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The genetical influence of the Matterhorn (Monte Cervino)

Introduction

The Matter valley and the Saas valley are two similarly situated side valleys of the Rhône river (Figure 1). This sets an ideal framework for comparison of population dynamics in the two valleys under almost identical evolutionary conditions. Therefore, allele frequencies of 14 hematological systems were analysed and genetical distances wer compupted.

Material and Methods

6 villages of the Saas valley and 7 of the Matter valley were compared.

8 erythrocyte enzymes (ACP, ADA, AK-1, ESD, GALT, GLO-1, 6-PGD, PGM) and 6 serum proteins (Alb, AMY, Bf, C3, GC, Hp) have been electrophoretically analysed

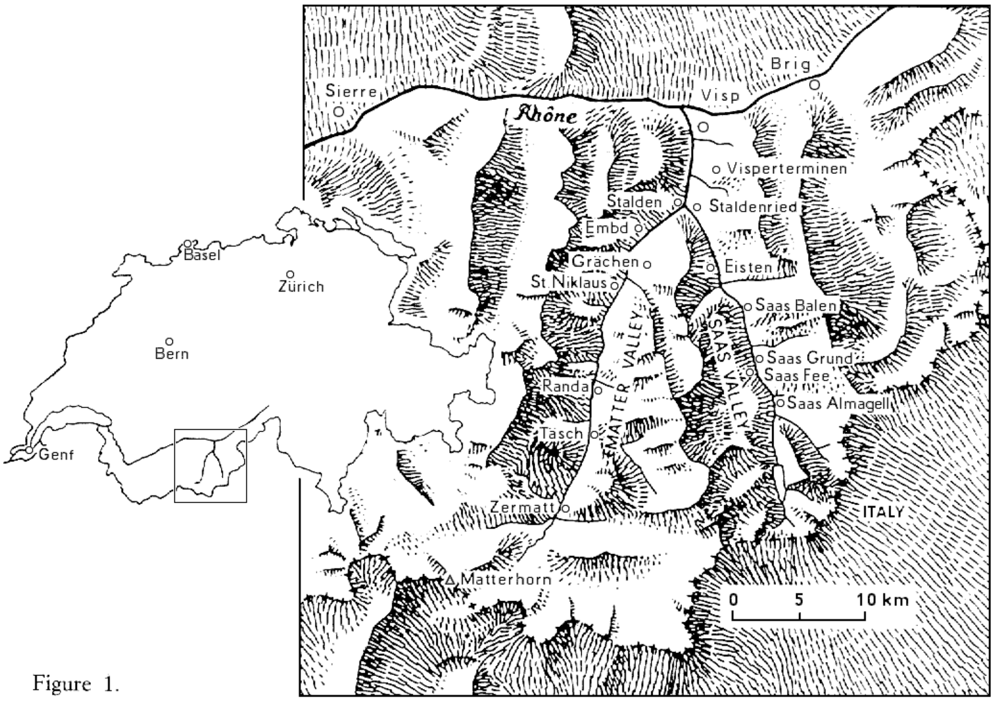

Figure 1.

for 883 individuals. Allele frequencies of the region around *Brig* (main Rhône valley) (Marks, 1983) and a representative sample of the whole Swiss population (e.g. Scheffrahn and Biedermann, 1981) have also been included in the comparison.

Cluster analysis was done using the genetical distance formula of Prevosti et al. (1975) and according to the unweighted pair-group method with average linkage (Sneath & Sokal, 1973). A computer program was used which is identified as NT8, version March 1982, developed by G. Bächli of the Zoological Institute, University of Zürich.

Results

Allele Frequencies

The frequencies show an irregular distribution through the villages of each valley. They do *not* fluctuate gradually to form a genetical cline (Figure 2).

This problem reflects the relative isolation of at least some of the villages in each valley (→ local Mendelian populations).

The frequencies in several systems differ distinctly between the two valleys.

An eventual exchange between the valleys, therefore, seems to be rather restricted. The genetical characteristics in both valleys have probably developed independently.

Cluster Analysis

All villages of the Matter valley were comprised in one cluster (Figure 3).

The cluster of the Saas villages is less distinctly defined. *Saas Almagell* for instance forms its own cluster, while *Saas Fee* is even included in the Matter cluster.

The sample of the whole Swiss population is also included in the Matter cluster, as well as the Brig sample (not shown here).

