two years observed. The average values for the provenances, however, were used for the stepwise regression analyses, as was suggested in studies by other investigators (KHALIS and DOUGLAS, 1979; LOOPSTRA and ADAMS, 1989), and the use of the provenance means ignored the intra-provenance and environmental variations.

Finally, it can be concluded that the distinct variation patterns in some phenological characteristics of *Cupressus sempervirens* (duration of summer and winter rest periods, time of the spring growth peak) imply that the natural selection of the species is directed to favour genotypes resistant to drought and low temperatures. On the other hand, the non-systematic variation of other group characteristics of the primary growth (date of winter peak, date of growth cessation in summer, duration of spring growth period) suggests that other factors in addition to natural selection also are involved. In this sense, it has to be considered that the natural forests around the Mediterranean have been generally disrupted by man and for centuries have been subjected to dysgenic selection. The discontinuous natural range of the species and the relatively small population could mean that genetic drift has also played a role in the pattern of provenance variation of growth rhythm.

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Allozyme Differentiation and Phylogeny of Cedar Species

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Summary

The isozyme variation patterns of 21 populations belonging to four Cedar species *(Cedrus libani, C. atlantica, C. deodara, C. brevifolia)* were studied at six loci (6PGD-B, LAP-A, LAP-B, IDH-A, DIA-A, PGI-B) by horizontal starch and polyacrylamide gel electrophoresis. Species specific alleles (DIA-A1 and LAP-A1 for *C. deodara,* IDH-A1 for *C. atlantica,* LAP-A3 for *C. libani* and *C. brevifolia*) and alleles with a particular geographic variation pattern (6PGD-B4 for *C. libani*) were detected in most of the species. Great variation was observed in heterozygosity levels among species which ranged from 0.136 *(C. deodara)* to 0.316 *(C. brevifolia)*. The construction of a dendrogram revealed five distinct clusters corresponding to the following taxa: i) *C. libani* ssp. *libani,* ii) *C. libani* ssp. *stenocoma,* iii) *C. libani* ssp. *brevifolia,* iv) *C. deodara,* v) *C. atlantica.*

Key words: Isozyme variation, phylogeny, *C. libani, C. brevifolia, C. atlantica, C. deodara.*

Introduction

The genus *Cedrus* includes coniferous evergreen species and is distributed in four geographically separated regions: a) Algeria and Morocco, b) Cyprus, c) Lebanon, Syria and Turkey and d) Afghanistan and the Himalayas (ARBEZ *et al.,* 1978; ARBEZ, 1987; M'HIRIT, 1987; VIDAKOVIC, 1991). According to TOTH (1980) and M'HIRIT (1987), *Cedrus* has an exceptional ability to perform well in a variety of soil and climatic conditions and to offer a considerable resistance to pests and fires.

Due to its exceptional adaptation in a variety of environmental conditions, *Cedrus* has been successfully introduced in many countries out of its natural distribution, firstly as an ornamental and secondly as a reforestation species.

Today, in spite of its ecological and economic importance, limited information concerning the amount and pattern of its genetic variability is available (FAO, 1989). According to a

number of provenance trials and taxonomic studies based on morphological and anatomical characteristics (HOLMBOE, 1914; ARBEZ, 1987; GREUTER *et al.,* 1984), there is no general consensus on its taxonomy, especially for those species growing in the Mediterranean basin.

Cedrus was first described as a genus by Trew in 1757 (ARBEZ, 1987) and most of the taxonomists agree now on the four species classification arrangement: *Cedrus atlantica* MANNETTI (1844) in Morocco and Algeria, *C. brevifolia* HENRY in Cyprus, *C. libani* A. RICH. (1823) in Lebanon, Syria and Turkey and *C. deodara* D. DON (1830) in Afghanistan and India (ZOLLER, 1981; HORA, 1981; MITCHEL, 1985; VIDAKOVIC, 1991).

In pertinent publications such as the Flora of Turkey (DAVIS, 1965) and the Med-Checklist (GREUTER *et al.,* 1984) all the Mediterranean Cedars are described as a single species, namely *Cedrus libani (C. libanitica)* with four sub-species: *C. libani* ssp. *atlantica* in Morocco and Algeria, *C. libani* ssp. *brevifolia* in Cyprus, *C. libani* ssp. *libani* in Lebanon and Syria and *C. libani* ssp. *stenocoma* in Turkey.

However, according to Flora Europeae (TUTIN *et al.,* 1964) and POLUNIN and EVERARD (1976), the genus *Cedrus* is divided in three species: *C. atlantica, C. libani* and *C. deodara.*

PANETSOS *et al.* (1992, 1993), carried out a first analyses on allozyme variation of Cedar species which showed that considerable intra- and inter-specific genetic differentiation exists, except for *C. deodara* where lack of variation was noticed.

On the other hand, MISHRA (1996) detected a minor polymorphism in natural populations of *C. deodara* from Himalayas.

Aim of this study was to estimate the genetic variability within the genus *Cedrus* and to clarify the taxonomic status of the genus by means of enzyme-gene systems.

