Comparison of Population Genetics of the Single Locus Probes pS194 and pL427-4

W. Martin*, H.H. Hoppe, M. Muche, Institut für Blutgruppenserologie und Genetik, Hamburg und L. Henke, Labor für forensische Blutgruppenkunde, Düsseldorf

Summary

Comparing population genetics of different laboratories for the single locus probes pS194 (D7S107) and pL427-4 (D21S112) it became evident that considerable differences of the distributions for the calculated KB values of the fragments were present. The forms of the distribution curves were identical for the same population, but deviations of the determined KB-values for the fragments were found according to the technique used. On the example of the two probes, these deviations can be shown to be linear corresponding to the electrophoresis technique: particularly according to the agarose concentration and -less- to the amount of DNA applied. By that, we have the possibility to combine population genetic data of different laboratories using different techniques after linear correction of the distribution tables or curves. Since this interdependence is valid for all probes, it is quickly possible to compile relatively extensive population genetic tables as a reliable basis for the statistical evaluation in cases of disputed paternity.

Introduction

Fragment size distributions of digested human DNA hybridized with different probes showed deviations in the calculated KB values owing to the techniques used. Dykes et al. could show that dependence especially exists upon the concentration of the agarose gel used for the run and the amount of DNA incorporated into the gel (Fig. 1). This interdependence seemed to be linear in the ranges of agarose concentration and amount of DNA usually used. The goal of our investigation was to find out how different population genetic studies with deviations in the KB values can be corrected and combined in order to get large fragment size distributions for different probes as a basis for a safe statistical evaluation in paternity testing.

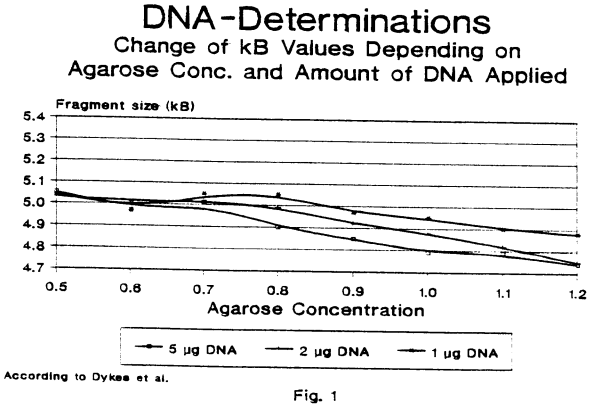

Fig. 1

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Material

Fragment size distributions of the probes pS194 (D7S107) and pL427-4 (D21S112) from Dykes (Denver, USA, Lab 1) and our own laboratory (Hamburg, Germany, Ham) are compared. The sample sizes were: pS194 n=1903 (Lab 1) and n=225 (Ham); pL427-4 n=330 (Lab 1) and n=100 (Ham).

Results and discussion

The deviations in the distributions are evident as shown in Fig. 2 (pS194) and Fig. 3 (pL427-4). Since the peakes of the distribution curves are obviously in the same distance from eachother, the reason for this shift must be a technical one. Experiments showed that changes in the agarose concentration not only led to differences in the running distance but also in the fragment sizes determined. Simple linear correction of the deviations in fragment size determinations gives identical distribution curves as shown in Fig. 4 and Fig. 5.

