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The characterization and structure of ϵ -globin gene
Perissodactyla

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To synthesize the ϵ -globin gene from Perissodactyla PCR was performed by using genomic DNA as template and synthesized primers. The PCR product was 1.475 Kb in length. The amplified ϵ -globin genes were cloned by using A-T cloning method, and their nucleotides were determined by using the Sanger's method. The structure of ϵ -globin gene amplified by PCR from Perissodactyla showed that it contained consensus CCAAT at position -85 site a Hogness-Goldberg box (ATA) at position -30 site, and an mRNA ribosomal binding sequence CTTCTC at position +8 site in the 5' flanking-region. The Amino acid sequence encoded by exon 1 and 2 (105 amino acids) of ϵ -globin gene was highly homologous to human's (84%), goat's (89%), respectively. The insert sequence in IVS 2 of ϵ -globin gene was not found. The ϵ -globin gene, as is typical of other β -like globin genes, contains three exons and two introns. The second intron (865 bp) of the ϵ -globin show different length, as human and goat, is 960 bp and 1039 bp in length. This difference is entirely due to a difference in the size of insertion element.

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P elements Distributed in Drosophilid Species In Korea

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The genus *Drosophila* were isolated from Korean national population (Cheju-Do) and examined for *P* element in the genome by using PCR with inverted repeat primers. five of the *P* elements in PCR product were found to be 2.9 kb, 1.3 kb, 1.15 kb, 0.55 kb and 0.45 kb elements. Southern blot analysis on the genus *Drosophila* were also performed with *Ava*II restriction enzyme. The results of Southern blot analysis showed that *P*-homologous sequences are essentially confined to the subgenus *Sophophora*. The strongest *P* hybridization occurs in species from the closely related *melanogaster* and *obscura* groups. The *D. melanogaster* *P* element is most similar to the elements from the *obscura* group.