Materials and Methods

Electrophoresis was carried out on haploid endosperms of germinated seeds (enhanced to germinate with cold stratification) with a radicle of 1 mm to 3 mm long.

The seed material was taken from 21 bulk stand collections that included six populations of *C. atlantica* (four from Algeria provided by INRFA, one from a French plantation provided by INRA and one from Morocco provided by the Station de Recherche Forestiere, Rabat-Maroc), ten populations of *C. libani* (four populations from Turkey and six from Lebanon provided by INRA), one of *C. brevifolia* provided by the Forest Service of Cyprus and four populations of *C. deodara* (one from an artificial plantation in France and one from Afghanistan provided by INRA) and two from India provided by Forest Research Institute of India and by Shimla Forest Research Institute respetively. The exact number of seed trees sampled from each popula-

Table 1. – Location of 21 populations of *Cedrus* sp..

No. of Population	Country	Provenance	Altitude (m)
Cedrus libani			
1	Turkey	Catalan	1100
2	Turkey	Sutlegen	1550
3	Turkey	Pozanti	1300
4	Turkey	Arslankoy	1800
5	Lebanon	Akkar East	1250-1450
6	Lebanon	Ain Zhalta	1300
7	Lebanon	Masser Chouff	1600
8	Lebanon	Akkar Ouest	1250-1800
9	Lebanon	Niha	–
10	Lebanon	Barouk	1700
Cedrus brevifolia			
11	Cyprus	Tripylos	900-1400
Cedrus deodara			
12	France	Art. plantation in France (Aude)	–
13	Afghanistan	Mirdesh	–
14	India	Chamba	–
15	India	Himachal Pradesh	–
Cedrus atlantica			
16	Algeria	Babors	1800-1850
17	Algeria	Ouarsenis	1500
18	Algeria	Djurdjura	1600-1650
19	Algeria	Aures	2030
20	France	Art. Plantation in France (Marcelly)	550-600
21	Morocco	Ich N' Timghilt	–

tion was not known, but as most of the above Institutions assured us, it was apparently greater than 100. The location and elevation of the examined populations are given in *table 1.*

All the enzyme systems tested, were resolved by means of horizontal starch gel (11% starch and 1% sucrose) electrophoresis technique (CHELIAK and PITEL, 1984), except for LAP which was resolved in Morpholine-Citrate buffer system pH 6.1 (CONKLE *et al.,* 1982) by using the horizontal polyacrylamide gel (7.5% w/v) electrophoresis technique (PASTEUR *et al.,* 1988).

Endosperms (megagametophytes) were dissected from germinated seeds and were homogenized individually by adding 0.20 M phosphate buffer (pH 7.5) (CONKLE *et al.,* 1982). The homogenates were analysed for 6-phosphogluconate dehydrogenase (6PGD; E.C.1.1.1.44), menadione reductase (MNR; E.C.1.6.99.2), phosphoglucose isomerase (PGI; E.C.5.3.1.9), diaphorase (DIA; E.C.1.1.1.40), glucose-6-phosphate dehydrogenase (G6PD; E.C.1.1.1.49), malate dehydrogenase (MDH; E.C.1.1.1.37), leucine aminopeptidase (LAP; E.C.3.4.11.1) and isocitrate dehydrogenase (IDH; E.C.1.1.1.42). The staining recipes were prepared according to CHELIAK and PITEL (1985). Gels were run under refrigeration (4°C) and constant amperages (60 mA for starch and 16 mA for polyacrylamide gel). The loci (isozymes) and the alleles within each locus (allozymes) were numbered in decreasing order of anodal mobility. "Null" isozymes, that lacked staining activity under the conditions of our assays, were specified by the letter "n".

The genetic parameters: He (expected average heterozygosity), A/L (mean number of alleles per locus), P (percentage of polymorphic loci) and D (genetic distance) were estimated according to NEI (1973, 1978). Cluster analysis, using the Unweighted Pair Group Method (UPGMA), was performed on the matrix of NEI's genetic distances.

Isozyme patterns of all enzyme systems were examined in random samples consisting of 75 to 100 endosperms from each population.

Results and Discussion

Five enzyme systems (IDH,6PGD, LAP, PGI, DIA) out of the eight tested were resolved with sufficient consistency and clarity while the rest were excluded because of unsatisfactory resolution in at least one Cedar species. Each of the resolved enzymes was coded by two loci but their electrophoretic patterns were sufficiently clear for genetic interpretation at only one locus (IDH-A, 6PGD-B, PGI-B, DIA-A), except of the LAP enzyme system in which both loci exhibited sufficient resolution. The isozyme banding patterns and the genetic control of the studied isozyme loci has been previously described by PANETSOS *et al.* (1992) and MISHRA (1996).