The Saas population as a whole is genetically more heterogenous and also more isolated from the main Rhône valley. The Matter population as a whole is genetically more homogenous.

Population Increase

Touristic activity and upcoming industry has led to an extensive population increase in some villages (Figure 4).

Large villages show smaller genetical distances relative to each other than to small villages (Figure 5).

Conclusions

In spite of supposedly similar evolutionary preconditions the two valleys differ remarkably in in their genetical composition.

Touristic and industrial activity led to population increase in only some of the villages.

Every intense increase in population in any village coincides with a reduced genetical distance to the main Rhône valley (Brig) and to the whole Swiss sample. Therefore, the increase probably can be attributed to immigration rather than to direct population growth within the villages.

A small increase predominates in the Saas populations. They have diverged in genetical composition due to isolation. The touristic centre of Saas Fee represents the only exception.

A great increase predominates in the Matter populations. They converge in genetical composition due to migration.

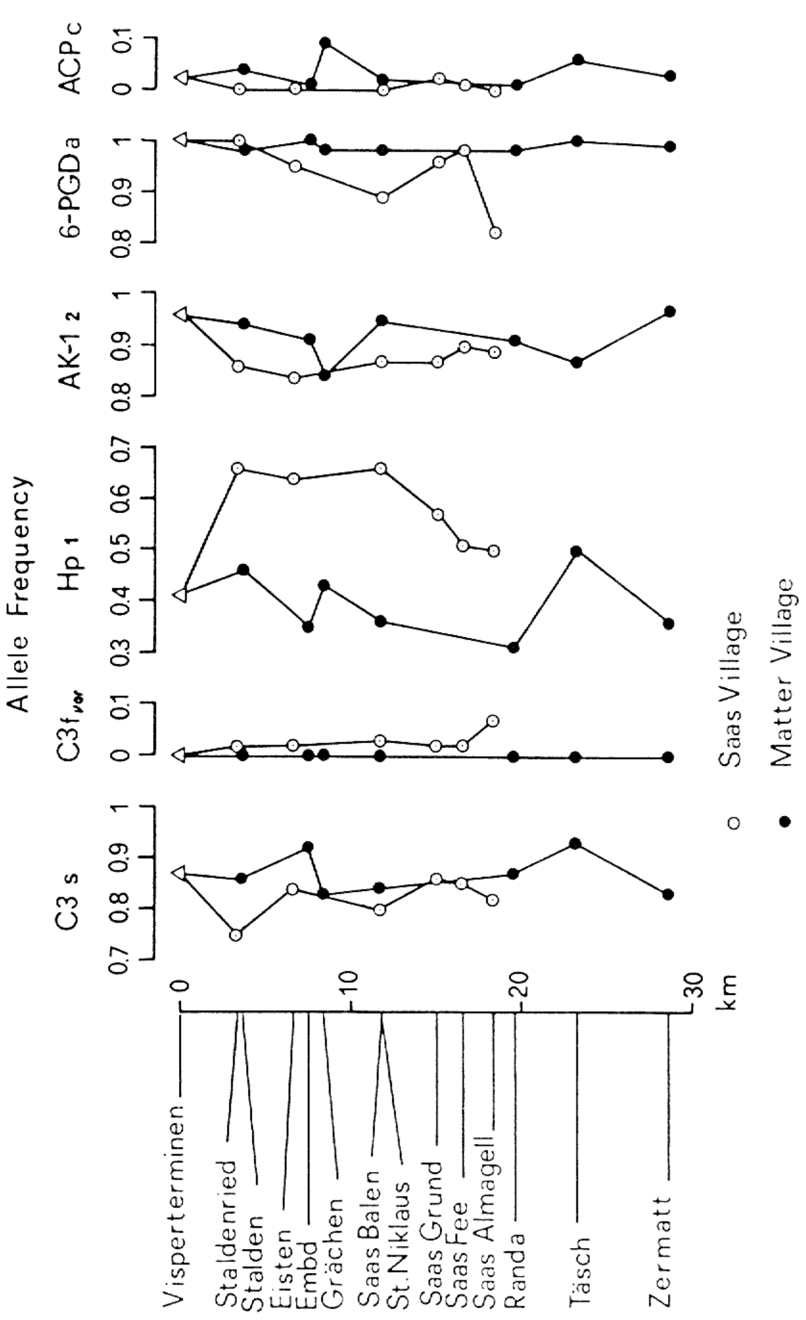
Allele Frequency
C3 s
0.7
0.8
0.9
1
C3f var
0
0.1
Hp 1
0.3
0.4
0.5
0.6
0.7
AK-1 2
0.8
0.9
1
6-PGD a
0.8
0.9
1
ACP c
0
0.1
0
10
20
30
km
Visperterminen
Staldenried
Stalden
Eisten
Embd
Grächen
Saas Balen
St. Niklaus
Saas Grund
Saas Fee
Saas Almagell
Randa
Täsch
Zermatt
○ Saas Village
● Matter Village

