

The Site of 5S RNA Genes in Primates

I. The Great Apes

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Abstract. A major site of genes for 5S RNA has been localized in representative members of the family Pongidae by means of hybridization in situ. These genes are shown to be concentrated in the most distal bands of the primate chromosome arm homologous to human chromosome 1q.

Introduction

Members of the primate family Pongidae are considered the closest living relatives of man. These primates show striking similarities to man in overall chromosome banding pattern, in agreement with independent criteria of relatedness. A more stringent criterion of homology is correspondence in the chromosomal assignments of genes. One example is the multisite distribution of rDNA which is characteristic of the Hominidae and Pongidae as contrasted to the single-site distribution found in the lar gibbon (Hylobatidae) and the Cercopithecine monkeys (Henderson et al., 1972, 1974a, b; Warburton et al., 1975; Evans et al., 1975). This distribution is not identical among the Pongids, but each of them has rDNA-bearing chromosomes that are homologous to human rDNA-bearing chromosomes by the criterion of banding pattern.

A major site of 5S RNA genes has been localized to a subterminal position on human chromosome 1q by means of hybridization in situ (Steffensen et al., 1974; Atwood et al., 1975). Here we report the localization of 5S RNA genes in the chimpanzees, *Pan troglodytes* and *Pan paniscus*, the mountain gorilla (*Gorilla gorilla beringei*) and the orangutan (*Pongo pygmaeus*). In each case a major site of 5S RNA genes is located in a subterminal position on an arm of chromosome 1 homologous by banding pattern to chromosome 1q in man.

Materials and Methods

Hybridization in situ with iodinated human 5S RNA was as described in Atwood et al. (1975). The specific activities of the RNA and the exposure times for the various preparations are listed separately in Table 1. Blood from two individuals of *Pan paniscus* and one individual of *G. gorilla beringei* was obtained from the Prince Leopold Institute for Tropical Medicine, Antwerp. Blood from *Pan troglodytes* was obtained from the Laboratory of Experimental Medicine and Surgery, New York, and blood from *Pongo pygmaeus* was obtained from the Oklahoma City Zoo. In each case slides were prepared from PHA-stimulated peripheral blood lymphocytes.

Results and Discussion

Chromosome 1 in the Pongidae is similar in banding pattern to human chromosome 1 (Supplement of the Paris Conference on Standardization in Human Genetics, 1975). The heterochromatic region near the centromere in human chromosome 1q is, however, reduced in the Pongid chromosomes. Consequently the shorter of the arms in all of the Pongid first chromosomes is the arm

