

## **Evaluation of Genetic Distances from the Origins of Comparative Culture Beech Cărbunaru-Maramureș-Baia Sprie**

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**Abstract.** One of the consequences of the most valuable populations represents the strategy plan of genetically resources utilization for export. It is known that in Romania exist centres of extremely valuable genes, with remarkable growing performances in different sides from Europe. In this way has creating the premises of reproduction forestry materials for enlarging of export with its. This way is available because these premises counting the environment's conservation and durable development principles al global level, which has promoted national strategies and a substantial growing of forest areas.

**Keywords:** diversity, Euclidian distance, basic diameter, survival, similarities

### INTRODUCTION

The present researches resemble the tremendously plasticity and the high beech genetic diversity, a quite "young" species, so that is was born the idea that it is important to be established which beech origins are most indicated for extreme spas, which origins produce high quality wood, which have the best growth, have the highest frost resistance, which of them have the highest recreational and landscape value or any other social use.

### MATERIALS AND METHODS

In the comparative culture of descent installed at Cărbunaru, Baia Sprie forest management unit, in the Maramureș County, where the study material was composed of 26 descents of beech (*Fagus sylvatica* L.), representative for 8 European countries, from almost the entire natural area of the species, including Romania, the seedling plants used in the setting up of the culture were two years old and came from the nursery of the Institute of Forest Genetics in Schalembeck, Germany.

The culture's area of settlement was in the H2 zone – The Ciceului Hills, with a cold and wet climate where the biggest area is represented by the beech hills, subareas H 240-Beech hills - main area species: beech, altitude range 500-700 m, while the experimental appliance for the culture was a 3x4 rectangular railing, with three repetitions, completely randomized, each unitary lot covering 10x10 m, and being made up of 50 plants placed on five rows with a 2 meter distancing in between and 1 meter distance within the row (Ienciu, Savatti, 2004).

For each analyzed characters there were calculated the main statistical parameters: the medium, the standard deviation, minimum and maximum values, the amplitude variation, variance and variance coefficient (Ceapoiu,1968).The facts' analyse was performed after the STATISTICA program (Complete Statistical System, StatSoft, Inc., 1991). For the graphics' marking there were used computer graphic programs from STATISTICA and Excel.

The similarity or differences (distances) study between the tested origins, based on the results registered for more characters, was made through the “cluster” analyzed, using the Euclidian distance from two points in the multidimensional space, determined by many vectors (characters), provided that there is no correlation between these (the determined position should not be influenced by covariance between the characters) (Lenfort-Buson, Vienne, 1985). For eliminating the results distortion, it was used the values standardization, which was carried out by replacing the gross value with the report between the difference from this value and the experience medium of the standard deviation.

The distance was calculated by using the formula:  $d_{xy} = [\sum_i (x_i - y_i)^2]^{1/2}$ , and the group was carried out with the “single linkage” method, where the distances between the groups are determined by the distance between the closest components (the closest neighbors) in the different types. This method is appropriate to the intended purpose and was preferred for other genetically distance types (Gregorius, 1984).

## RESULTS AND DISCUSSION

There were calculated the Euclidian genetic distances, that allowed the contacts' establishment between the origins but also the group depending on the existing similarities. If we take into consideration the survival, it is found that the origins are divided into two big parts (Fig. 1). First part contains 12 origins from France, Denmark, Sweden and Germany and the second part includes 13 origins from Germany, Slovakia, Slovenia, Ukraine and Romania.