Figure 2.

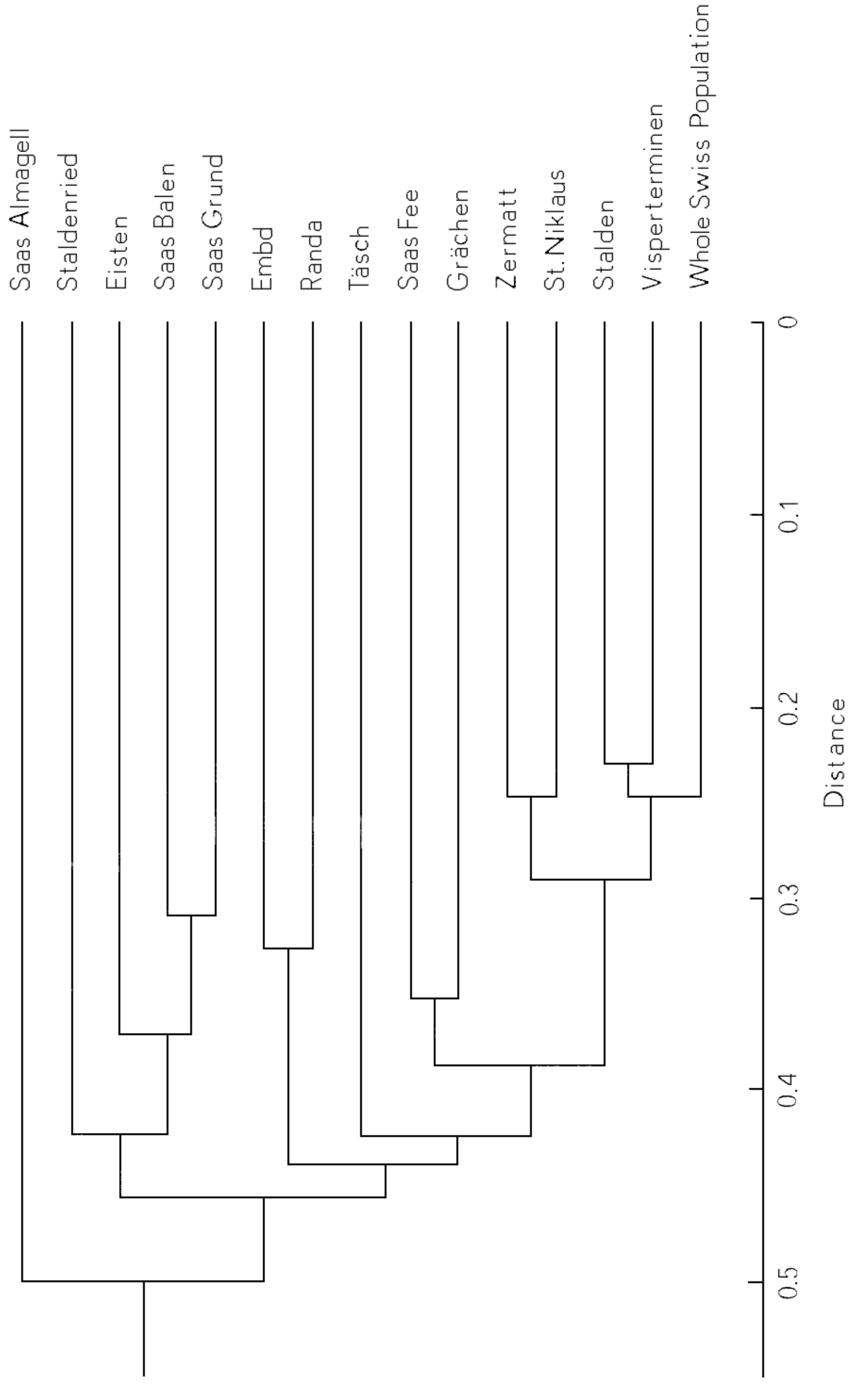
Saas Almagell
Staldenried
Eisten
Saas Balen
Saas Grund
Embd
Randa
Täsch
Saas Fee
Grächen
Zermatt
St. Niklaus
Stalden
Visperterminen
Whole Swiss Population
0
0.1
0.2
0.3
0.4
0.5
Distance

Figure 3.

