 1990; KORSHIKOV, 1996).

The aim of our study was to conduct a comparative analysis of the genetic variation and of the structure of *Pinus sylvestris* L. populations, degrading due to damaging effect of emissions from large chemical enterprises and which are not exposed to their effect in the south-east of Ukraine.

Materials and Methods

Small isolated populations of *Pinus sylvestris* from residual pine stands of the Kremenskoye wood, located in the second sandy terrace of the Severskiy Donets river on the territory of Rubezhansk-Severodonetsk-Lisichansk industrial agglomeration were the objects of our investigations. Trial plots (A, B and G) were laid in 1988 respectively 0.3 km, 2 km and 15 km from big chemical enterprises, producing nitrogenous fertilizers and plastics, the emissions of which are a complex mixture of organic and inorganic compounds, where toxic gases – ammonia, oxides of nitrogen and sulphur dominate. 30 kilometres from those plants there was laid the trial plot C, it was 2 km from the factory, producing organic dyes. The trial plot IX was laid in the Upper Severskiy Donets, more than 100 km from the emissions' provenance. The plantations studied are mainly presented by pure 60 to 80 and 100-year old pine stands. The peculiarity of the trial plot A is that about 50% of plants are stag-headed, and in the course of our researches, starting since 1988 some plants got perished. The untimely elimination and stag-headed trees were not observed in plants of the three other trial plots. When the production capacities of chemical plants were very high and accordingly emissions were highest possible, needles of plants from the zone of acute stress-emission impact (A and B) were severely damaged, their life span did not exceed 2 years and surplus sceleton branches dying off being also observed. In plants of the background zone of pollution G and also of the trial plot C and ecologically pure habitat IX the needles were weakly damaged and the duration of their life was 3 years to 4 years. For the last 7 years to 8 years due to the production decline and decrease of chemical plants emissions, in particular plants of the trial plots A and B the lifetime of needles reached 3 years. Damaging effects of emissions from chemical plants do not cause annual decrease of seed productivity (calculating on one female cone) even in plants of degrading population (A) (KORSHIKOV, 1996). The seeds of plants from the degrading populations (A, B) preserve germination, however, a current annual increment, observed in particular favourable years in control populations is not formed. Mature plants were employed for the genetic analyses, the quantity of them was: A - 44, B - 56, C - 54, G - 25, IX - 46. 20 to 80 cones were gathered from each tree. To determine a genotype of a maternal tree using electrophoresis we analyzed 10 to 20 endosperms of seeds which were chosen at random from the total sampling. The electrophoresis of enzymes of homogenates of endosperms was conducted in vertical blocks of 7.5% polyacrylamide gel with separating gel pH 8.9, using tris-glycin electrode buffer, pH 8.3 (DAVIS, 1964; KOROCHKIN et al., 1977).

9 enzymes were analysed: glutamateoxaloacetatetransaminase (GOT, enzyme classification (E.C.) 2.6.1.1), glutamatedehydrogenase (GDH, E.C. 1.4.1.2), superoxidedismutase (SOD, E.C. 1.15.1.1), leucineaminopeptidaze (LAP, E.C. 3.4.11.1), malatedehydrogenase (MDH, E.C. 1.1.1.37), acid phosphatase (ACP, E.C. 3.1.3.2), alcoholdehydrogenase (ADH, E.C. 1.1.1.1), diaphorase (DIA, E.C. 1.6.4.3) and – malic-enzyme (ME, E.C. 1.1.1.40).

To assess the level of genetic variation and partition of *Pinus sylvestris* populations there were used standard techniques and indices most frequently and successfully employed in population-and-genetic studies: observed (H_o) and expected heterozygosity, a mean number of alleles per locus (n_0), the proportion of polymorphic loci according to 95% and 99% criteria. The analyses of the genetic structure and the extent of partition of *Pinus sylvestris* stands were performed, using S. WRIGHT's F-statistics (GURIES and LEDIG, 1982) and M. NEI's G-statistics (1975). Allele and genotypic heterogeneity of compared populations were evaluated by standard χ^2-test.