Table 2 presents the allozyme frequencies among the 21 tested Cedar populations. Altogether, 24 alleles were detected among the populations of the analyzed species. Only three alleles (PGI-B2, IDH-A2, DIA-A2) were present in all the populations studied while some other alleles e.g. IDH-A1, LAP-A1, DIA-A1, could be considered as species-specific. Among the 6 loci tested, PGI-B and 6PGD-B were the most variable (6 allozyme variants), whereas the IDH-A and LAP-A loci showed the minimal variation (3 allozyme variants). All these variants are depicted schematically in *figure 1.* Allozyme frequencies varied by species and populations and imply that considerable genetic differentiation exists among the species and populations. Among the 6 loci tested, LAP-A and 6PGD-A loci possess alleles with diagnostic value providing strong evidence for discrimination of the genus *Cedrus* into distinct taxa and even for identification of the provenance of some populations within the species (*Figure 2* and *3*).

The IDH-A locus was fixed at IDH-A2 allele in all Cedar species except for *C. atlantica* in which IDH-A1 allele was present at low frequencies. Monomorphic behaviour of the IDH system was also reported by MISHRA (1996) in *C. deodara* populations.

Although in the previous works (PANETSOS *et al.,* 1992, 1993) the LAP-A locus appeared to be monomorphic in all Cedar spe-

Table 2. – Allozyme frequencies of six enzyme gene loci for 21 populations of Cedar sp..

Species & Provenances	DIA-A				IDH-A			LAP-A			LAP-B			
	a1	a2	a3	a4	a1	a2	a3	a1	a2	a3	b1	b2	b3	b4
C. libani														
1. Catalan	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	1.00	0.00	0.00	0.96	0.04	0.00
2. Sutlegen	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.90	0.10	0.00	0.93	0.07	0.00
3. Pozanti	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.90	0.10	0.00	0.91	0.09	0.00
4. Arslankoy	0.00	0.94	0.00	0.06	0.00	1.00	0.00	0.00	0.94	0.06	0.00	0.90	0.10	0.00
5. Akkar East	0.00	0.82	0.09	0.09	0.00	0.94	0.06	0.00	0.06	0.94	0.00	0.76	0.24	0.00
6. Zhalta	0.00	0.96	0.00	0.04	0.00	1.00	0.00	0.00	0.06	0.94	0.00	0.72	0.28	0.00
7. Masser Chouff	0.00	0.88	0.00	0.12	0.00	1.00	0.00	0.00	0.09	0.91	0.00	0.80	0.20	0.00
8. Akkar Ouest	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.00	0.00	1.00	0.00	0.83	0.17	0.00
9. Niha	0.00	0.81	0.07	0.12	0.00	1.00	0.00	0.00	0.05	0.95	0.00	0.80	0.20	0.00
10. Barouk	0.00	0.85	0.00	0.15	0.00	1.00	0.00	0.00	0.05	0.95	0.00	0.80	0.20	0.00
11. C. brevifolia	0.00	0.83	0.16	0.01	0.00	1.00	0.00	0.00	0.87	0.13	0.00	0.82	0.18	0.00
C. deodara														
12.	0.14	0.86	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.15	0.85	0.00	0.00
13.	0.04	0.96	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.23	0.59	0.18	0.00
14.	0.10	0.90	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.20	0.80	0.00	0.00
15.	0.02	0.98	0.00	0.00	0.00	1.00	0.00	1.00	0.00	0.00	0.18	0.82	0.00	0.00
C. atlantica														
16.	0.00	1.00	0.00	0.00	0.20	0.80	0.00	0.00	1.00	0.00	0.12	0.00	0.76	0.12
17.	0.00	1.00	0.00	0.00	0.12	0.88	0.00	0.00	1.00	0.00	0.16	0.00	0.66	0.18
18.	0.00	1.00	0.00	0.00	0.28	0.72	0.00	0.00	1.00	0.00	0.08	0.00	0.92	0.00
19.	0.00	1.00	0.00	0.00	0.08	0.92	0.00	0.00	1.00	0.00	0.12	0.00	0.88	0.00
20.	0.00	1.00	0.00	0.00	0.04	0.96	0.00	0.00	1.00	0.00	0.00	0.00	1.00	0.00
21.	0.00	1.00	0.00	0.00	0.10	0.90	0.00	0.00	1.00	0.00	0.08	0.00	0.84	0.08

(continuation *table 2*)