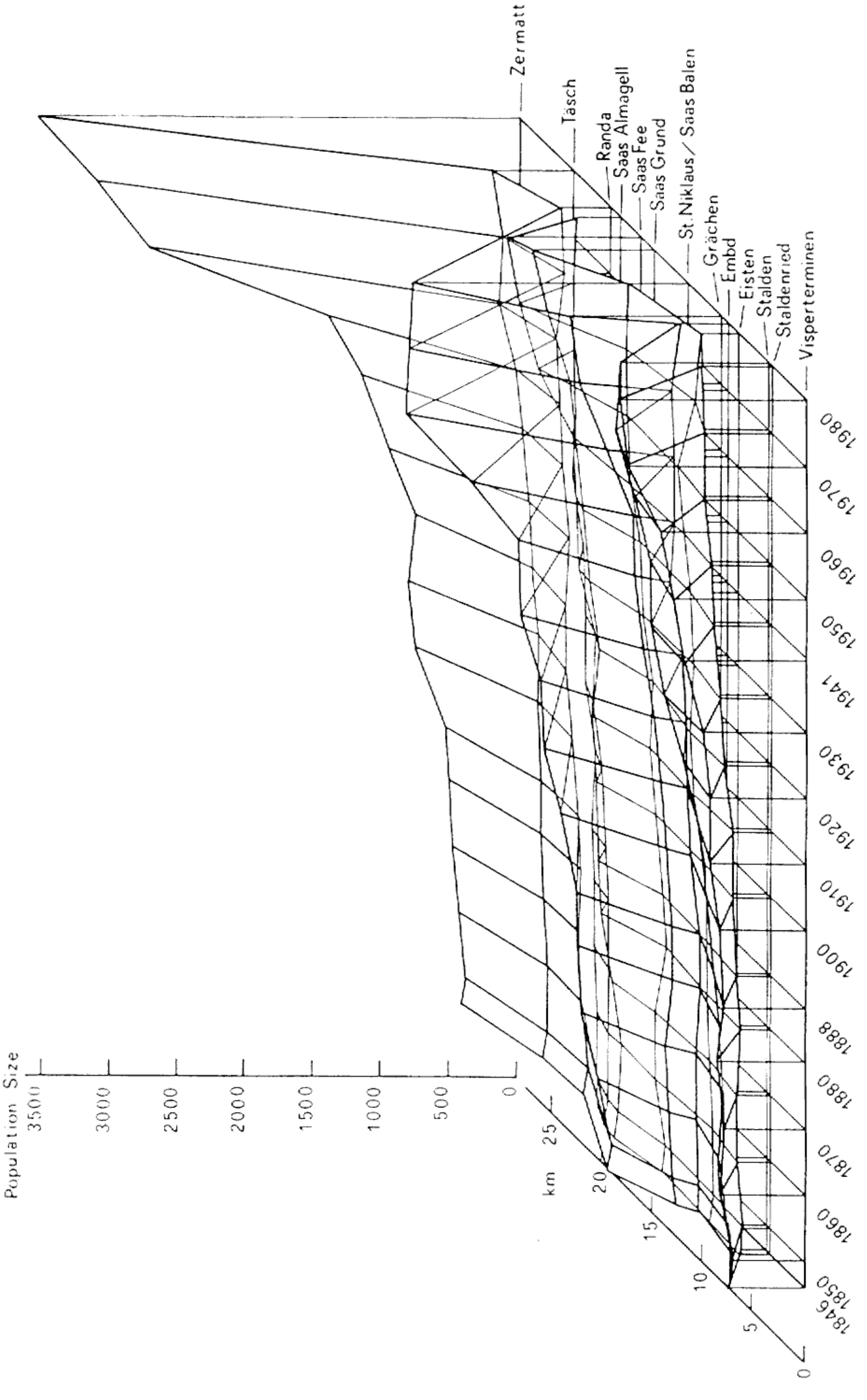
Population Size
3500
3000
2500
2000
1500
1000
500
0
km
0
5
10
15
20
25
Zermatt
Täsch
Randa
Saas Almagell
Saas Fee
Saas Grund
St. Niklaus / Saas Balen
Grächen
Embd
Eisten
Stalden
Staldenried
Visperterminen
1846
1850
1860
1870
1880
1888
1900
1910
1920
1930
1941
1950
1960
1970
1980

Figure 4.