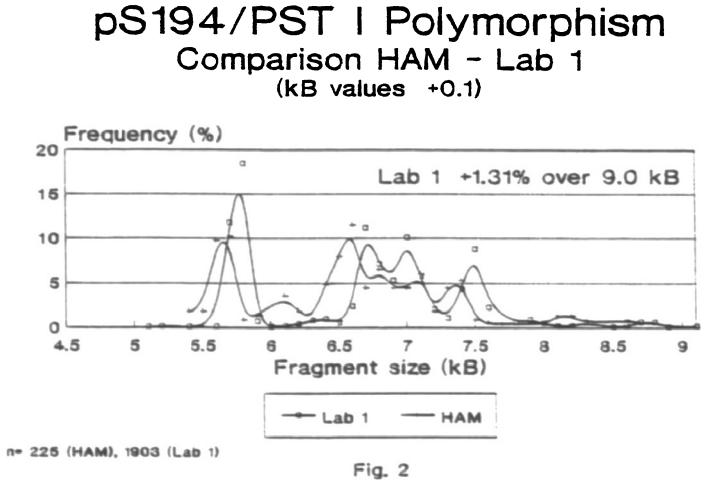

Fig. 2

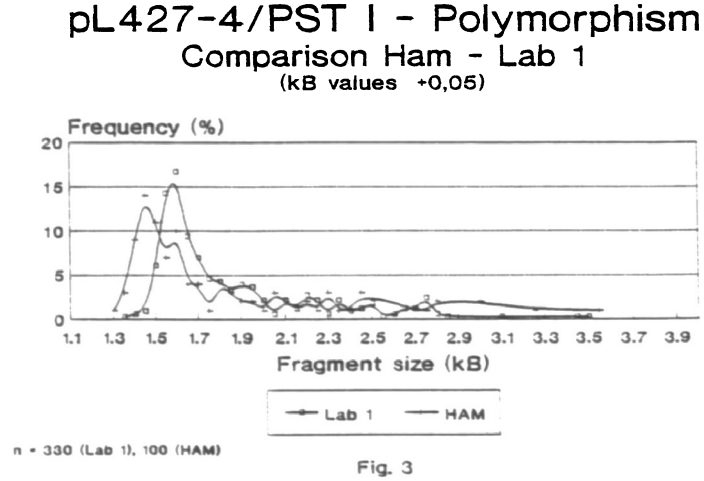

Fig. 3

The KB value for the correction can easily be ascertained by determining the KB value of the distance of the main peak of a distribution curve. Persisting small differences in distributions will not influence the correctness of the statistical evaluations , since these calculations have to be done with a certain range (e.g. ± 2% KB) of the actual KB value determined for a fragment. If, in addition, the calculations are performed with a minimum frequency of 0.01, possible errors are eliminated, while the information remains high enough as to the proof of paternity.

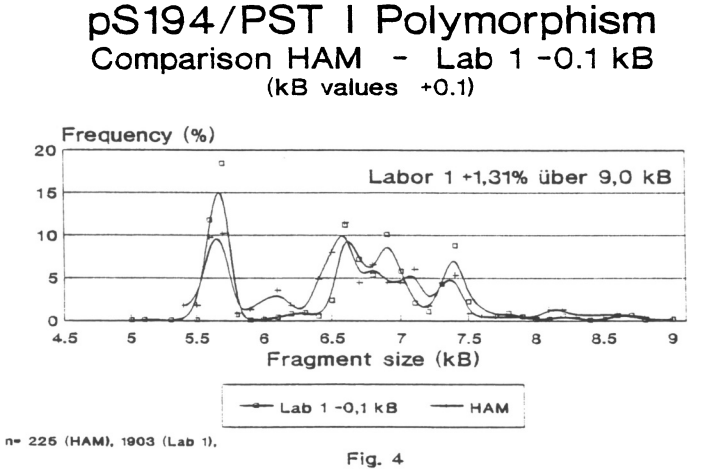

Fig. 4

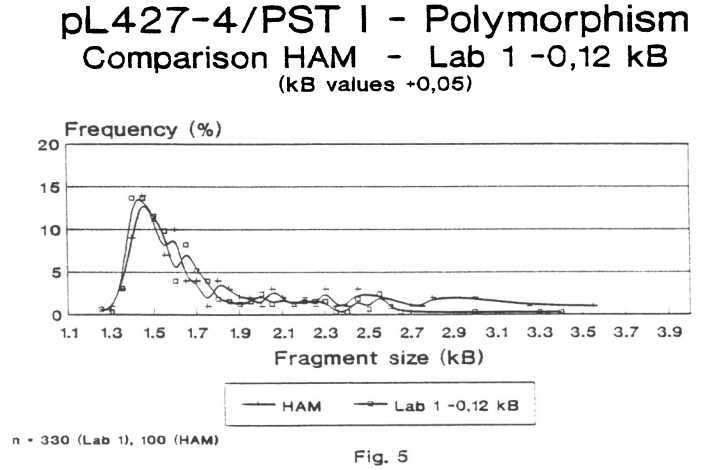

Fig. 5

As the examples of the probes pS194 and pL427-4 show, it is possible to combine population genetic data of different laboratories using different techniques after linear correction of the distribution tables or curves. Since this interdependance is valid for all probes, it is quickly possible to compile relatively extensive population genetic tables as a reliable basis for the statistical evaluation in cases of disputed paternity.