

A Chromosome Landmark Separating Sumatran and Bornean Agile Gibbons

H. Hirai¹, H. Wijayanto², H. Tanaka¹, A.R. Mootnick³, D. Iskandriati²,
D. Perwitasari-F², D. Sajuthi²

¹Primate Research Institute, Kyoto University, Inuyama, Aichi 484-8506, Japan;

²Primate Research Centre, Bogor Agricultural University, Bogor 16151, Indonesia;

³International Center for Gibbon Studies, Santa Clarita, CA 91380, USA

Email: hirai@pri.kyoto-u.ac.jp

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Identification of agile and Mueller's gibbons is difficult and has resulted in numerous cases of misidentification in zoos and primate institutions. The use of misidentified gibbons has an adverse affect on genetic and evolutionary investigations. The identification of agile gibbons is

compounded by the fact that the species classification is still debatable. Recently the agile gibbon was shown to have a new chromosome mutation, whole arm translocation between chromosomes 8 and 9 (WAT8/9) (van Tuinen et al. 1999; Hirai et al. 2003). It was speculated that Sumatra and Borneo (Kalimantan) agile gibbons (SAG and BAG) are different in the WAT8/9. Therefore, we addressed this question to clarify the species identification of gibbons. We examined a total of 50 gibbons (19 SAGs, 19 BAGs, and 12 Mueller's Bornean gibbons). Their chromosomes were analysed using a chromosome painting technique with probes of human chromosomes 5 and 17, these being the best probes to detect WAT8/9. Molecular phylogenetic analysis with TSPY sequences was also performed to look at molecular clustering of the three species of gibbons. WAT8/9 might have occurred between chromosomes 9 and inverted 8 (8-2). Most haploid sets of SAGs (8/38, 79%) demonstrated the variation, but this was not the case in the other two groups. This chromosomal difference between the three groups corresponded to molecular phylogenetic clusters constructed by alignment of TSPY sequences. Thus, the variation might have occurred in SAG after isolation between the two island populations. Moreover, all the heterozygotes showed only one pair of chromosomes 9|8-2 and 8-2, so that another inverted chromosome (8-1) was probably selected by inversion heteromorphism.