Species & Provenances	6PGD-B						PGI-B					
	b1	b2	b3	b4	b5	b6	b1	b2	b3	b4	b5	b6
C. libani												
1. Catalan	0.00	1.00	0.00	0.00	0.00	0.00	0.00	0.64	0.32	0.04	0.00	0.00
2. Sutlegen	0.00	0.65	0.00	0.35	0.00	0.00	0.00	0.84	0.04	0.44	0.02	0.02
3. Pozanti	0.02	0.42	0.00	0.56	0.00	0.00	0.00	0.76	0.00	0.20	0.04	0.00
4. Arslankoy	0.02	0.50	0.00	0.48	0.00	0.00	0.00	0.40	0.06	0.50	0.04	0.00
5. Akkar East	0.00	0.18	0.04	0.56	0.22	0.00	0.00	0.37	0.00	0.63	0.00	0.00
6. Zhalta	0.00	0.17	0.17	0.63	0.03	0.00	0.00	0.40	0.00	0.60	0.00	0.00
7. Masser Chouff	0.00	0.11	0.00	0.89	0.00	0.00	0.00	0.44	0.00	0.56	0.00	0.00
8. Akkar Ouest	0.00	0.08	0.03	0.52	0.37	0.00	0.00	0.55	0.00	0.45	0.00	0.00
9. Niha	0.00	0.12	0.00	0.88	0.00	0.00	0.00	0.50	0.00	0.50	0.00	0.00
10. Barouk	0.00	0.04	0.04	0.92	0.00	0.00	0.00	0.55	0.00	0.45	0.00	0.00
11. C. brevifolia	0.00	0.80	0.00	0.20	0.00	0.00	0.00	0.30	0.28	0.25	0.05	0.12
C. deodara												
12.	0.00	0.00	0.00	1.00	0.00	0.00	0.12	0.88	0.00	0.00	0.00	0.00
13.	0.00	0.00	0.00	1.00	0.00	0.00	0.24	0.76	0.00	0.00	0.00	0.00
14.	0.00	0.00	0.00	1.00	0.00	0.00	0.18	0.82	0.00	0.00	0.00	0.00
15.	0.00	0.00	0.00	1.00	0.00	0.00	0.25	0.75	0.00	0.00	0.00	0.00
C. atlantica												
16.	0.00	0.00	0.00	0.00	1.00	0.00	0.05	0.32	0.00	0.50	0.13	0.00
17.	0.00	0.00	0.00	0.00	1.00	0.00	0.05	0.35	0.00	0.48	0.12	0.00
18.	0.00	0.00	0.00	0.00	1.00	0.00	0.05	0.48	0.00	0.14	0.33	0.00
19.	0.00	0.00	0.00	0.00	1.00	0.00	0.06	0.33	0.00	0.58	0.03	0.00
20.	0.00	0.00	0.00	0.00	1.00	0.00	0.00	0.40	0.00	0.36	0.24	0.00
21.	0.00	0.00	0.00	0.00	0.94	0.06	0.00	0.24	0.00	0.76	0.00	0.00

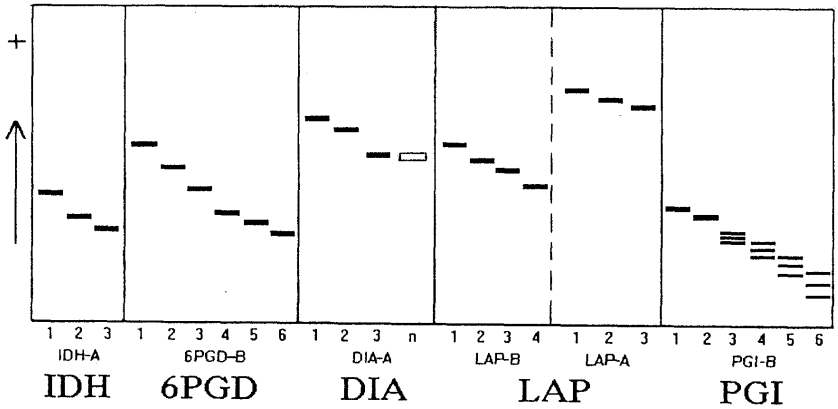


Figure 1. – Representative illustrations of allozyme band patterns observed in six loci in megagametophyte tissues of 21 Cedar populations.