Results and Discussion

As a result of electrophoretic analysis of 9 enzymous systems stable manifestation of their activity zones on the gel plates and satisfactory genetic interpretation were obtained for 22 isozymous loci, four of which Sod-1, Sod-2, Sod-3 and Mdh-1 were monomorphic in all the five populations of *P. sylvestris* (*Table 1*). Out of 18 polymorphic loci the biggest allele representation was characteristic of the locus Adh-1 – six alleles, including null-allele, and the least one was typical of loci Gdh, Me-2 and Sod-4 – two alleles. The frequency of the main allele occurence, designated as 1.00, was higher than 0.500 for all the polymorphic loci in all the five populations (*Table 1*). Differences in structure and frequencies of alleles (between the populations studied) concerned mainly rare electrophoretic versions. In the overwhelming majority of cases their frequencies were low and did not exceed 0.100. According to the character of alle-

Table 1. – Alleles frequences, observed (Ho) and expected(He) heterozygosities in *P. sylvestris* L. populations, differently exposed to emission impact of chemical plants in the south-east of Ukraine.

Locus Heterozygosities Alleles	Populations				
	A	B	C	G	Ix
1	2	3	4	5	6
Gdh					
1.00	0,625	0,518	0,625	0,560	0,707
1.12	0,375	0,482	0,375	0,440	0,293
Ho	0,295	0,571	0,500	0,440	0,413
He	0,469	0,499	0,469	0,493	0,414
Got-1					
0	0	0,018	0	0	0
0.90	0	0,018	0,019	0	0
1.00	0,989	0,955	0,972	0,980	0,989
1.10	0,011	0,009	0,009	0,020	0,011
Ho	0,023	0,089	0,056	0,040	0,022
He	0,022	0,087	0,055	0,039	0,022
Got-2					
0	0	0,009	0,009	0,081	0
1.00	0,614	0,527	0,639	0,520	0,652
1.12	0,386	0,464	0,341	0,399	0,337
1.20	0	0	0,009	0	0,011
Ho	0,545	0,339	0,481	0,680	0,478
He	0,474	0,507	0,475	0,564	0,461
Got-3					
1.00	0,625	0,705	0,722	0,600	0,685
1.15	0	0,009	0	0	0
1.50	0,375	0,286	0,278	0,400	0,315
Ho	0,386	0,518	0,333	0,600	0,500
He	0,469	0,421	0,401	0,480	0,432
Me-2					
1.00	0,983	0,962	0,880	0,920	0,930
1.15	0,017	0,038	0,120	0,080	0,070
Ho	0,034	0,077	0,240	0,160	0,140
He	0,033	0,073	0,211	0,147	0,130
Me-3					
0	0	0	0	0	0,012
1.00	0,759	0,811	0,740	0,619	0,651
1.20	0	0	0	0	0,023
1.25	0,241	0,189	0,260	0,381	0,302
1.40	0	0	0	0	0,012
Ho	0,483	0,346	0,520	0,760	0,465
He	0,366	0,307	0,385	0,472	0,484
Sod-4					
0.90	0,068	0,027	0,037	0,060	0,033
1.00	0.932	0.973	0.963	0.940	0.967

1	2	3	4	5	6
Ho	0,136	0,055	0,074	0,120	0,065
He	0,127	0,053	0,071	0,113	0,064
Mdh-2					
0	0	0,010	0	0	0
1.00	0,951	0,970	0,980	0,981	0,945
1.08	0,049	0,020	0,020	0,019	0,055
Ho	0,098	0,060	0,040	0,040	0,111
He	0,093	0,059	0,039	0,037	0,104
Mdh-3					
0	0,012	0,010	0,030	0,040	0,011
0.86	0,329	0,360	0,240	0,440	0,300
1.00	0,659	0,630	0,730	0,520	0,655
1.12	0	0	0	0	0,023
1.15	0	0	0	0	0,011
Ho	0,634	0,580	0,460	0,760	0,556
He	0,457	0,473	0,409	0,534	0,480
Mdh-4					
0.90	0,012	0,030	0,095	0,060	0
1.00	0,720	0,810	0,755	0,660	0,636
1.20	0,037	0,030	0	0,040	0
2.50	0	0,050	0	0,020	0,046
3.50	0,231	0,080	0,150	0,220	0,318
Ho	0,415	0,160	0,340	0,600	0,409
He	0,427	0,333	0,398	0,510	0,492
Dia-1					
0	0	0	0	0	0,022
0.85	0	0	0	0,060	0
0.90	0,216	0,260	0,150	0,260	0,322
1.00	0,784	0,720	0,650	0,680	0,634
1.15	0	0,020	0,200	0	0,022
Ho	0,250	0,480	0,380	0,560	0,489
He	0,339	0,414	0,515	0,466	0,493
Dia-2					
0.90	0	0,010	0,040	0,021	0,011
1.00	0,909	0,910	0,870	0,937	0,967
1.10	0,091	0,080	0,090	0,042	0,022
Ho	0,091	0,140	0,220	0,120	0,067
He	0,165	0,165	0,233	0,120	0,064
Dia-4					
0.89	0,045	0,050	0	0,040	0,033
1.00	0,955	0,940	0,950	0,960	0,967
1.10	0	0,010	0,050	0	0
Ho	0,068	0,120	0,100	0,080	0,067
He	0,086	0,114	0,095	0,077	0,064
Adh-1					
0	0,011	0	0	0	0
0.89	0,011	0,010	0,042	0	0,011
1.00	0,920	0,840	0,833	0,955	0,856

