Genetic Characterization of an Isolated Alpine Population Using Seroprotein Markers: Vallouise (Briançonnais)

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Abstract

The aim of the "Dauphiné Project" is to reconstruct, with a wide perspective and multidisciplinary approach, the anthropological history of some mountain populations in both the French and Italian parts of the Dauphiné. Mountain populations present peculiarities that make them interesting to anthropology: living in difficult climatic conditions, continuous biological and socio-economic adaptation.

The present study is an analysis of some seroprotein markers in blood samples of subjects living in mountain communities in the Western Alps and native to the area for at least two generations.

The data for these seroprotein systems are the first results of the biological study of populations of the Western Alps. Thus they are an important contribution to our otherwise scanty knowledge about the distribution of these polymorphisms in the populations under study.

Communication

The Vallouise is a small valley about 12 Km from Briançon in the Hautes-Alpes department, situated in the French part of the Dauphiné. It is a region closed between tall mountains which in the past were an obstacle to exchanges and communication of any kind, thus contributing to the constant isolation of the inhabitants.

The Vallouise population is particularly interesting: the inhabitants have become rather homogeneous due to the processes of adaptation to the alpine ecosystem and the long period of endogamy caused by geographical isolation and an almost total absence of immigration.

There is a clear need to collect data from this population since there is the risk that it may disappear or at least lose its interesting genetic characteristics acquired through isolation.

Therefore, we have genetically characterized the Vallouise community using three seroprotein markers: the third component of complement (C3), the group specific component (Gc) and properdin B factor (Bf), very

important markers in human genetics research.

The sample consists of adult males and females carefully selected on the basis of their origin in the valley for at least two generations.

Determination of the C3, Gc and Bf systems was performed by cellulose acetate electrophoresis followed by immunofixation with specific antiserums (anti-Gc, anti-C3, anti-Bf).

The results were compared with those in the literature on northern European and Mediterranean populations in order to identify origins and microevolutionary processes, as well as biotransformations related to environmental adaptation.

To analyze the genetic relationships between the populations, we applied statistical procedures (*maximum likelihood*) and multivariate analyses (principal components and cluster analysis) (1-2).

The serum polymorphism analyses revealed only one rare polymorphism for properdin, the STF variant; the polymorphisms of the other proteins are the commonest ones, although they exhibit peculiar allele frequencies (Tab I.).

		Alleles frequencies
C ₃	S	0,4268
	F	0,5732
Ge	1	0,5933
	2	0,4067
Bf	S	0,5800
	F	0,4200

Tab. I

For example, the low frequency of the GcI allele (0,59 vs. the European average 0,73) places the Vallouise population among European populations with the lowest frequencies; indeed it represents a much lower limit than the lowest values found in Europe: Germans (0,68) and Polish (0,66). Moreover, there are high frequencies of the Gc2 allele (0,40), exceptional in Europe although high frequencies have also been observed in Sweden, Finland and in a region of the Pyrenees, and of the C3F allele (0,57), high with

respect to other European populations.

gene pool of the Vallouise population.

The results can probably be interpreted as the combined effect of drift and very low local gene flow. Comparison with other populations of northern Europe and the Mediterranean area generally shows that the Vallouise population presents mainly European characteristics. However, some peculiar aspects have emerged, probably attributable to the strong geographical isolation but also revealing the possibility of past contacts with northern European peoples (fig. 1, 2). Indeed, invasions by such populations are historically documented and it is likely that the traces of these dominations are not only historical but also remain in the

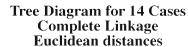
Reference

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- 2. Felsenstein J., Cladistics, 1989, 5: 164.

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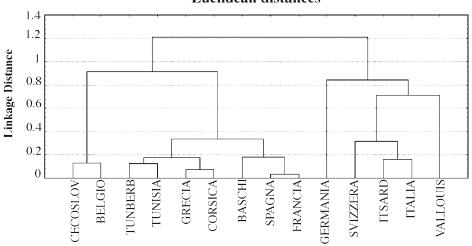


Fig. 1 - Cluster analysis of the seroprotein polymorphisms in various European and North African populations

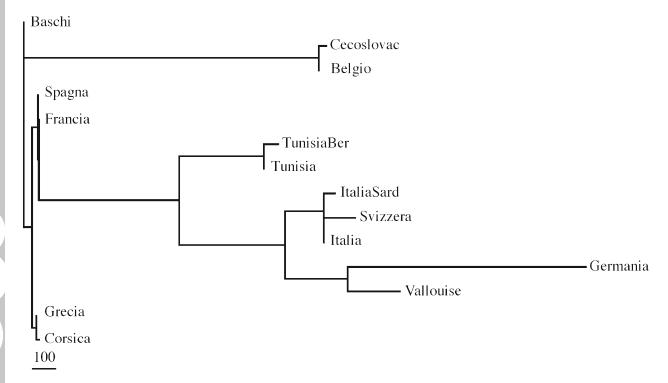


Fig. 2 - Dendrogram obtained according to the maximum likelihood principle