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Primates, including 420 species and 73 breeds (IUCN 2013.2 IUCN Red Threatened Species List), are an important mammal radiation with a rich diversity of morphological, behavioral and ecological adaptations. Today, non-human members of this order are mainly limited to tropical or subtropical regions of Asia, Central and South America and Africa. Fossil records show that primates have been more widely distributed in the past, including in North America and Europe (Covert, 2002). Despite the great interest of evolutionary biologists in this radiation, many issues related to their origin and diversification remain unclear. The traditional appearance of primate origin emerges and diversified crown primates or eucopaths (that is, all descendants of the last common ancestor of living species), which appeared shortly after the Cretaceous-Paleogene (K-Pg) border (explosive model). According to this model, the sudden anmation of dinosaurs and the radiation of flowering plants (angiosperms) opened a new set of ecological niche that placental mammals (Eutheria) and birds (Neoaves) could benefit from (Conroy, 1990; Rose, 2006). As a result, these groups of animals, which remained quite small and encrypted during the Cretaceous period, underted rapid adaptive radiation shortly after the mass extinction 65 million years ago (Rose, 2006; Wible et al., 2007; O'Leary et al., 2013). The main line of evidence supporting the explosive model is the absence of euprimate fossils before the K-Pg border. The earlier fossil euprimates date from the beginning of the Eocen age and 56 Ma (Miller et al. 2005; Smith et al. 2006; Williams et al. 2010). The best known representatives of these early euprimates were two groups of Omomyoidea (e.g. Teilhardina and Melanerimia) and Adapoidea (e.g., Cantius and Donrussellia), possibly related to living haplorhines and strepsirrhines, respectively (Gingerich, 1986; Martin, 1993; Ni et al., 2004; Miller et al., 2005; Smith et al., 2006; Rasmussen, 2007). North African Altiatlasius koulchii (Sigé et al., 1990) dated a little earlier, the late Paleocenite dated about Ma 57, but is not a clear euprimate (Rasmussen, 2007; Williams et al., 2010). Finally, plesiadapiforms, which have been included in the Primates row in the past, are most recently found in fossil records between the Cretaceous and early Eocele, most samples of which were recovered deposits from the Paleocenia (56-66 Ma). However, in contemporary taxonomas, none of these fossils are involved in euprimates and are thought to represent a different root group before the origin of either euprimates (Bloch and Silcox, 2001; Bloch and Boyer, 2002; Bloch et al., 2007; Silcox et al., 2007) or a non-primate group of mammals is probably associated with primates or colugos (Martin, 1968; Cartmill, 1972; Wible and 1987; Beard and Houde, 1989; Beard, 1990, 1993; Kay and Thorington, 1990; Kay et al., 1992). Analysis of molecular data provided a very different scenario for the origin and diversification of primates. Molecular studies have revealed dates of deviation older than any known euprimatfosil, citing the origin of Crown primates before the K-Pg limit (63.7-95.0 Ma; Springer et al., 2003, 2012; Chatterjee et al., 2009; Fabre et al., 2009; Meredith et al., 2011; Perelman et al., 2011; Jameson et al., 2011; Wilkinson et al., 2011). This view of primate origins agrees with a series of molecular studies on mammals diversification that suggest that modern placental lineages are of deep cretaceal origin to most (Madsen et al., 2001; Murphy et al., 2001; Springer et al., 2003; Bininda-Emonds et al., 2007; Meredith et al., 2011), although there are no fossils showing the clear morphological properties of the crown group Placentalia (Wible et al., 2007; O'Leary et al., 2013). Unlike the explosive model, these studies place the origin of öther orders in the cretaceous, extending a long insurance model (the origin of the orders extends deep into the Cretaceous, with the origin of the main intraordinal lineages close to K-boundary Pg) or a short insurance model (both the interordinal and intraordinal variety appear deep in the Cretaceous) (Springer et al al. , 2003; Bininda-Emonds et al., 2007; Meredith et al., 2011). While molecules are expected to underestimate times of differentiation (Steiper and Young, 2008), early genealogy dates extracted from molecular studies show that a significant part of primate evolutionary history (~20-25 million years) is missing. Let a possible source of conflict between paleontological and molecular models of primate origin lie in the calibration of molecular clocks. To turn molecular evolutionary distance estimates into chronological time, a series of well-dated fossils with well-supported phylgenetic placement are required. These calibration points are critical to molecular historicalization because they are the only source of information about absolute time (Steiper and Young, 2008; Ho and Phillips, 2009; Parham et al., 2012). The three main problems may affect the use of fossil information when predicting times of differentiation using molecular sequences: 1) the selection of inappropriate fossils; 2) lack of fossil records in some areas of the tree; and 3) the distribution of a fossil in phylgenetic placement (for example, placing a root form in a crown group). Although these problems have long been considered critical to staying in a molecular tree (Raaum et al. 2005; Rutschmann et al., 2007; Steiper and Young, 2008; Ho and Phillips, 2009), still underestimate the challenge of choosing the right calibration points (Pyron, 2010; Dornburg et al., 2011; Parham et al., Many molecular studies suffer from a non-rigorous use of paleontological record, which may contain a significant error in fossil calibration and provide misleading estimates of deviation (Graur and Martin, 2004). Here we are transferring one of the largest time-adjusted phenogens of primates predicted using full mitochondrial genome sequences. Mitogenomic analyses have been shown to be useful in predicting phylogenetic reconstruction and deviation time at different taxonomic levels and in different groups, including amphibies (Zardoya et al., 2003; Zhang et al., 2005; Zhang and Wake, 2009), birds (Pereira and Baker, 2006; Slack et al., 2007; Pacheco et al., 2011), fish (Inoue et al., 2003, 2010; Miya et al., 2003) and mammals (Arnason and Janke, 2002; Arnason et al., 2002, 2004, 2008). Mitochondrial genomes have traditionally been used in phylgenetic and phylological analyses of animal taxa. The use of mitochondrial DNA (mtDNA) has several advantages: lack of recombination, time combined quickly, relatively high substitution rates, high copy number and haploidia. For these reasons, it has been claimed that mitochondrial gene trees estimate the history of deviation between species more than other loci (Moore, 1995). Today, multilocus phylogenies are very common (Jameson et al., 2011; Perelman et al., 2011; Springer et al., 2012), but the nuclear lodge used in these studies is usually quite short<1500 