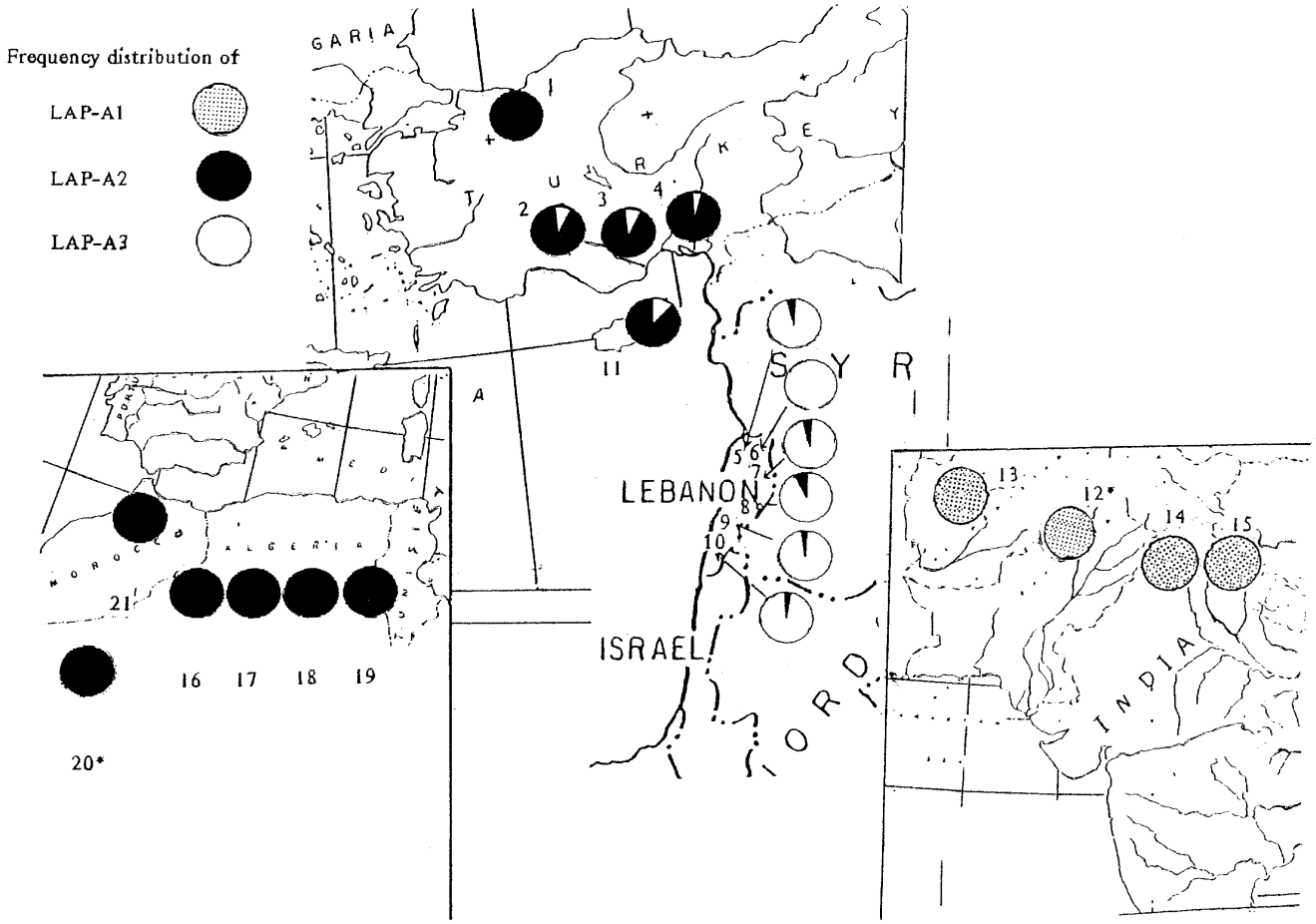
cies, under our electrophoretic conditions (Morpholine buffer system, polyacrylamide gel) variation was observed among species and populations probably due to the better resolution among the enzyme variants.

The LAP-A locus was fixed for the LAP-A1 allele in *C. deodara* and LAP-A2 allele in *C. atlantica,* while the same locus was nearly monomorphic in the Turkish and the Lebanese populations of *C. libani* for different alleles, LAP-A2 and LAP-A3 alleles respectively *(Figure 2).* The monomorphic behaviour of the LAP-A locus in *C. deodara* was also reported by MISHRA (1996).

Regarding to the LAP-B locus, *C. libani* and *C. brevifolia* are discriminated from the other species by the presence of LAP-B2 and LAP-B3 alleles at high and low frequencies respectively, while *C. atlantica* is characterized by the high frequency of the LAP-B3 allele. On the other hand, *C. deodara* is characterized by the high frequency of the LAP-B2 allele in conjunction with the presence of the LAP-B1 allele. Among the *C. deodara* populations studied, the Afghan one was unique in the presence of the LAP-B3 allele. Two of the observed variants in the Himalayan populations of *C. deodara,* were also found by MISHRA (1996). The LAP-B4 allele was present only in some populations of *C. atlantica* (pop. 16, 17, 21).

Out of the six alleles at the PGI-B locus, five were found in *C. brevifolia* (B2, B3, B4, B5, B6). PGI-B6 allele could be considered as a unique allele for *C. brevifolia* although in one Turkish population (pop. 2) appeared as rare. The above is in agreement with the findings of previous works (PANETSOS *et al.,* 1992, 1993).

Allele PGI-B1 was detected at low frequencies in *C. deodara* and in many populations of *C. atlantica,* as well. Higher frequencies of the PGI-B2 allele were recorded in *C. deodara* and in some Turkish populations and ranged from 64% to 88%. MISHRA (1996) also reported the appearance of two allozymes in the PGI-B locus in *C. deodara* populations. The higher frequencies of PGI-B3 allele appeared in *C. brevifolia* (0.28) and in the northernmost Turkish population (0.32). Finally, the higher frequency of PGI-B4 allele was recorded in the Moroccan population (0.76). Regarding the PGI-B locus, it is worth mentioning that two alleles (B1, B2) appeared as single band while the rest alleles (B3, B4, B5, B6) as a triple-band *(Figure 1).* As it can be seen from the data *(Table 2),* the PGI-alleles coding for single-



*) Art. plantation in France

Figure 2. – Frequency distribution of the LAP-A locus in 21 populations of Cedar sp..

band isozymes dominate in *C. deodara* and in some Turkish populations of *C. libani,* whereas the alleles coding for triple-band isozymes occur more frequently in *C. atlantica* and *C. brevifolia.* In *Picea abies* and *Pseudotsuga menziesii,* BERGMANN (1975) found that, acid phosphatase alleles coding for single-band enzyme dominate in colder zones of the distribution range of the species while the alleles coding for double-band enzymes occur more frequently in all moderate climatic zones.