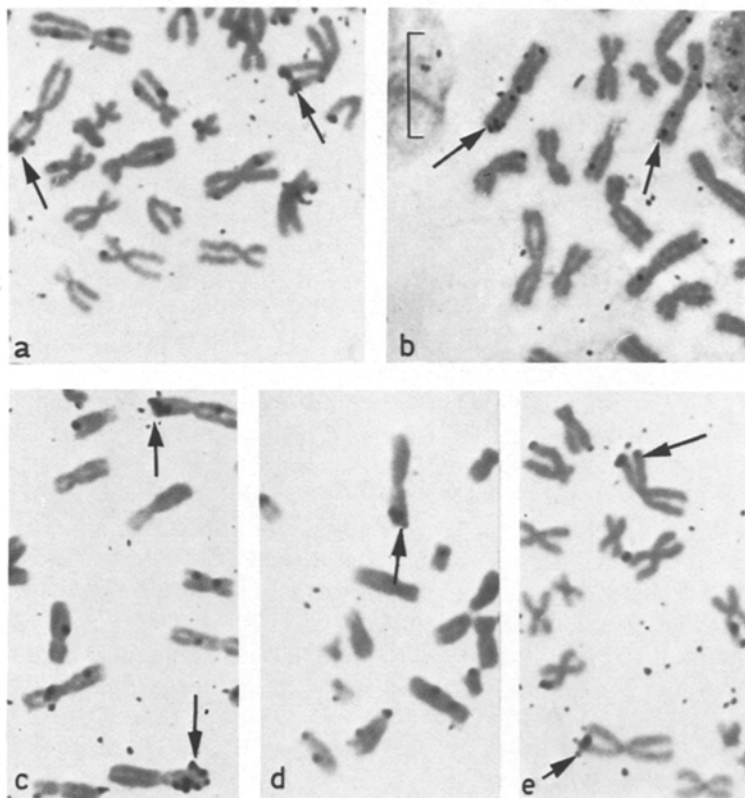


Fig. 1a-e. Labelling of 1q with ¹²⁵I 5S RNA. **a** *Homo sapiens*. **b** *Pan paniscus*. **c** *Pan troglodytes*. **d** *Pongo pygmaeus*. **e** *Gorilla gorilla beringei*

homologous to human 1q by banding pattern. After hybridization it was possible to distinguish the arms of chromosome 1 in the apes on the basis of length. Metaphase plates were chosen under low power for clarity and well-spread chromosomes and photographed for analysis. Inspection of at least 25 metaphases from each species revealed that the major grain clusters were near the distal end of the arm homologous to human 1q (Fig. 1). Grain counts were made over the distal third of 1q and compared with grain counts over the rest of 1q, the full length of 1p, and at least one other identifiable chromosomal region of length comparable to 1q. These results, including data from human preparations in the same series of experiments, are given in Table 1. It may

Table 1. Distribution of label among chromosomal regions

	<i>Homo sapiens</i>	<i>Pan paniscus</i>	<i>Pan troglodytes</i>	<i>Pongo pygmaeus</i>	<i>Gorilla gorilla beringei</i>
Number of plates examined	56	51	38	27	35
Specific activity of 5S RNA (dpm/ $\mu\text{g} \times 10^8$)	2.4	2.4	4	4	2.4
Time of exposure (days)	30-40	30-40	18-21	18-21	30-40
Total grains	3,721	3,244	2,654	2,622	2,491
Chromosomal region:					
A. Distal third of 1q (% haploid length = ~1.5)					
% total grains	11.7	11.7	7.5	8.5	10
Mean number of grains/2 chromatids	3.9	4.0	3.0	4.5	3.6
Expected number of grains/2 chromatids	0.5	0.5	0.5	0.7	0.5
B. Remainder of 1q (% genome = ~3.1)					
% total grains	2.3	1.4	1.3	1.8	2.3
Mean number of grains/2 chromatids	0.8	0.5	0.5	0.9	0.8
Expected number of grains/2 chromatids	1	1	1.1	1.5	1.1
C. 1p (% genome = ~4.4)					
% total grains	3.6	3.1	3	3	2.8
Mean number of grains/2 chromatids	1.2	1.1	1.2	1.6	1
Expected number of grains/2 chromatids	1.5	1.4	1.5	2.1	1.6
D. Control arm (% genome = ~4.5)					
% total grains	3.5	2	2.2	1.7	3
Mean number of grains/2 chromatids	1.2	0.9	1.3	1.8	1.1
Expected number of grains/2 chromatids	1.5	1.4	1.6	2.2	1.6

be noted that this type of analysis does not exclude the possibility of minor sites of 5S RNA genes in locations other than chromosome 1, but none of the preparations used here gave the impression that such sites were present.

The site-associated grain counts in Table 1 do not suggest any species differences in the number of 5S RNA genes present at the site. On the assumption that the efficiency of hybridization is in the same range as that for rDNA (~3%), it can be calculated that the site in 1q comprises at least 80–120 genes for 5S RNA in the primates studied.

Our results indicate that the 5S RNA site in chromosome 1q was present in a common ancestor of the Pongidae and Hominidae. Studies in progress to locate the 5S RNA genes in other primate groups may permit inferences concerning more remote branching points in primate evolution.

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