bp)= compared= to= the= large= size= of= mitochondrial= genomes= (=>(16,000 bp). Mitochondrial genomes also show more information content per base than nuclear DNA (Anderson et al., 1982; Cummings et al., 1995). Finally, the high number of mitochondria copies in each cell facilitates the obtaining and sorting of mitogenomic data, especially in low-quality samples such as museums and fossil specimens (Briggs et al., 2009; Krause et al., 2010; Rowe et al., 2011; Mason et al., 2011; Guschanski et al., 2013). Therefore, mitochondrial evolutionary history can provide a significant set of comparative data in studies where good knowledge is not only valuable in its own right, but also mtDNA is the only genetic marker available. Mitochondrial genomes within primates are widely used in phylgenetic studies at family or breed level (Raaum et al., 2005; Sterner et al., 2006; Hodgson et al., 2009; Chan et al., 2010; Chiou et al., 2011; Guschanski et al., 2013; Zinner et al., 2013), but to date only two extensive mitogenomic studies have been conducted, including all the main primate lineages (Matsui et al., 2009; Finstermeier et al., 2013). Here we brought together all mitochondrial genome sequences from sixty-two primate species (including eleven new sequences) to represent sixteen families living within the Primate order. The objectives of this study are (i) the evolutionary relationships of primates mitokondriyal genom dizileri, (ii) primatlar içinde ve dışında seçilen farklı fosil kalibrasyonlarının sıra içindeki farklılaşma zamanlarını nasıl etkilediğini araştırmak ve (iii) gelecekteki çalışmalarda kullanılmak üzere uyumlu fosil kalibrasyonları paketi geliştirmek. Üç strepsirrhines 'i temsil eden on bir tür için tam mitokondriyal genom dizilimi yaptık (Daubentonia madagascarensis, Mirza coquereli ve Otolemur crassicaudatus) ve sekiz Eski Dünya maymunu (Allenopithecus nigroviridis, Cercopithecus diana, C. lhoesti, C. mitis, Erythrocebus patas, Cercocebus torquatus, Lophocebus aterrimus ve Mandrillus sphynx) (Tablo 1). Bu örneklerden elde edilen komple genom dizileri GenBank'a ({type:entrez-nucleotide-range,attrs:{text:KJ158462-KJ158463 katılım numaraları altında yatırılır.,start_term:KJ158462,end_term:KJ158463,start_term_id:597710934,end_term_id:597710948}}KJ158462-K JJ158463 ve {type:entrez-nucleotide-range,attrs:{text:KJ434955-KJ434963,start_term:KJ434955,,end_term:KJ434963,start_term_id:597955520, end_term_id:597955632}}KJ434955-KJ434963 (Tablo 1). Bu çalışmada kullanılan diziler. Scientific nameCommon nameNCBI Accession NoReferencePrimates Strepsirrhini Lorisiformes Lorisidae Loris tardigradusSlender loris{type:entrez-nucleotide,attrs:{text:NC_012763,term_id:238908467,term_text:NC_012763}}NC_012763Matsui et al., 2009 Nycticebus coucangSlow loris{type:entrez-nucleotide,attrs:{text:NC_002765,term_id:14010665,term_text:NC_002765}}NC_002765Arnason et al., 2000 Perodicticus pottoPotto{type:entrez-nucleotide,attrs:{text:NC_012764,term_id:238866862,term_text:NC_012764}}NC_012764Matsui et al., 2009 Galagidae Galago senegalensisSenegal galago{type:entrez-nucleotide,attrs:{text:NC_012761,term_id:238866834,term_text:NC_012761}}NC_012761Matsui et al., 2009 Otolemur crassicaudatusaThick-tailed galago{type:entrez-nucleotide,attrs:{text:KJ434961,term_id:597955604,term_text:KJ434961}}KJ434961This study Chiromyiformes Daubentoniidae Daubentonia madagascariensisaAye-aye{type:entrez-nucleotide,attrs:{text:KJ158462,term_id:597710934,term_text :KJ158462}}KJ158462This çalışma 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hubbardorumHubbard'ın sportif