

POSSIBILITY OF INTERSPECIES GENE FLOW AMONG GIBBON SPECIES

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Most of primate species are endangered, and estimation of genetic diversity of each species is important for primate conservation studies through evaluation of uniqueness of each subpopulation and estimation of gene flow with surrounding species. We thus developed database of PCR primers for primates, called "PRIM-PRIM" (<http://sayer.lab.nig.ac.jp/primprim/>). Human-Rhesus macaque genomic alignment sequence data were downloaded from Ensembl database, and 2303 introns of protein coding genes were chosen as candidates for estimating nucleotide level diversity of catarrhine primates. We provide PCR primers for all 2303 introns in PRIM-PRIM database. This database was constructed by Kawai Yosuke.

We used 58 primer pairs to check if these can really produce authentic nucleotide sequences. Gibbon genomic DNA samples collected by Ishida Takafumi were used; 11 *Hylobates lar*, 5 *H. agilis*, 4 *H. muelleri*, 4 *H. pileatus*, 1 *H. moloch*, and 11 *Symphalangus syndactylus*. Nucleotide sequencing was conducted in Saitou Laboratory. Saitou Naruya and Suzuki Rumiko performed sequence analysis. So far, *H. lar* and *S. syndactylus* do not show any evidence of gene flow by checking phylogenetic trees for intron sequences. Nucleotide sequencing for the remaining species is under way. We will present results of this sequencing effort at this talk. Though PRIM-PRIM database was made based on human-macaque sequence comparison, it may be possible to apply these PCR primers for non-catarrhine primate species because of sequence conservation.

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