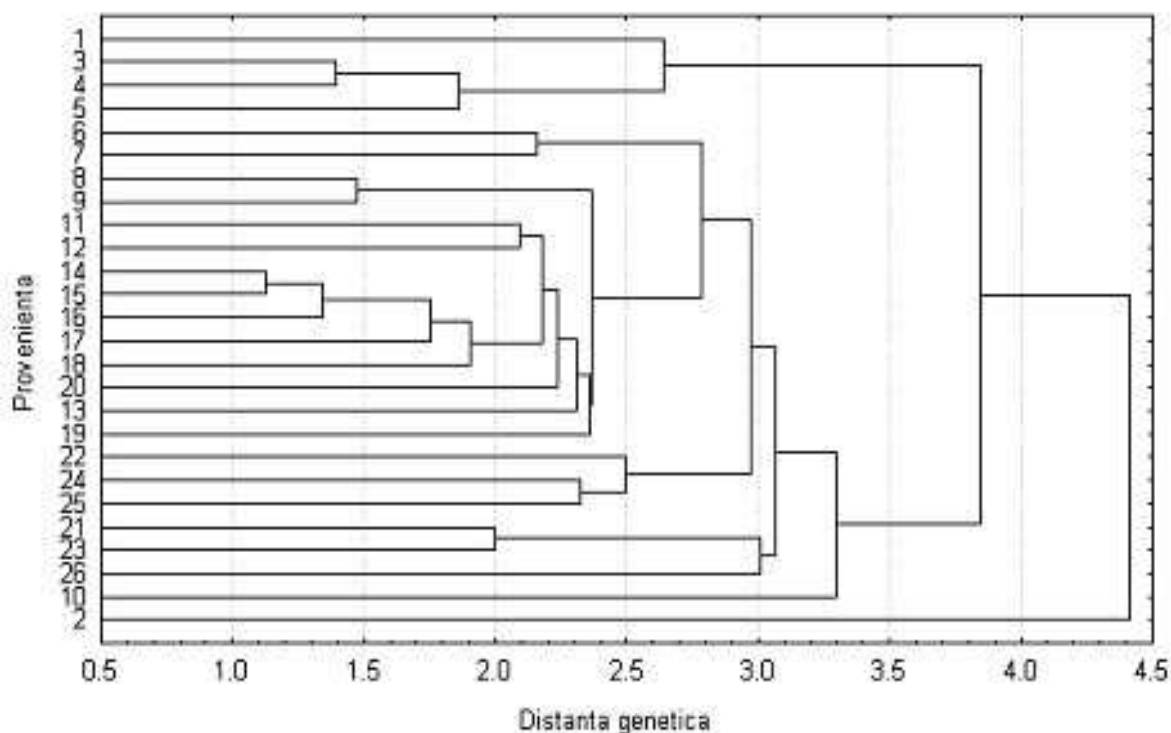


Fig. 1. The Euclidian genetic distance of the beech origins depending on the survival in the comparative culture Baia Sprie-Cărbunaru-Maramureș

It is noted that all the three origins from France behave differently, namely the 11-F.D. origin des Charmettes - France and 23-F.D. de Villafans – France are parts of the first group, while the 18- F.D. de Ligny en Barrois - France origin is not part of the two big groups, but is

close related to them. The origins from Germany do not belong to the same part, four of them belong to the first part, the other ten belong to the second. It is noticed that the origins situated on high altitudes, like the origin 137-Postojna - Slovenia and 150-Sovata (25) - Romania belong to the same part.

The highest level of differentiation is registered between the origin 18- F.D. de Ligny en Barrois - France that was separately grouped, between this and the others is the highest genetic distance.

For the entire height, the origins' group was different so that there are registered three big groups, two origins namely the origin 92-Elmsten-Sii Appenthal - Germany and 104-Zwiesel - Germany are separately grouped (Fig. 2).

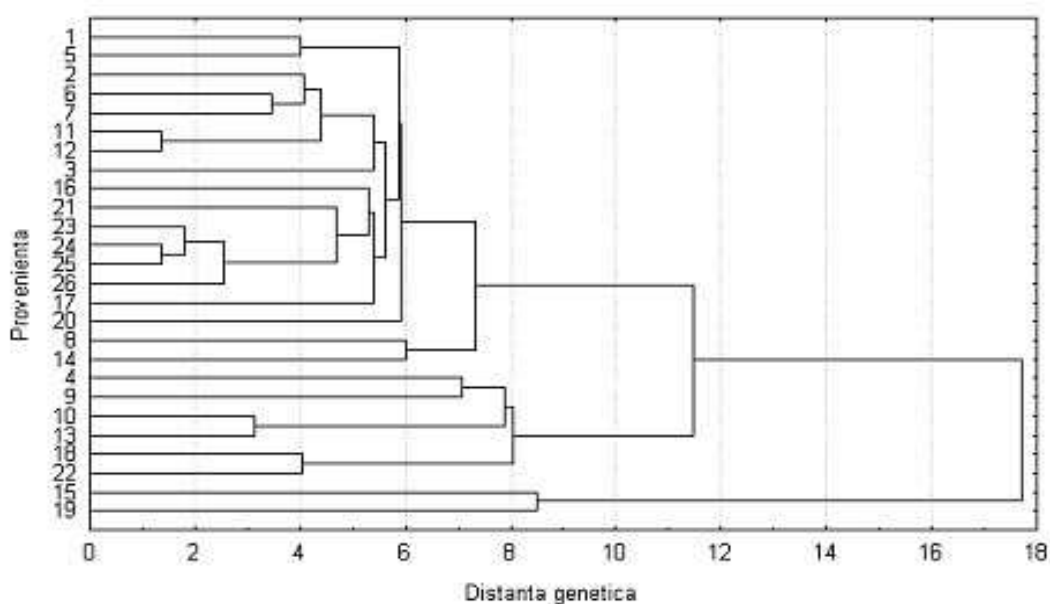


Fig. 2. The Euclidian genetic distance of the beech origins depending on the entire height of the comparative culture Baia Sprie-Cărbunaru-Maramureș