lemur{type:entrez-nucleotide,attrs:{text:NC_014453,term_id::304322880,term_text:NC_014453,term_text:NC_014453}}NC_014453Lei at al., 2010 Indridae Propithecus coquereliCoquerel's sifaka{type:entrez-nucleotide,attrs:{text :AB286049,term_id :194247742,term_text:AB286049}}AB286049Matsui ve ark., 2007 Haplorrhini Tarsiformes Tarsiidae Tarsius bancanusHorsfield's tarsier{type:entrez-nucleotide,attrs:{text:NC_002811,term_id:14602225,term_text:NC_002811}}NC_002811Schmitz 2002b Tarsius syrichtaPhilippine tarsier{type:entrez-nucleotide,attrs:{text:NC_012774,term_id:238866974,term_text::NC_012774}}NC_012774Matsui ve al., 2009 Anthropoidea Platyrrhini Cebidae Aotus lemurinusLemurine gece maymun{type :entrez-nükleotid,attrs:{text:FJ785421,term_id:227122185,term_text:FJ785421}}FJ785421Hodgson ve ark., 2009 Cebus albifronsWhite önlü kapuçin{type:entrez-nucleotide,attrs:{text:AJ309866,term_id:13940255,term_text:AJ30986666}}AJ309866Arnason ve ark., 2000 Saimiri 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maymun{type:entrez-nucleotide,attrs:{text:KJ434962,term_id:59795561 ,term_text:KJ434962}KJ434962Bu çalışma Cercocebus torquatusaYakalı mangabey{type:entrez-nükleotit,attrs:{text :KJ43495 ,term_id:597955576,term_text:KJ434959}}KJ434959Bu çalışma Cercopithecus dianaaDiana maymun{type:entrez-nükleotid,attrs:{text:KJ434958,term_id::597955562,term_text:KJ434958}KJ434958Bu çalışma Cercopithecus lhoestiaL'Hoest's monkey{type :entrez-nükleotid,attrs:{text:KJ434957,term_id:597955548,term_text:KJ434957}}KJ434957Bu çalışma Cercopithecus mitisaBlue monkey{type:entrez-nucleotide,attrs:{text:kJ435548,term_text:KJ434957}KJ434957Bu çalışma Cercopithecus mitisaBlue monkey{type:entrez-nucleotide ,attrs{text:KJ43548,term_text:KJ434957}}KJ434957Bu çalışma Cercopithecus mitisaBlue monkey{type:entrez-nucleotide,attrs:{text:text:,term_id:597955534,term_text:KJ434956}}KJ434956This çalışma Chlorocebus aethiopsGrivet{type:entrez-nucleotide,attrs:{text:NC_007009,term_id:term_id::NC_007009:term_text NC_007009}, NC_007009Raaum 2005 Chlorocebus pygerythrusVervet monkey{type:entrez-nucleotide,attrs:{text:NC_009747,term_id:156471191,term_text :NC_009747}}}NC_009747Wertheim & Worobey , 2007 Chlorocebus sabaeusGreen monkey{type:entrez-nucleotide,attrs:{text:EF597503,term_id:147712874,term_text:EF597503}}EF597503Wertheim & Worobey, 2007 Chlorocebus tantalusTantalus monkey{type:entrez-nucleotide,attrs:{text:NC_009748,term_id:156471205,term_text:NC_009748}}}NC_009748Wertheim & Worobey, 2007 Erythrocebus patasaPatas çalışma Lophocebus aterrimusaBlack tepeli mangabey{type:entrez-nükleotid,attrs:{text:KJ434960,term_id:597955590,term_text:KJ434960}KJ434960Bu çalışma Macaca sylvanusBarbary apeNC 00276Ar4, etna.etna 2000 Macaca mulattaRhesus monkey{type:entrez-nucleotide,attrs:{text:NC_005943,term_id::49146236,term_text:NC_005943}}NC_005943Gokey ve ark., 2004 Macaca fasikülerYengeç yiyen makak{type:entrez-nucleotide,attrs:{text:NC_012670,term_id:229772910,term_text:NC_012670}}NC_012670Yi ve ark. , unpub. Macaca thibetanaPere David'in makaque{type:entrez-nucleotide,attrs:{text:NC_011519,term_id:211908556,term_text:NC_011519}}NC_011519Li ve ark., 2009 Mandrillus sfenksaMandrill{type:entrez-nucleotide,attrs:{text:kJ444 963,term_id:597955632,term_text:KJ434963}}KJ434963Bu çalışma Papio hamadryasHamadryas baboon{type:entrez-nucleotide,attrs,{text:NC_001992term_id,,term_text::term_text NC_001992}NC_001992Arnason 1998 Theropithecus geladaGelada{tipi :entrez-nükleotid ,attrs:{text:FJ785426,term_id:22712255,term_text:FJ785426}}FJ785426Hodgson ve ark., 2009 Hominoidea Gorilla GorillaWestern