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Advances of the phylogenetic relationships in gibbon

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Abstract. Gibbons are a family (Hylobatidae) of ape species endemic to the rainforests of the mainland and islands of Southeast Asia, including four well-recognized genera (Hylobates, Nomascus, Symphalangus, and Hoolock). Most gibbon species are known as considered “endangered” or “critically endangered” (IUCN 2009). This present article gives a review on the research progress of phylogenetic relationships between gibbon species and closely related genera utilizing a range of different traits (e.g., vocalization, morphology, karyotype, mtDNA, Y chromosomes, Autosomes, Alu, and whole genome). Our aim held great potential to clarify more directions in researches on identification of genetic relationship, to provide reference for molecular biology research and useful information for further gibbon research.

Keywords: Gibbon, Phylogenetic relationships, Progress.

1 Introduction

The gibbon is a small sized ape, found inhabiting the dense jungles and tropical rainforests across south-east Asia. Gibbons are a family (Hylobatidae) of ape species endemic to the rainforests of the mainland and islands of Southeast Asia, including the Malay Peninsula, Sumatra, Borneo, Java and Mentawai Islands (Fig. 1) [1]. They belong to the lesser ape family, which are the closest relatives of the great ape family (Hominidae, including chimpanzees, orang-utans, bonobos, gorillas and humans), and share a common ancestor with other hominoids roughly 16–20 Mya [2].

Gibbons are currently divided into four well-recognized genera (Hylobates, Nomascus, Symphalangus and Hoolock) that have very different karyotypes and diploid chromosome counts which vary from 2n = 38 - 52. Overall, 17 gibbon species have been identified. Most gibbon species are considered “endangered” or “critically endangered”, and the Hainan gibbon (Nomascus hainanus), with approximately 20 extant individuals, is the rarest primate in the world [3].

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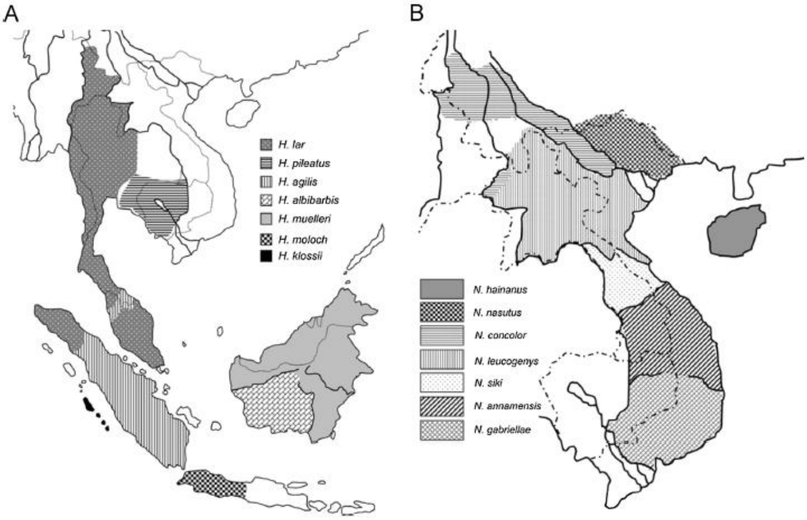

Fig. 1. Approximate geographic distribution of Hylobates (A) and Nomascus (B) species. Dotted and solid lines indicate country borders and major rivers, respectively [1].

2 Research progress on the phylogenetic relationships in gibbon

Despite their conservation importance and despite a lot of studies utilizing a range of different traits (e.g., vocalization, morphology, karyotype, mitochondrial DNA (mtDNA) variation, and nuclear sequence variation), the phylogenetic relationships between gibbon species and genera remain unresolved (see Fig. 2 and Table 1).