1	2	3	4	5	6
1.02	0,058	0,150	0,094	0,045	0,100
1.05	0	0	0	0	0,012
1.08	0	0	0,031	0	0,021
Ho	0,114	0,120	0,333	0,080	0,267
He	0,150	0,272	0,295	0,086	0,257
Adh-2					
0	0	0	0	0	0,011
0.90	0,114	0,120	0,146	0,045	0,091
1.00	0,875	0,860	0,854	0,955	0,898
1.10	0,011	0,020	0	0	0
Ho	0,205	0,100	0,167	0,080	0,156
He	0,221	0,246	0,249	0,086	0,185
Lap-1					
0	0,011	0,010	0	0	0
0.95	0,091	0,100	0,200	0,040	0,077
0.97	0	0	0	0	0,013
1.00	0,898	0,890	0,800	0,960	0,910
Ho	0,182	0,220	0,360	0,080	0,179
He	0,185	0,198	0,320	0,077	0,166
Lap-2					
0	0,011	0	0	0,020	0
0.95	0,023	0,070	0,020	0,060	0,012
1.00	0,875	0,880	0,930	0,880	0,910
1.05	0,091	0,050	0,050	0,040	0,078
Ho	0,159	0,120	0,140	0,240	0,179
He	0,225	0,218	0,132	0,220	0,166
Acp					
0.94	0,102	0,152	0,261	0,180	0,119
0.97	0	0	0	0	0,036
1.00	0,796	0,803	0,729	0,560	0,524
1.02	0,102	0,045	0,010	0,260	0,321
Ho	0,462	0,321	0,292	0,440	0,571
He	0,346	0,330	0,400	0,586	0,607

les frequencies change, directional one-locus selection, depending on an extent of emissions impact, does not occur in the populations researched. The values of observed (H_o) and expected (H_e) heterozygosity were sufficiently similar. Although in populations from the zone of acute emission impact (A, B) there were observed six cases (five were in the population B), when deficiency of heterozygotes exceeded or was practically 50%. In three other populations that was found only in one version in the locus Adh-2 in the population C.

Out of 68 alleles of polymorphic loci found in 225 trees analyzed, 55 were in the joint sampling of plants of A and B populations and 62 were in populations C, G and IX (*Table 2*). 92 genotypes were detected in 5 populations studied. Their least number 68 was typical of populations from the zone of acute emission impact and in conventionally control populations (G, C, IX) 81 genotypes were revealed. Valid interpopulation allele heterogeneity (by the standard χ^2-test) was detected for 4 and genotypic – for 6 out of 18 polymorphic loci. Mean values of observed and expected heterozygosities are close enough in 13 loci, but in the other five either surplus of heterozygotes accounting for 23% (Mdh-3 and Me-3) or their deficiency which was 45% at a maximum for the locus Adh-2 were detected. The populations studied did not differ in the portion of polymorphic loci, which was 81.8% according to 99% criterion (*Table 3*). A mean number of alleles per one locus in the degrading population A was the same as in the population G or close to C, which are in the zone of the background pollution. Maximum allele and genotypic representation in loci was characterictic of the IX population, not exposed to any effect of pollutants. Nearly the same level of such representation was found in the population B, severely damaged by emissions from chemical plants. A bit lower level of heterozygosity was observed in two populations from the zone of acute emission impact. Mean values of expected and observed heterozygosity in damaged-weakened

Table 2. – Number of alleles and genotypes, heterogeneity of their frequencies, values of heterozygosity for 18 polymorphic loci in *Pinus sylvestris* L. populations, differently exposed to airpollutants effect.