gorilla{type:entrez-nucleotide,attrs:{text:NC_001645,term_id:5835149,term_text:NC_001645}}NC_001645Horai ve ark., 1995 Homo neanderthalensisNeanderthal{type:entrez-nucleottide,attrs:{text:AM948965,term_id:195972535,term_text:AM94 88965}}AM948965Green ve ark., 2008 Homo sapiensHuman{type:entrez-nucleotide,attrs:{text:EF061150,term_id :256946671 ,term_text:EF061150}}}EF061150Friedlaender ve ark., 2007 Homo sp. (Denisovan)Denisova hominin{type:entrez-nucleotide,attrs:{text:FR695060,term_id:315466581,term_text:FR695060}}FR695060Krause et al., 2010 Hylobates agilisAgile gibbon{type:entrez-nucleotide,attrs:{text:NC_014042,term_id:295065480,term_text:NC_014042}NC_014042Matsudaira & Ishida, 2010 Hylobates larWhite elli gibbon{type:entrez-nucleottide,attrs:{text:NC_002082,term_id:5835820 ,term_text :NC_002082}}}NC_002082Arnason ve ark., 1996 Hylobates pileatusPileated gibbon{type:entrez-nucleotide,attrs,{text:NC_014045,term_id:2950655510,term_text:NC_014045}}NC_014045Matsudaira & Ishida, 2010 Nomascus sikiGüney beyaz yanaklı gibbon{type:entrez-nucleotide,attrs:{text:NC_014051,term_id:2950655580,term_text:NC_014051}}NC_014051Matsudaira & Is hihida, 2010 Pan paniscusPygmy şempanze{type:entrez-nucleotide,attrs:{text:D38116 ,term_id:643684,term_text :D38116}}}D38116Horai ve ark., 1995 Pan troglodytesCommon & Carr, 2007 Pongo abeliiSumatran orangutan{type:entrez-nucleotide,attrs:{text:X97707,term_id:1743294,term_text:X97707}}X97707Xu & Arnason, 1996 Pongo pygmaeusBornean orangutan{type:entrez-nucleotide,attrs:{text:NC_001646,term_id:5835163,term_text:NC_001646}}}NC_001646Horai ve ark., 1995 Symphalangus syndactylusSiamang{type:entrez-nucleottide,attrs:{text:NC_014047,term_id:295065538,term_text:NC_014047}}NC_014047Matsudaira & Ishida , 2010Non-primat memelisEuarchontoglires Dermoptera Galeopterus variegatusSunda uçan lemur{tipi :entrez-nükleotid,attrs:{text:NC_004031,term_id:21449889,term_text:NC_004031}}NC_004031Arnason ve ark., 2002 Galeopterus variegatusSunda uçan lemur{type:entrez-nucleotide,attrs:{text:AF460846,term_id:26284395,term_text:AF460846Schmitz ve ark., 2002a Rodentia Cavia porcellusGuinea pig{type:entrez-nucleotide,attrs:{text:AJ222767,term_id:5679797,term_textAJ222767}}AJ222767D'Erchia ve ark., 1996 Cricetulus griseusChinese hamster{type :entrez-nucleotide,attrs :{text:NC_007936,term_id:91176202,term_text:NC_007936}}NC_007936Partridge ve al., 2007 Glis glisFat dormouse{type:entrez-nucleotide,attrs:{text:NC_001892,term_id:5835484term_text,:NC_001892}NC_001892Reyes et., 1998 Mus musculusMouse{type:entrez-nucleotide,attrs:{text:NC_005089,term_id:34538597,term_text::NC_005089}}}NC_005089Bayona-Bafaluy et al., 2003 Rattus norvegicusBrown rat{type:entrez-nucleottide attrs :{text:AJ428514,term_id:19577313,term_text:AJ428514}}AJ428514Nilsson ve ark., 2003 Sciurus vulgarisSquirrel{type:entrez-nucleotide,attrs:{text:AJ238588,term_id:8347068,term_text:AJ238588}}AJ238588Reyes ve ark., 2000 Lagomorpha Lepus europaeusEuropean hare{type:entrez-nucleotide,attrs:{text:AJ421471,term_id::21425393,term_text:AJ421471}}AJ421471Arnason ve ark., 2002 Ochotona collarisCollared pika{type:entrez-nucleotide,attrs:{text:NC_003033,term_id:15055558 term_text :NC_003033}}}NC_003033Lin ve ark., 2002 Oryctolagus cuniculusRabbit{type:entrez-nucleotide,attrs,{text:NC_001913,term_id:5835526,term_text:NC_001913}}NC_001913Gissi}NC_001913Gissi 1998Laurasiatheria Carnivora Canis familiarisDog{type:entrez-nucleotide,attrs:{text:NC_002008,term_id:17737322,term_text:NC_002008}}NC_002008Kim ve ark., 1998 Felis catusYerli kedi{type:entrez-nucleottide,attrs:{text:U20753,term_id::1098523 