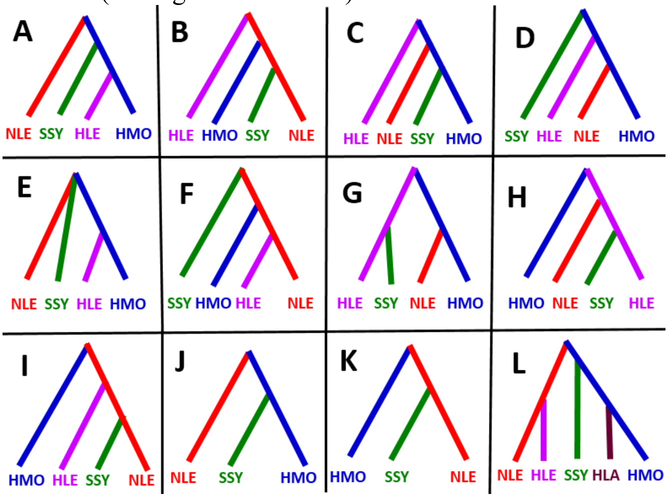

Fig. 2. Schematic of different phylogenetic trees for the four gibbon genera. The trees represented in letter A to L have been proposed as the results of previous studies and corresponded to the code in Table 1. NLE: *Nomascus*; SSY: *Symphalangus*; HLE: *Hoolock*; HMO: *Hylobates*.

Studies based on morphological and vocal traits have tended to support either Nomascus and Hylobates (Code A in Fig. 2) [4, 6] or Hoolock and Hylobates (Code E in Fig. 2) [5, 6] as sister taxa, while a study based on chromosomal rearrangements placed Nomascus and Symphalangus as sister taxa (Code B in Fig. 2) [7].

Table 1. The code represented different phylogenetic relationships utilizing a range of different traits.

Traits Code	Vocalization	Morphology	Karyotype	mtDNA	Ychromosomes	Autosomes	*Alu*	Whole genome
A				[8] -D-loop;[9] -Cytb;[10] -Cytb				
B			[7]	[11] -COII;[12] -D-loop		[3]		
C				[13]- ND3 and ND4;[14]-COII; ND4 and ND5; [15] – including 10 gene				
D		[4]						
E	[5]	[6]						
F							[21]	
G						[20]		
H								[22,23]
I				[16]-Mitochondrial genome sequences		[1]		
J					[19]			
K				[2,17]-Mitochondrial genome sequences				
L				[18]-Mitochondrial genome sequences				

Note: Each code was represented by a letter. The phylogenetic relationships represented in letter A to L corresponded to the code in Fig. 2. "-"denote the mtDNA sequence fragment used in the study.

The global taxonomy for gibbons remains very controversial based on mtDNA research. Based on mtDNA D-loop gene [8]; and Cytb gene [9, 10], their result supported Hylobates and Hoolock as sister groups (Code A in Fig. 2). However, results of Zehr (1999) [11] and Whittaker et al (2007) [12] based on mtDNA COII and D-loop gene respectively, were similar to the previous karyotype research (Code B in Fig. 2). Takacs et al. [13] (ND3 and ND4 genes); Israfil et al. [14] (COII; ND4 and ND5); and Springer et al. [15] (including 10 mtDNA genes) showed Symphalangus and Hoolock as sister groups (Code C in Fig. 2).

Some mitochondrial genome sequences studies have supported Symphalangus and Hylobates as sister groups (Code I in Fig. 2) [16] but Matsudaira and Ishida (2010) [2] and Finstermeier et al. (2013) [17] support for a Symphalangus and Hylobates pairing (Code K in Fig. 2). Fan et al. (2016) [18] supported that Nomascus and Hoolock while Symphalangus and Hylobates both as sister groups (Code L in Fig. 2).

Studies of nuclear sequence variation (with or without mtDNA variation) have also been inconsistent, with Symphalangus and Nomascus [3] (Code B in Fig. 2); Symphalangus and Hoolock [20] (Code G in Fig. 2); and Symphalangus and Hylobates [1] (Code I in Fig. 2) identified as possible sister taxa.

An Alu-based phylogeny of gibbons by Meyer et al. (2012) [21] demonstrate significant support for Symphalangus as the most basal lineage within the family. Their findings also place Nomascus as a derived lineage, sister to Hoolock, with the Nomascus–Hoolock clade sister to Hylobates.

To Examine phylogenetic relationships among gibbon genera, Carbone et al. (2014) [22] and Veeramah et al. (2015) [23] using whole genome sequence both supported Hoolock and Symphalangus are likely sister taxa (Code H in Fig. 2).

3 Summary

In a word, from the above-mentioned studies attempting to elucidate the phylogenetic relationships among gibbons using vocalization, morphology, karyotypes, mitochondrial DNA (mtDNA), the Y chromosome, short autosomal sequences, and whole genome sequence have been inconclusive. To examine the relationships among gibbon genera in more depth, a much broader geographic sampling will be vital for inferring the phylogenetic relationships among extent gibbon species.

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