Locus	Number of alleles and genotypes						Heterogeneity index χ^2		Heterozygosity in the total sampling of plants	
	in the total sample		in damaged-degrading (A,B)		of the background zone (C,G) and on the not polluted territory (IX)		allele	genotypic	observed (Ho)	expected (He)
	alleles	genotypes	alleles	genotypes	alleles	genotypes				
Got-1	4	4	4	4	3	3	10,86(12)	10,84(12)	0,049	0,048
Got-2	4	7	3	4	4	7	32,03(12)***	58,10(24)***	0,480	0,493
Got-3	3	4	3	4	2	3	7,12(8)	15,53(12)	0,453	0,438
Gdh	2	3	2	3	2	3	8,31(4)	14,78(8)	0,453	0,474
Sod-4	2	2	2	2	2	2	2,74(4)	1,26(4)	0,085	0,081
Mdh-2	3	3	3	3	2	2	7,66(8)	9,62(8)	0,071	0,068
Mdh-3	5	7	3	4	5	7	21,24(16)	25,76(24)	0,578	0,471
Mdh-4	5	9	5	7	5	7	47,35(16)***	52,83(28)**	0,357	0,431
Me-2	2	2	2	2	2	2	5,58(4)	5,98(4)	0,129	0,118
Me-3	5	5	2	2	5	5	15,82(16)	19,91(16)	0,507	0,414
Dia-1	5	9	3	4	5	9	87,30(16)***	99,02(28)***	0,420	0,452
Dia-2	3	5	3	4	3	4	10,72(8)	15,47(16)	0,131	0,157
Dia-4	3	4	3	4	3	4	16,13(8)	23,45(12)*	0,089	0,090
Acp	4	5	3	4	4	5	76,58(12)***	49,76(16)***	0,405	0.455
Adh-1	6	7	4	5	5	5	23,32(20)	78,14(24)***	0,193	0.230
Adh-2	4	5	3	4	3	4	11,88(12)	15,30(16)	0,146	0.212
Lap-1	4	5	3	3	3	4	18,68(12)	21,10(16)	0,221	0,209
Lap-2	4	6	4	6	4	5	13,48(12)	16,34(20)	0,158	0,189

– ( ) liberty extent, differences are significant: * – at P < 0.95, ** – at P < 0.99, **** – at P < 0.9999

Table 3. – Values of the main genetic polymorphism indices in *Pinus sylvestris* L. populations in the south- east of Ukraine, exposed to the impact of emissions from chemical plants (A, B), in the zone of the backgroud pollution (C, G) and not exposed to the effect of pollutants (IX).

Populations	Number of trees	Number of polymorphic loci (P_{99})	Mean number per locus of		Heterozygosity		Wright's fixation index
			alleles	genotypes	observed (Ho)	expected (He)	
A	44	0,818	2,273	2,773	0,208 ± 0,012	0,212 ± 0,012	0,019
B	56	0,818	2,591	3,136	0,201 ± 0,011	0,217 ± 0,012	0,074
Mean		0,818	2,682	3,318	0,204 ± 0,008	0,216 ± 0,008	0,051
C	54	0,818	2,318	2,862	0,229 ± 0,012	0,234 ± 0,012	0,021
G	25	0,818	2,273	2,824	0,267 ± 0,015	0,231 ± 0,015	-0,156
Ix	46	0,818	2,682	3,141	0,233 ± 0,012	0,231 ± 0,012	-0,009
Mean		0,818	3,000	3,864	0,238 ± 0,007	0,232 ± 0,007	-0,026
Mean within species	225	0,818	3,273	4,364	0,223 ± 0,006	0,225 ± 0,006	0,009

