Chromosome Evolution in Primates

Fig. 1, Comparison of the chromosomes of *Homo sapiens* (USA; left) and common chimpanzee, *Pan troglodytes* (PTR; right). The 11 symbols indicate 11 of 12 of the 11 modifications recognized in the cladogram. The 12th modification involves a gain in heterochromatin in many chromosomes of the chimpanzee, not rendered visible by this staining technique (R-banding).

Fig. 2. Hypothetical ancestral karyotype for all living primates (PRI). This karyotype has been reconstructed from chromosomes still existing in several Platyrrhini and Prosimii, and quite closely resembles the reconstructed ancestral karyotype for Carnivora.

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Cladogram indicating evolutionary relationships among primates, established from sequences of chromosome rearrangements reconstituted through comparison of the karyotypes of more than 100 living species and subspecies. The presumed ancestral karyotype of all living primates (PRI) is illustrated in figure 2. From this starting point, a short trunk may be common to all Prosimii, but this is not certain (dotted line), as tree-shrews (TUP) are not clearly linked to primates. Lorisiformes and Lemuriformes diverged very early, and the aye-aye (DMA) was isolated very early from the common trunk with Lemuriformes. All the other families of Lemuriformes emerged from a common ancestral population (LEM). The only clear case of dichotomic evolution is observed in sportive lemurs (LEP). The karyotype of *Tarsius syrichta* differs completely from that of all other primates studied and does not allow any phylogenetic inference for Tarsiiformes.

The common trunk for all simians or Anthropoidea (PRI→SIM), like that for all New World monkeys, the Platyrrhini (SIM→PLA), is rather short. From the ancestral platyrrhine population (PLA) there is a radiation of various families and subfamilies, without an obvious common trunk for Cebidae. Saimiri (SAI) is not closely linked to Cebus (CCA and others), as proposed by certain authors, but shares some chromosome rearrangements with Pitheciinae (PPI, CCR). The common trunk for Old World monkeys and apes, the Catarrhini (SIM→CAT) is fairly long, as is that for Old World monkeys, the Cercopithecoidea (CAT→CER). From the common ancestral population for Cercopithecoidea, three separate branches lead to leaf monkeys (Colobinae), to baboons, macaques and related forms, and to *Cenopithecus* and related genera. *Cercopithecus* species have undergone very complex evolution, many chromosome rearrangements being shared by diverse groups of species. This indicates populational or network evolution. All species stem from an initial populational evolu-

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Primates

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o Pericentric inv

• Other inv

□ Robertsonian translocation

■ Other translocation

† Fission

EEL ← Shift

NCO * ^omP^ex 0Γ unspecified rearrangement

a Modification of heterochromatin

C- -^ HSA

aΣ 1/8 it

in* 9 GGO PPV

Fig. 3. Examples of inversions (inv) observed in human pathology which reconstitute chromosomes found normally in certain other primates: chimpanzee (PTR), gorilla (GGO) and orang-utan (PPY). These inversions thus correspond to either reverse or convergent mutations. For chromosome 5, the 2 inversions similar to PTR5 were induced with radiation.

tion. *Alouatta nigroviridis* (ANI) has remained the most primitive in chromosome terms, occupying an intermediate position. Subsequently, a common trunk for all other arboreal species emerged and gave rise to another very complex populational evolution.

Following a common trunk for Pongidae + Hominidae (CAT→PON), the orangutan separated first. Then populational evolution occurred at the end of a common trunk for man (HSA), chimpanzees (PTR and PPA) and gorilla (GGO). The phylogenetic position of gibbons could not be determined on the basis of chromosome data. Overall, there are no major discrepancies between these inferences from chromosome data and consensus views of primate systematics. N.B.: (1) the relative rarity of true dichotomic evolution, which is frequently replaced by populational evolution when a number of closely related species can be studied, and (2) the strong tendency for accumulation of a given type of chromosome rearrangement in a particular group

of species: inversions in Pongidae + Hominidae; fissions and shifts in Cercopithecus, and Robertsonian translocations in Prosimii.

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