ANALYSIS OF AUSTRALIAN, BLACK, CAUCASIAN, CHINESE AND AMERINDIAN POPULATIONS WITH HYPERVARIABLE DNA LOCI

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SUMMARY

Population genetic studies in australian aborigine, american black, chinese, caucasian and amerindian populations were performed with several highly polymorphic DNA loci. PstI-digested samples from random individuals were hybridized to probes recognizing 5 hypervariable loci (i.e. D2S44, D4S163, D14S13, D17S79, D18S27). Results showed that the american black population had the highest level of heterozygosity (92%) followed by caucasian (89%) and chinese (84%). In australians it was 78% while in the various amerindian populations it varied from 74 to 84%. In general, the distributions of DNA fragments show that the most common polymorphic DNA fragments of a locus were within the same size range in all populations. The distinguishing feature of each population was the relative frequency of particular group of alleles. Some of these allele groups showed statistically significant differences between some of the populations. For example, alleles >9.0 Kb in size, in D14S13, or from 4.5 to 4.7 Kb, in D18S27, were two or more times more rare in caucasians than in the other populations.

INTRODUCTION

The high level of heterogeneity found in several DNA loci containing variable number of tandem repeats has made them an extremely useful tool for the identification of individuals. Although the most of the initial evaluation of this type of loci was performed in the American caucasian or black population (Baird et al. 1986, Balazs et al. 1989, Chimera et al. 1989) other smaller populations have been examined (Flint et al. 1989, Kidd et al. 1991). The purpose of this report is to extend these studies to Chinese, Australian aborigine and several Amerindian populations of North America.

MATERIALS AND METHODS

Blood samples. DNA from North American caucasian and black individuals were obtained from samples submitted for paternity testing. Chinese samples represent Han individuals from different regions of China. Australian aborigines were collected from individuals in the Northern Territories. Samples of Amerindians from USA were

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collected at three different indian reservations representing, Cheyenne, Navajo and Pima tribes. Samples from "Maya" individuals were collected in Mexico, in the Yucatan peninsula (Kidd et al.1991). DNA isolation, digestion with PstI, fractionation and hybridization was performed as described by Balazs et al.(1989).

RESULTS AND DISCUSSION

Analysis for several VNTR loci, in different populations shows similar size range distributions of DNA fragment sizes. The largest world populations (i.e. caucasian, black, chinese oriental) have the broadest distribution and highest heterogeneity in fragment sizes. This is partly reflected in the average heterozygosity of the 5 markers examined. The three major ethnic groups show the highest level of heterozygosity (i.e. black: 0.92; caucasian: 0.89; chinese: 0.83). However, native north american populations show a range of values from 0.72 to 0.84. This indicates that the variety of alleles in these four amerindian populations remains high. The heterozygosity of australian aborigines is similar to those of amerindians (i.e: 0.78).

The distinguishing feature of each population is the relative frequency of certain group or size ranges of DNA fragments. For example: in D2S44 DNA fragments in the 10 to 11 Kb size range are 2 to 3 times more common in amerindian, australians and chinese than in caucasians. D17S79 alleles, in the size range of 3.9 to 4.1 Kb and for D18S27 alleles, from 4.5 to 4.7 Kb, are 2 to 3 times more rare in caucasians than in all the other populations. D14S13 has a broad distribution of DNA fragment sizes in all populations, but alleles from 9 to 16 Kb in size are more common in australian, chinese and amerindian populations than in american black and caucasians. The most common D4S163 alleles were found between 6 and 9 Kb. Other rare alleles were found from about 3.4 to <6 Kb and from >9 to 16 Kb in size.

In summary, the analysis of several VNTR loci indicate that these genetic markers are very heterogeneous and highly informative in a large variety of populations. In addition, the application of more rigorous quantitative analysis of this type of data may be a useful tool for population genetic studies.

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