populations A and B were lower accordingly by 7.9% and 16.7% and allele and genetic representation per locus – by 11.9% and 16.5% lower, than in the three populations with conventionally healthy plants. At an average a small surplus of heterozygotes is typical of those control populations and some deficiency of them is characteristic of populations degrading due to damaging effects of pollutants. On the whole the differences between observed and expected heterozigosity (according to χ^2-test) were insignificant in the studied *Pinus* populations. In exposed populations mean values of calculated heterozygosity (H_e) were slightly lower and of observed one (H_o) were less by STUDENT's criterion ($t_{0.95}$) than in the control populations. Thus the exposed populations (A and B) yield to the populations of the background zone of pollution (C and G) and the population not exposed to any pollution effect (IX) in respect to the most significant adaptive index – an average level of heterozygosity. This can be linked with the fact that specimens with high heterozygosity are also in a number of untimely eliminating trees in the degrading populations. Earlier we have shown that the sampling of plants most tolerant to pollutants in these populations has a level of heterozygosity close to average (KORSHIKOV, 1996). From a position of the optimum genic diversity concept marked decrease or excessive increase of heterozygosity under stress are equally unfavourable for normal functioning of populations. On the whole mean value of expected heterozygosity for *P. sylvestris* in the investigated by us part of its distribution in marginal, including also degrading populations, was by 28.9 % lower than in central and marginal populations of Eastern Europe and Siberia (GONCHARENKO et al., 1993) and by 23 % higher than in German-Lithuanian-Urals populations of this species (SHIGAPOV et al., 1995). Three of five populations (A, IX, C) and on the whole native stands of *P. sylvestris* in the outlying part of the range studied by us are in a state of equilibrium by HARDY-WINBERG; nearly coinciding values of expected and observed heterozygosity testify to it (*Table 3*). The calculations of parameters F (Fis and Fit) confirm once more an equilibrium state of the populations studied and low values of Fst and Gst coefficients witness about their low differentiation degree (*Table 4*). Interpopulation genetic variation of five *P. sylvestris* populations in the south-east of Ukraine accounts only for 1.5%. The contribution of particular polymorphic loci into this variability varied from 0.6% (Sod-4) to 6.7% (Acp). It should be noticed that the portion of the interpopulation variation within a vast range from the Baltic Coast of Germany to the Urals and Siberia (Russia) was about 3%

Table 4. – Values of Fis, Fit, Fst and Gst indices for 22 loci in *Pinus sylvestris* L. populations in the south-east of Ukraine.

Locus	Fis	Fit	Fst	Gst
Gdh	0,033	0,051	0,018	0,018
Got-1	-0,020	-0,012	0,008	0,007
Got-2	0,019	0,037	0,018	0,012
Got-3	-0,042	-0,034	0,008	0,009
Sod-1	0	0	0	0
Sod-2	0	0	0	0
Sod-3	0	0	0	0
Sod-4	-0,045	-0,041	0,004	0,006
Mdh-1	0	0	0	0
Mdh-2	-0,043	-0,035	0,007	0,007
Mdh-3	-0,242	-0,225	0,013	0,016
Mdh-4	0,179	0,201	0,028	0,031
Me-2	-0,074	-0,054	0,019	0,019
Me-3	-0,236	-0,218	0,015	0,021
Dia-1	0,056	0,099	0,045	0,029
Dia-2	0,134	0,145	0,013	0,013
Dia-4	0,003	0,018	0,014	0,010
Acp	0,048	0,107	0,062	0,067
Adh-1	0,152	0,163	0,013	0,016
Adh-2	0,273	0,280	0,009	0,009
Lap-1	-0,074	-0,055	0,017	0,026
Lap-2	0,130	0,138	0,010	0,008
Mean	0,011	0,026	0,015	0,015

(GONCHARENKO et al., 1993; SHIGAPOV et al., 1995). A low degree of genetic differentiation of *P. sylvestris* populations studied by us is corroborated by small values of NEI's genetic distance coefficients (*Table 5*), the mean value of which was 0.008. This

Table 5. – NEI'S genetic coefficient (1972) between *Pinus sylvestris* L. populations in the south-east of Ukraine.

Populations	A	B	C	G	Ix
A	0,000	0,004	0,006	0,007	0,007
B		0,000	0,006	0,010	0,013
C			0,000	0,014	0,011
G				0,000	0,006
Ix					0,000

testifies to the proximity of genofonds of the studied populations. It is remarkable that the values of this coefficient for the population A, degrading due to emission impact, and for the other four populations did not exceed even an average level. The biggest genetic similarity was detected between damaged-degrading populations A and B (Dn = 0.004) and maximum was in populations of the background zone of pollution C and G (Dn = 0.014). As to the literary data NEI's genetic distance coefficient was 0.017 for 18 *P. sylvestris* populations in Eastern Europe and Siberia (GONCHARENKO et al., 1993) and 0.010 for eight populations from Germany, Lithuania and Russia (SHIGAPOV et al., 1995). A dendrogram, created on the basis of NEI's genetic distance coefficients, visually demonstrates the genetic similarity between populations A and B and also G and IX, which are united into two independent groups (*Figure 1*).