The 6PGD-B locus was fixed for the 6PGD-B4 allele in *C. deodara.* The 6PGD-B5 allele was fixed in all *C. atlantica* populations except for the Moroccan population in which a rare allele (6PGD-B6) was also present.

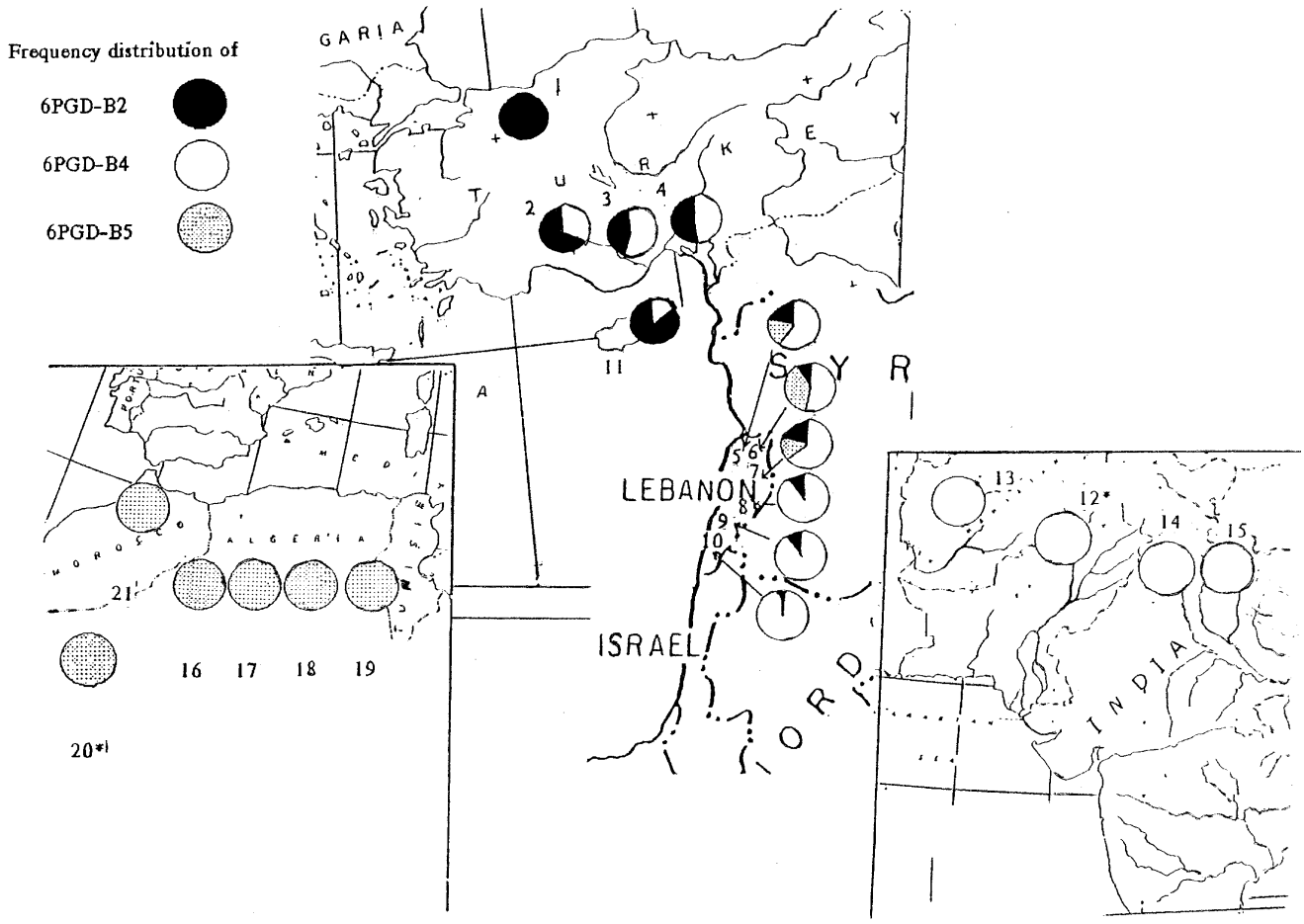
On the contrary, *C. libani* can be characterized by the presence of the 6PGD-B2, 6PGD-B3, 6PGD-B4, 6PGD-B5 alleles in a wide range of frequencies. The allele frequency data *(Table 2, Figure 3)* show a latitudinal cline pattern variation in *C. libani* (from North to South) at the 6PGD-B2 and 6PGD-B4 alleles, dividing the species into two distinct geographical races (Turkey and Lebanon). Similar conclusions were reached by ARBEZ *et al.* (1978) who noticed a clear distinction between Lebanese and Turkish populations by using morphological traits. Clinal variation patterns of allozyme frequencies have also been reported for Norway spruce (BERGMANN, 1975, 1978), Douglas fir (YANG *et al.,* 1977; YEH and O'MALLEY, 1980), Greek and Silver firs (BERGMANN and KOWNATZKI, 1988; SCHROEDER, 1989; SCALTSOYIANNES *et al.,* 1997 and submitted).