term_text :U20753}}U20753Lopez ve ark., 1996 Perissodactyla Equus caballusHorse{type:entrez-nucleotide,attrs:{text:NC_001640,term_id:5835107,term_text:NC_001640}}NC_001640Xu & Arnason, unicornisGreater Indian rhinoceros{type:entrez-nucleotide,attrs:{text:NC_001779,term_id:5835331,term_text:NC_001779}}NC_001779Xu et al., 1996 Cetartiodactyla Balaenoptera musculusBlue whale{type:entrez-nucleottide,attrs:{text:NC_001601,term_id:5834995,term_text:NC_001601}}NC_001601Arnason et al., 1993 Balaenoptera physalusFinback whale{type:entrez-nucleottide,attrs:{text:X61145,term_id:12772,term_text:X61145}}X61145Arnason et al., 1991 Bos TaurusCow{type :entrez-nucleotide,attrs:{text:NC_006853,term_id:60101824,term_text:NC_006853}}NC_006853Chung,and Ha, unpub. Hippopotamus amphibiousHippopotamus{type:entrez-nucleotide,attrs:{text:AJ010957,term_id:4127863,term_text:AJ010957}}AJ010957Ursing & Arnason, 1998b Lama pacosAlpaca{type:entrez-nucleotide,attrs:{text:NC_002504,term_id:9755345,term_text::NC_002504}}NC_002504Ursing et al., 2000 Ovis ariesSheep{type:entrez-nucleotide,attrs:{text:AF010406,term_id:3445513,term_text:AF0104 }}}AF010406Hiendleder et al., 1998 Physeter catodonSperm whale{type:entrez-nucleottide,attrs:{text :NC_002503 term_id:34582601,term_text:NC_002503}}NC_002503Arnason et al., 2000 Sus scrofaPig{type:entrez-nucleotide,attrs:{text:AJ002189,term_id:4220565,term_text:AJ002189}}AJ002189Ursing & Arna, 1998aAfrotheria Hose Elephas maximusAsiatic elephant{type:entrez-nucleotid,attrs:{text:NC_005129,term_id:10712207 ,term_text:NC_005129}}NC_005129Rogaev et al., 2006 Loxodonta africanaAfrican elephant{type:entrez-nucleotide,attrs:{text:NC_000934 ,term_id :6137801,term_text:NC_000934}}NC_000934Hauf et al., 2000This genomes were added to a data set containing mitochondrial genomes consisting of 51 other primates, representing mitogenomes of 23 other species representing all major taxonomic lineages and the main lineages in Boreoeutheria. Rooting was done using two afrotheria species, Elephas maximum and Loxodonta africanus, generally considered externally accepted as mammals' phylogens Boreoeutheria (Murphy et al., 2001; Arson and Janke, 2002; Springer et al., 2003; Bininda-Emonds et al., 2007; Arnason et al., 2008; Meredith et al., 2011; Song et al., 2012). A total of 87 mammalic genomes were included in phylgenetic analysis. DNA was removed and isolated from blood or tissue samples using the QIAamp DNA Micro Kit (Qiagen, Inc.), following the protocol provided by the manufacturer. A list of examples with location, sample lem, and GenBank participation number is reported in Appr. Table A1. All samples are currently stored in the Molecular Anthropology laboratory at New York University. Mitochondrial genomes were sequenced with long-templated PCR, which raising mitochondrial pseugenes in the nuclear genome (numts) (Thalmann et al., 2004; Raaum et al., 2005). We used the same approach previously used in Raaum et al. (2005), Sterner et al. (2006), Hodgson et et. (2009) and Chiou et al. (2011). In short, a set of independent amplification linings is designed for each species that strengthens the entire mtDNA genome in long pieces overlapping two or more. PCR reactions were carried out with a long-range PCR kit (Expand Long Template PCR System, Roche). Sorting products were analyzed on 3730 DNA Analysis System (Applied Biosystems, Foster City, CA). The sequences were then assembled and edited using Sequencher 4.1 (Gene Codes, Corp., Ann Arbor, MI). In addition to eleven newly sequenced genomes, fifteen of the primate genomes used in