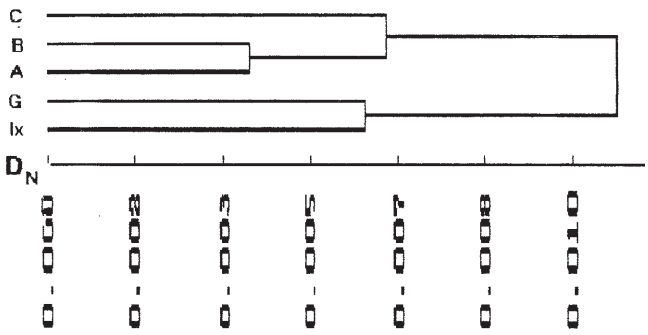

Figure 1. – Dendrogram of the extent of genetic differentiation of 5 *Pinus sylvestris* L. populations in the south – east of Ukraine, created on the basis of NEI'S genetic distance coefficient.

It is considered that at the borders of ranges under extreme conditions of existence genetic diversity should decrease and interpopulation differentiation of a species has to increase (NIEBLING and CONKLE, 1990). For example, marginal populations of *Picea glauca* in the subarctic region of Canada had comparatively high genetic differentiation. However there are a lot of data, testifying to the absence of the pronounced differentiation of coniferous populations within one geographic region or spatialy isolated territories (YEH et al., 1986; YEH. and EL. KASSABY, 1980; PLESSAS and STRAUSS, 1986). Changes of conifers genetic parameters do not always occur under conditions of industrially polluted environment. The directional change of alleles frequences and the most common genotypes were found in four age groups (embryos of seeds, 3 to 10 year old trees, 10 to 30 year old trees and older ones) of *P. sylvestris*, exposed to the effect of steelworks' emissions (PRUS-GLOWACKI and NOVAK-BROWY, 1989). The decrease of heterozygosity by 12% and increase of the mean alleles number by 8% were detected in naturally renewed 10 to 15 year old *P. sylvestris* populations near the zink enterprise (PRUS-GLOWACKI and NOVAK-BROWY, 1992). In *P. sylvestris* populations from the

south Urals, grown in industrially polluted zones, a bigger number of rare alleles was observed compared to populations from ecologically pure habitats (SHIGAPOV et al., 1995; BACHTIYAROVA et al., 1995). In the studied *P. sylvestris* population (A), degrading through untimely death of some plants of long-term (more than thirty years) damaging effects of toxic emissions from chemical plants there does not occur a noticeable change of prevailing alleles frequences (1.00) in any of 18 polymorphic loci compared to the control populations, though the genotypic representation is poorer mainly because of a smaller portion of heterozygotes with rare allele versions. In the population B, significantly damaged by emissions, where the death of plants insignificantly exceeds a natural level there was not observed a noticeable loss of allele and genetic diversity. The decrease of intrapopulation components of genic diversity in the demographically oldest element of the degrading population (A) does not increase the degree of its differentiation compared with the control populations. On the whole these facts may witness that single-directed changes in the genetic structure of the oldest element of degrading populations do not take place. It is not excepted that stochastic change of genes frequences may occur in such populations in case of decrease of emissions effect to the level, which allows natural regeneration in subsequent generations. In will be a result of an incidental genetic drift through the destruction of evolutionary laid bases of their adaptive genetic structure, which occured as a result of the decrease in the number and the lack of regeneration of populations.

Thus, a slightly lower level of genetic diversity was observed in the degrading (through damaging effects of emissions from chemical enterprises of the south-eastern Ukraine) marginal *P. sylvestris* populations, than in the populations, not exposed to the effect of pollutants.

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Sensitivity of Diameter Growth to Annual Weather Conditions in Scots Pine Provenances at a Central Siberian Location

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Summary

Eight tree-ring characteristics (tree ring width, latewood and earlywood widths and densities, maximum and minimum densities and latewood percentage) were measured densitometrically in 16 Scots pine provenances in the southern taiga, Central Siberia. Age trends were excluded by standardization. It was found that the sensitivity coefficient of latewood width, latewood and maximum densities and latewood percentage has a tendency to decrease in relation to the increasing latitude of seed sources. Northern provenances utilise only the energy resources (heat and light) during the first half of the growing season effectively. The correlation of tree ring series between the local provenance and the other provenances decreases in relation to the increasing latitude difference between seed origins. As a whole, the values of the normalized Euclidean distance, correlation and synchronicity coefficients between the local provenance and the other provenances prove that, for most of the provenances, the interannual variability of the chosen tree ring characteristics reflects the prevailing

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