C. brevifolia, seems to be closer to the southern Turkish populations and it is discriminated from them by the higher frequency of 6PGD-B2 allele (0.80).

Comparison diaphorase (DIA) and menadione reductase (MR) zymograms revealed that the fastest migrating zones of the DIA enzyme system was identical to the MR-A zone. Among the four allozymes of the DIA-A locus, DIA-A2 allele was common in all species and populations while the DIA-A1 allele was present at a low frequencies (2% to 14%) only in *C. deodara* and it could be considered as a species specific allele. The DIA-A3 and DIA-A4 alleles appeared in *C. brevifolia* and some populations of *C. libani* at low frequencies. Absence of polymorphism at this locus was reported by MISHRA (1996) in *C. deodara* populations.

The high allozyme differentiation between *C. atlantica* and *C. libani* in many loci tested justifies their separation into two distinct species. The above is in disagreement with the findings of PANETSOS *et al.* (1992) who raised doubts about the separation of the two species into distinct taxa. One explanation of the previous discrepancy is that the previous work was mainly based on plant material that originated from arboreta where probably for some Cedar species identification problems occur.

On the basis of allelic frequencies we calculated the main parameters of genetic variability (He, P, A/L) were calculated. The values of the above parameters varied among the species *(Table 3).* For instance, *C. brevifolia* exhibits the highest values



*) Art. plantation in France

Figure 3. – Frequency distribution of the 6PGD-B locus in 21 populations of Cedar sp..

of heterozygosity (0.316) whereas *C. deodara* the lowest one (0.136). The levels of genetic variability among the species are in correspondence with the findings of PANETSOS *et al.* (1992) and MISHRA (1996), and comparable with other conifer species (LEDIG, 1986; GONCHARENKO *et al.,* 1994; SCALTSOYIANNES *et al.,* 1994). Nevertheless, the low heterozygosity noticed in *C. deodara* was also confirmed by MISHRA (1996) and was attributed to the fact that all populations of *C. deodara* shared the same ancestral gene pool. It should be noted that among the 21 populations studied, the two European populations, originating from artificial plantations in France (pop. 12, pop. 20), exhibited the lowest values of heterozygosity.

Genetic affinity among Cedar populations and species was quantified using NEI's genetic distance coefficient (D_N) (NEI, 1978). The D_N values, obtained for the 21 populations, are listed in *table 4.* The highest genetic distance among the species (*Table 4),* was noticed between *C. deodara* and *C. atlantica* (pop. 12 and pop. 21), while the lowest one was noticed between populations belonging in the same taxa (e.g. pop. 7 and pop. 9, pop. 12 and pop. 14).

The dendrogram *(Figure 4)* of the Cedar populations, based on UPGMA clustering, was constructed by using the D_N, and provides new information about the phylogenetic relationships among populations and species. In particular, the 21 populations are arranged into five distinct clusters corresponding to the following taxa: i) *C. libani* ssp. *libani* (for Lebanese populations), ii) *C. libani* ssp. *stenocoma* (for Turkish populations), iii) *C. libani* ssp. *brevifolia* (for the Cyprian population), iv) *C. deodara* (for Himalayan and Afghan populations) and v) *C. atlantica* (for African populations).

Although in the above cluster analysis, a distinction was noticed between *C. libani* and *C. atlantica,* our findings seem to be in agreement with the classification of the Flora of Turkey (DAVIS, 1965) and the Med-Checklist (GREUTER *et al.,* 1984) in which all Mediterranean Cedar species were treated as subspecies of *C. libani (*or *C. libanotica).*

In addition, even though the similarity between *C. brevifolia* and the isolated northern Turkish population was unexpected, events like convergent evolution and genetic drift may have caused this similarity, even though artificial seed transfer from Cyprus to North Turkey, in the distant past, may not be excluded.

