J. Hum. Ecol., 7 (1): 55-57 (1996)
PRINT: ISSN 0970-9274 ONLINE: 2456-6608
DOI: 10.31901/24566608.1996/07.01.11

Is the Y/F-Index Suitable For Population Genetic Studies?

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KEY WORDS Y/F-Index. Y-Lenght Polymorphism. Computer Supported Analysing Systems.

ABSTRACT In the late 1960's and 1970's the Y-length polymorphism was used in many population genetic studies. Most of these investigations were made with the Y/F-index. In this study the value of this method is critically discussed applying a computer supported analysing system.

INTRODUCTION

Extreme variations of the length of the Y-chromosome were first discussed at the London Conference (1963). Cohen et al. (1966) showed that the length of the Y-chromosome varied not only from individual to individual, but also from population to population. The heterocromatic region of the end of the long arm has been considered responsible for the variation of the length of the Y-chromosome (Schnedl, 1971; Nielsen and Friedrich, 1972). The reason for this length polymorphism was discussed by some authors assuming a strong winding up of the chromatin (Wennström and De La Chapelle, 1963; Court Brown, 1967), while others supposed a duplication or deletion inside the heterochromatic segments (Wahlström, 1971; Verma et al., 1978).

In the late 1960's and the 1970's, several investigations were made with the Y/F-index. Table 1 shows the results of these investigations. They were carried out with different techniques: Different staining methods and different methods of measuring the length of the chromosomes. So, the question is, is it possible to compare the results of these investigations? The aim of this study is to discuss whether it is recommendable to employ the Y-length polymorphism in the form of Y-indices in population genetic studies.

MATERIALS AND METHODS

Blood samples were taken from unrelated students of the University of Bremen. Standard protocols were used for metaphase preparations and Giemsa staining. Five well spread metaphase plates from each individual were scanned into the computer. The picture of the metaphase plate were optimized with the software OPTIMAS 4.0. The measurement of the chromosomes was also done with this software. Figure 1 shows a scanned metaphase plate as it is seen on the computer screen. To study the length varition among Y-chromosomes, the Y/F index was calculated as follows: Y/F = total length of the Y-chromosome/average length of the F-group chromosomes (19 and 20). The F-group chromosomes were measured diagonally from one end of chromatid A to the other end of chromatid B and the Y-chromosome was mesured from the end of the short arm to the end of the long arm.

RESULTS AND DISCUSSION

It was not possible to make reproducible measurements. At first, we recognized that it was not unimportant which diagonal of the F-group chromosomes was measured, because some of them were shorter than the others. The reason for variation of the index therefore, could be the technique of metaphase preparation: the average length of the F-group chromosomes varied considerably. So, the Y/F index also varied considerably, within the same metaphase. Secondly, it was not possible, when measuring the same chromosome twice, to obtain the same measurement. Calculating with the results of the dif-

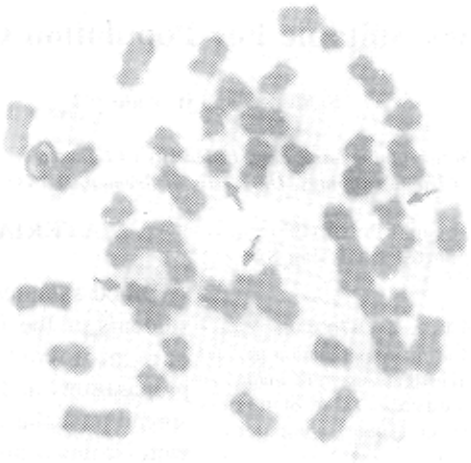

Fig. 1. Scanned metaphase

Tabl. 1 : Y/F-Indices in different populations

Population	*n*	*Y/F*	*SD*	*References*
crim. Swedish	106	0.89	0.09	Akesson & Wahlström (1977)
norm. Swedish	49	0.88	0.07	Akesson & Wahlström (1977)
ment.Danish	162	0.89	0.07	Christensen & Nielsen (1974)
norm. Danish	140	0.84	0.07	Christensen & Nielsen (1974)
newb. Danish	104	0.84	0.07	Nielsen & Friedrich (1972)
crim. Danish	407	0.94	0.07	Nielsen & Friedrich (1972)
newb. Danish	140	0.83	-	Nielsen & Henriksen (1972)
crim. Danish	151	0.88	-	Nielsen & Henriksen (1972)
Danish	100	0.88	-	Zeuthen & Nielsen (1973)
crim. Germans	50	0.88	0.06	Schweinger & Wild (1974)
norm. Germans	50	0.90	0.08	Schweinger & Wild (1974)
Austrians	40	0.98	-	Schnedl (1971)
crim. French	50	0.92	0.08	Benezech et al. (1976)
norm. French	50	0.92	0.08	Benezech et al. (1976)
Nubians	29	0.93	-	Nasjleti et al. (1979)
Japanese	11	0.87	0.05	Makino & Tagaki (1965)
USA White	60	1.02	-	Verma et al. (1978)
crim. Canadians	84	1.03	0.09	Soudek & Laraya (1975)
norm. Canadians	38	0.97	0.06	Soudek & Laraya (1975)
newb. Indians	170	0.81	0.09	Potluri et al., (1987)
Rajputs	100	0.09	0.14	Gosh & Singh (1975)
Punjabis	100	0.80	0.10	Gosh & Singh (1975)
Caucasians	60	1.02	0.09	Verma et al. (1983)
USA Black	60	1.09	0.10	Verma et al. (1983)
East-Indians	70	1.20	0.10	Verma et al. (1983)
Japanese	20	1.00	0.11	Cohen et al. (1966)
Indians	20	0.88	0.15	Cohen et al. (1966)
USA Black	20	0.92	0.09	Cohen et al. (1966)
East-Europ. Jewish	20	0.10	0.10	Cohen et al. (1966)
Anglo-Saxons	20	0.86	0.09	Cohen et al. (1966)
Jats	400	0.88	0.16	Kenue (1979)cf Potluri et al. (1987)

crim : criminal ment. : mentally retarded norm.: normal newb. : new borns

ferent measurements, the Y/F index varied considerably.

Considering the results of these investigations using the analysing-system OPTIMAS 4.0. the results obtained by the different authors, shown in table 1 have to be seen in a different way: Most of the cited authors made slides of their metaphase plates and projected them to a screen, where measurements were made. It seems that a computer supported analysing system, like OPTIMAS 4.0, with the option of optimizing the picture in contrast, brightness and also size, must be a more precise system for measuring very small objects like chromosomes.

Even if the authors cited in table 1 have not had these problems of non-reproducible measurements, the standard deviations of most of these investigations are too large to distinguish different populations. And, the range of most Y/F-indices, therefore, is not spread wide enough to make statements concerning the relationship of different populations. Also, within one population it seems not clear whether there is just "one" Y/F index, or whether the Y/F index is obtained by chance, like in the different Danish samples.

It seems, therefore, that indices of the Y-chromosome, like the Y/F-index, are not suitable for population genetic studies. It seems much more informative to study Y-specific DNA-polymorphisms, like Restriction Fragment Length Polymorphisms (RFLP's) or Variable Number of Tandem Repearts (VNTR's)

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