It was found, that in this case the origins from France belong to different parts, but the group is not the same for the survival namely the origin 11-F.D. des Charmettes - France and 18-F.D. de Ligny en Barrois – France belong to the first part and the origin 23-F.D. de Villafans - France belong to the second part. Also, the origins from Germany are not grouped together, two of them belonging to the first part, four to the second one, six to the third and the other two being separately grouped, like mentioned above.

The origins from Slovakia also belong to two groups, namely 129-Smolenice - Slovakia and 130-Trencin - Slovakia to the second part and 137-Postojna - Slovenia belong to the third group. The Romanian origins belong all to the second part. Concerning to the genetic differentiation, it was registered that the two German populations that are separately grouped, have the highest level of differentiation comparing to the other studied populations.

In case of the basic diameter the origins are also divided into three parts that are different from the others obtained (Fig. 3).

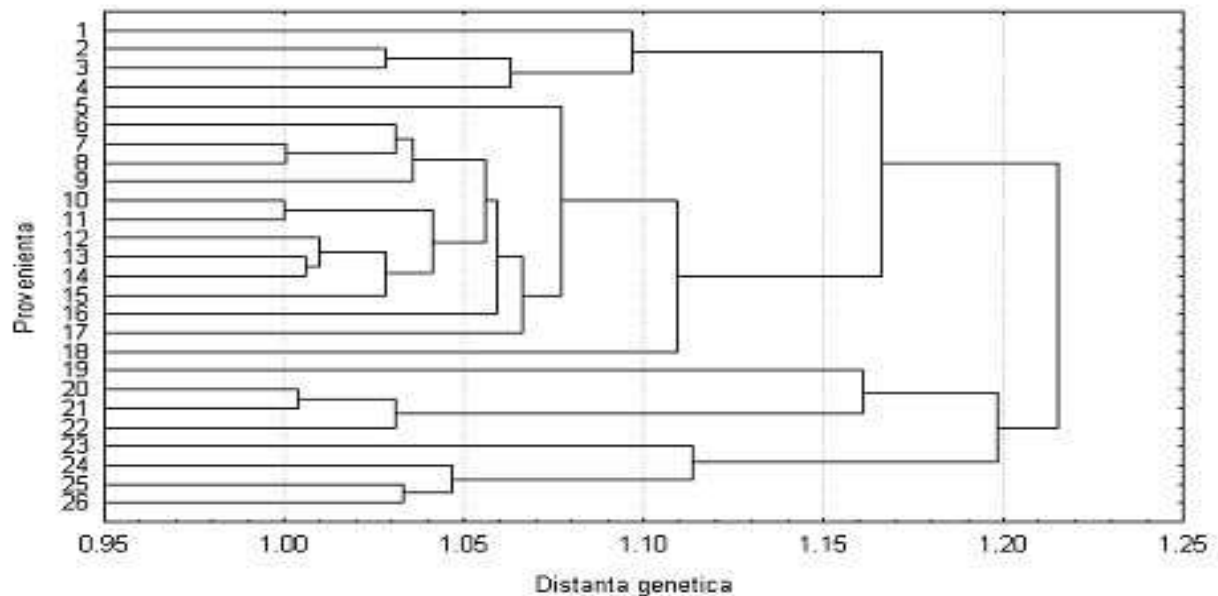


Fig. 3. The Euclidian genetic distances of the beech origins depending on the basic diameter of the comparative culture Baia Sprie-Cărbunaru-Maramureș

For this character the origins from France belong to the first group, which also includes 26-Glorup - Denmark. The German origins belong to the second part, except 99-Ehingen - Germany and 104 – Zwiesel - Germany that belong to the third one.

The origins from Slovakia are also grouped together in the third part, which also includes the two Romanian origins, this group registers the highest level of differentiation comparing to those of the second part.

## CONCLUSIONS

By estimating the genetic distances between the beech origins there could be determined the similarities and differences between the populations, so it was resembled the level of similarity and divergence but also the behavior of the Romanian origins, which register a high level of differentiation comparing to the others. This represents an important aspect for selecting them in order to use these as reproductive forest material.

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