this study were previously sequenced in the NYU Molecular Anthropology laboratory by applying the technique described above (see Raaum et al. 2005; Sterner et al. 2006; Hodgson et al. 2009). All genomes obtained from GenBank (61) were analyzed in the data set to minimize the presence of nuclear copies of mitochondrial genes (numts). First, we turned all protein-encoding mitochondrial genes into amino acids to check for the presence of early stop kodons and frame-changing additions or deletions. Then, for each protein-encoding gene and RNA sequence, we built a neighbor-joining tree to identify any sequence that showed unusual phylgenetic placement. Heavy threaded protein encoder genes and RNA sequences (2 rRNA and 22 tRNA) were automatically extracted from full genome sequences using a Perl script written by jah for this purpose, according to GenBank annnations. The D-loop was kept out of the dataset due to alignment difficulties due to its high variability. In addition, the ND6 gene has been shown to be encoded on the mitochondrial L-strand, which has a different nucleotide composition than H-strands, and has a poor phylgenetic signal because they are excluded from the final alignment (Gissi et al., 2000; Miya and Nishida, 2000). Protein-encoding genes are then aligned according to the corresponding amino acid translations using TranslatorX software (Abascal et al., 2010). Since homology is best defined by the triplets of nucleotides at the amino acid level and the evolution of DNA as an overdoor of genetic code, this software translates DNA sequences into AMINO acids, aligns amino acid sequences, and then reverses alignment for nucleotide sequences. We allowed the software to automatically identify the most likely reading frame (minimizing the number of stop codeons) and used MUSCLE (Edgar, 2004) to perform protein alignment. The secondary structures of the RNA arrays (rRNA and tRNAs) are aligned with the reference. Due to root and loop structures, it is defined when considering the secondary structure of the best RNA sequences of homologous regions. This approach was advocated to improve not only the alignment itself, but also phylegenetic tree reconstruction (Kjer and Honeycutt, 2007; Stocsits et al., 2009; Letsch et al., 2010). We hired two different structure-informed alignment methods for RNA arrays: RNAsalsa (Stocsits et al., 2009) and RAF (Do et al., 2006, 2008). Specially designed to align ribomal RNAs, RNAsa uses pre-existing information of the RNA structure to predict the secondary structure in RNA arrays at the same time and align it to secondary build information. As reported in the literature, we used the secondary structures of Bos Taurus (Springer and Douzery, 1996; Burk and Douzery, 2002; Stocsits et al., 2009) to align the remaining 86 arrays in our dataset. The RA RA (RNA Alignment and Folding) uses an algorithm for simultaneous alignment and consensus folding of unsalted RNA arrays. Unlike RNAsalsa, the RAF does not need pre-existing information about the secondary structure, but defines possible matching and alignment deterrings for each nucleotide and achieves simultaneous alignment and folding (Do al., 2006, 2008), and then compares the results of two candidate alignments to identify possible discrepancies. The resulting alignments (12 protein coding genes, 12S and 16S rRNA and 22 tRNA) were concatened with a relaxed approach after removing problem areas using gblocks 0.91 (Talavera and Castresana, 2007). Gblocks eliminates all poorly aligned regions in a dataset and has been shown to be particularly