ORAL COMMUNICATIONS

10.1 Correspondence of chromosome segments in low numbered (Equidae) and high numbered (Rhinocerotidae) Perissodactyla, and genetic confirmation of an F1 Black x White Rhinoceros hybrid by FISH and microsatellite analysis

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Conserved chromosomal segments in the Black Rhinoceros, Diceros bicornis (2n=84), and its African sister-species the White Rhinoceros, Ceratotherium simum (2n=82), were detected using Burchell's Zebra (Equus burchelli, 2n=44) chromosome-specific painting probes supplemented by subset of those developed for the Horse (Equus caballus 2n=64). In total, 41 and 42 conserved autosomal segments were identified in C. simum and D. bicornis respectively. Twenty one rearrangements (20 fissions and 1 fusion) are necessary to convert the Zebra karyotype into that of the White Rhinoceros. One fission distinguishes the karyotype of Black Rhinoceros from C. simum. The hybrid status of a single Black Rhinoceros/White Rhinoceros cross was examined. Conventional cytogenetics, FISH and assignment tests of nine microsatellite loci, several of which comprise alleles that are private to each species, confirmed the specimen's hybrid status. The F1 showed a likelihood ratio of belonging to the White Rhinoceros sample population (n=7) vs the Black Rhinoceros sample population (n=119) of 1.1 indicating that it was almost equally likely to belong to the one species as to the other. All data are consistent with the specimen having received half its genetic complement from a White Rhinoceros and the other half from a Black Rhinoceros making the F1 the first verified incident of hybridization within the Rhinocerotidae.

10.2. Molecular cytogenetic conservation of human aphidicolin-induced fragile sites in Papionini (Primates) species

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Introduction

Fragile sites are specific chromosomal loci that present non-random gaps and breaks under specific culture conditions and they are considered structural features of mammalian chromosomes. Previous comparative cytogenetic studies in Primates indicated that human fragile sites are mapped to the equivalent fragile sites in the long-tailed macaque (Macaca fascicularis). In this study we aimed to test whether the hypothesis of fragile sites conservation would be sustained in a wider range of species and could be confirmed by molecular methods.

Material and Methods

Blood samples and cell line: peripheral blood samples from one female mandrill (M. sphinx, MSP) and a fibroblast cell line from a long-tailed macaque (M. fascicularis, MFA). Cell cultures were processed under standard conditions in order to obtain chromosome preparations. FISH of BAC clones: Six BAC clones (three from human chromosome 1 and three from human chromosome 7), which are mapped to chromosome bands known to harbor common fragile sites, were chosen by reference to the FISH mapped BAC NCI database (NCI, Bethesda MD; http://cgap.nci.nih.gov).

Results and Discussion

The BAC probes used in this experiment were hybridised to human metaphases first to determine the hybridisation conditions and then to confirm chromosome locations. The BACs were then hybridised to primate metaphase spreads. The results of the cross-species hybridisations show that the BACs colocalize with fragile regions in the two non-human primates. Thus they confirm at the molecular level that the chromosome bands, which contain human, macaque and mandrill fragile sites are indeed homologous.