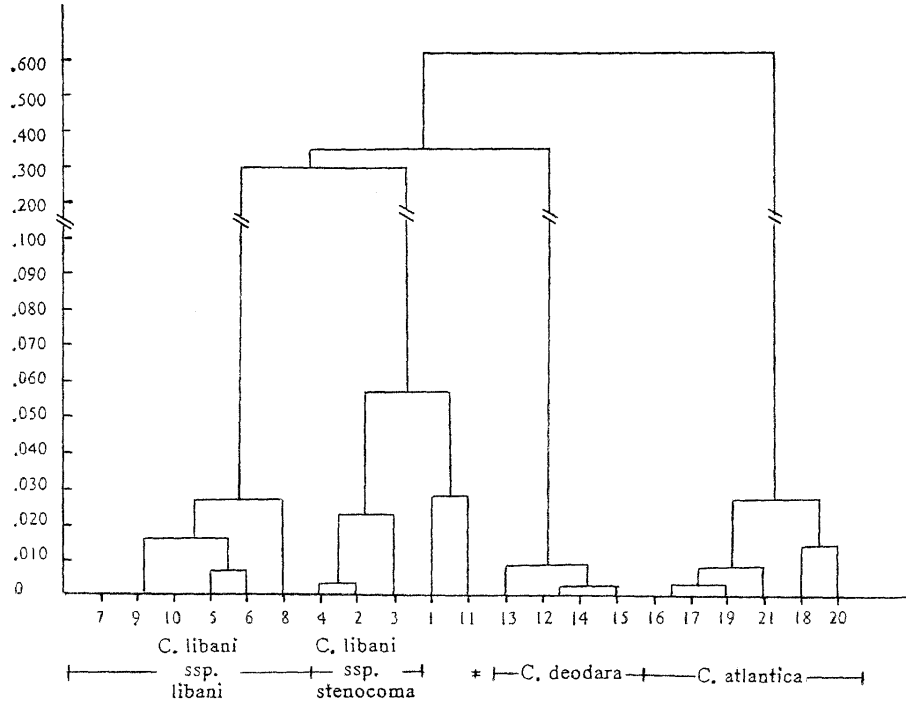
The present allozyme analysis provided important information on the variation of the genus *Cedrus* and filled, at least partly, gaps in our knowledge. Further studies on the genus are needed to expand our knowledge about its taxonomy and the extent of inter- and intra-populational variation which will help to develop strategies in applied and basic genetic research of Cedar species.

Table 3. – Genetic variability in 21 populations of *Cedrus* sp..

Species & Populations	Mean number of alleles per locus A/L	Percentage of loci polymorphic P (%)	Expected Heterozygosity He
C. libani			
1	1.50	33.3	0.096
2	2.17	66.6	0.225
3	2.00	66.6	0.207
4	2.33	83.3	0.254
5	2.50	100.0	0.332
6	2.17	83.3	0.272
7	1.83	83.3	0.235
8	1.83	50.0	0.229
9	2.00	83.3	0.245
10	2.00	83.3	0.225
Mean	2.03	73.3	0.232
C. brevifolia			
11	2.50	83.3	0.316
C. deodara			
12	1.50	50.0	0.119
13	1.67	50.0	0.170
14	1.50	50.0	0.134
15	1.50	50.0	0.119
Mean	1.54	50.0	0.136
C. atlantica			
16	2.00	50.0	0.228
17	2.00	50.0	0.229
18	1.83	50.0	0.202
19	1.83	50.0	0.155
20	1.50	33.3	0.124
21	1.83	66.6	0.158
Mean	1.83	50.0	0.183

Table 4. – Estimates of NEI's genetic distance coefficient based upon data from 6 loci between 21 populations of *Cedrus* sp..

Pop.	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21
1	*	.049	.080	.081	.441	.428	.457	.431	.471	.487	.028	.503	.543	.509	.500	.495	.464	.507	.498	.490	.518
2		*	.023	.004	.239	.229	.236	.258	.256	.268	.025	.370	.397	.372	.361	.394	.368	.458	.387	.408	.382
3			*	.024	.245	.226	.210	.236	.222	.220	.071	.261	.288	.266	.262	.409	.380	.429	.408	.405	.423
4				*	.232	.222	.216	.262	.239	.248	.039	.357	.378	.357	.346	.372	.348	.445	.364	.388	.353
5					*	.007	.016	.014	.017	.024	.301	.371	.379	.371	.362	.557	.537	.660	.526	.562	.510
6						*	.010	.023	.014	.016	.297	.340	.337	.338	.328	.591	.569	.685	.557	.586	.541
7							*	.034	.000	.000	.318	.283	.291	.283	.276	.677	.650	.773	.644	.673	.628
8								*	.034	.033	.335	.326	.339	.327	.319	.539	.512	.603	.519	.537	.523
9									*	.000	.333	.281	.293	.282	.278	.723	.694	.809	.687	.710	.678
10										*	.356	.262	.273	.264	.260	.723	.692	.795	.689	.705	.686
11											*	.483	.500	.483	.470	.420	.397	.466	.411	.416	.413
12												*	.013	.000	.005	.923	.867	.912	.905	.887	.958
13													*	.007	.007	.790	.747	.779	.768	.755	.819
14														*	.001	.900	.844	.895	.882	.871	.934
15															*	.879	.826	.880	.863	.855	.912
16																*	.000	.021	.002	.012	.009
17																	*	.030	.005	.016	.012
18																		*	.035	.014	.063
19																			*	.010	.003
20																				*	.027
21																					*



*) *C. libani* ssp. *brevifolia*

Figure 4. – Dendrogram of genetic distances of 21 Cedar populations.

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