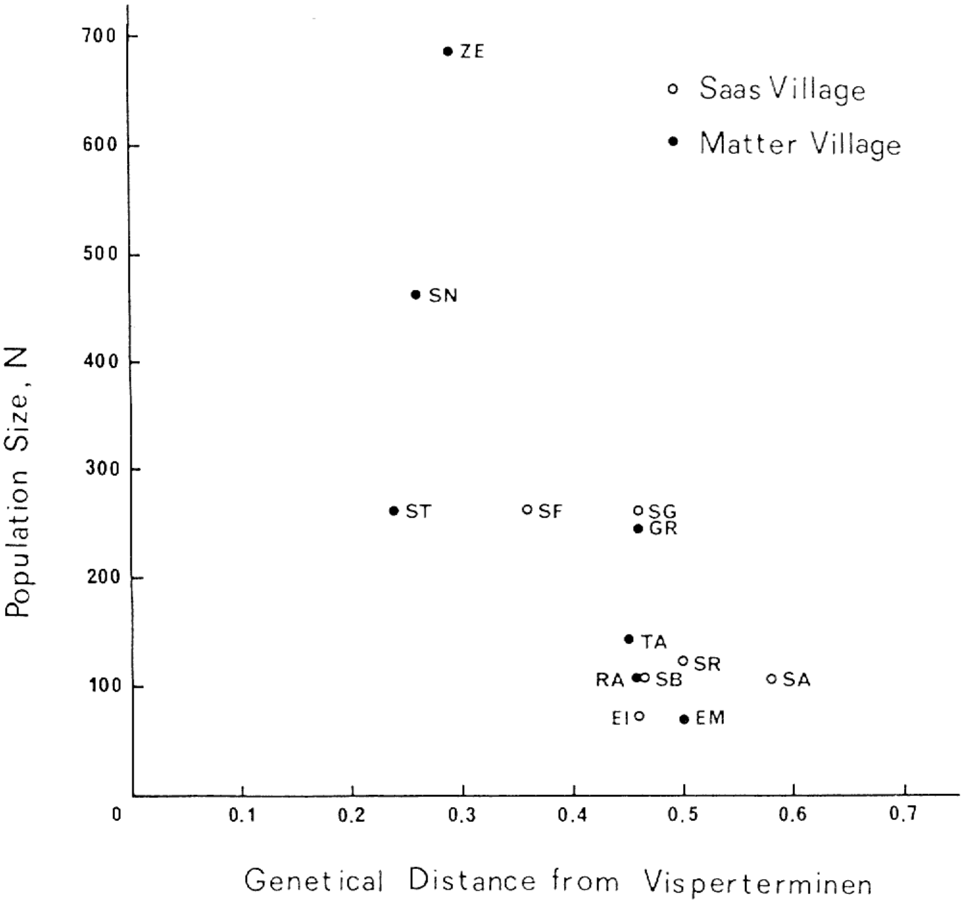

Figure 5.

Acknowledgments

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References

Marks E. 1983. *Hämatogenetische und populationsgenetische Studie über die Bevölkerung des mittleren Rhonetales (Kt. Wallis).* Unpubl. Diplomarbeit, Anthropol. Inst. Univ. Zürich.

Prevosti A., Ocaña J. and Allonso G. 1975. Distances between populations of *Drosophila subobscura* based on chromosome arrangement frequencies. *Theoretical and Applied Genetics*, 45: 231-241.

Scheffrahn W. and Biedermann V. 1981. Demography and serogenetics of an isolated population in the Swiss Alps. In: *Referate 9. Internat. Tag. Ges. Forens. Blutgruppenkunde, Bern,* pp. 83-88.

Sneath, P. H. A. and Sokal R. R. 1973. *Numerical taxonomy.* W. H. Freeman and Co., San Francisco.