effective in phylgenetic studies, including very different arrays (Castresana, 2000; Talavera and Castresana, 2007). Gblocks selects blocks to delete after a number of repeatable requirements, including non-contiguous locations, lack of space positions, and the absence of large segments such as high protection of side positions. Gblocks options were run with Minimum Length A Block = 10 (5 for RNA) and Allowed Space Positions = Half. A total of 11,022 bp from 12 protein-encoding genes, 1,313 bp from the 22 tRNA genes and 1,708 bp from the two rRNA genes were precisely aligned. The individual alignments then formed a master alignment equivalent to approximately 83% of the mitochondrial genome to create a total main alignment of 14,043 bp using SequenceMatrix v1.7.6 (Vaidya v., 2011) software. For both Bayesian and maximum probability (ML) analyses, we evaluated six different divisions of the mitochondrial genome: 1) no divisions (MT0); 2) four sections (protein-encoding genes, 12S rRNA, 16rRNA and 22 tRNA) (MT4); 3) Five sections, the same as the previous one but two different sections of protein coding genes (i) separated position 1 and 2 and (ii) codeon position 3 (MT5); 4) six sections consisting of three sections for two rRNAs (12S and 16S) and 22 tRNA, and three sections for three kodon positions of protein codeon genes (MT6); 5) Fifteen sections in which 12 protein-encoding gedies are treated as independent sections (MT15); and 6) Each protein codanci gene is treated as a separate section of different codon positions, and the three RNA divisions (MT39) are 39 sections. The nucleotide substitution model for each section was selected from 24 models using the Akaike Information Criterion (AIC) (Posada and Buckley, 2004), as applied in MrModeltest v2.3 (Nylander, 2004). For each of the data sections, we evaluated variable sites and parsimony-informative sites in all taksas and only in-group (primates) (Table 2). Array properties and models are selected for each data partition partitionPartitionNO. sitesAll taxaOnly primatesModel VSPISVSPISAll genes140439080824483967532GTR+I+G12S rRNA691349308286244GTR+I+G16S rRNA1017489389419313GTR+I+Gall tRNAs1313777643652514GTR+I+GAll protein-coding genes110227465690470396461GTR+I+G pos136742277203320921827GTR+I+G pos236741568127013411075GTR+I+G pos1+273483845330334332902GTR+I+G pos336743620360136063559GTR+I+GIndividual protein-coding genes ATP6681499465477434GTR+I+G pos1227163151156134GTR+I+G pos2227112929880GTR+I+G pos3227224222223220GTR+I+G ATP8225198190193176GTR+G pos17564596255GTR+G pos27564626154GTR+G pos37570697067GTR+G COI1569807727752694GTR+I+G pos1523198153164135GTR+I+G pos252396627650GTR+I+G pos3523513512512509GTR+I+G COII696443408417385GTR+I+G pos1232134121124111GTR+I+G pos223281606649HKY+I+G pos3232228227227225GTR+I+G COIII804463426443406GTR+ I+G pos1268131110122101GTR+I+G pos226872586250GTR+I+G pos3268260258259255GTR+I+G CYTB1143747961714648GTR+I+G pos1381221200209182GTR+I+G pos2381147114126102HKY+I+G pos3381379377379364GTR+I+G NADH1963640599601556GTR+I+G pos1321203180176160GTR+I+G pos2321118101110681GTR+I+G pos3321319318319315GTR+I+G NADH2105084847878829GTR+I+G pos1350274252258230GTR+I+G pos2350226192185159GTR+I+G pos3350348343345340GTR+G NADH3360248231234219GTR+I+G pos112078716964GTR+I+G pos212054455042GTR+I+G pos3120116115115113GTR+G NADH413861002911951864GTR+I+G pos1462319287297258GTR+I+G pos2462225179197157GTR+I+G pos3462458445457449GTR+I+G NADH4L297222205204186GTR+I+G pos19974686860GTR+I+G pos29951404030GTR+G pos39997979696GTR+I+G NADH518481348125312651154GTR+ I+G pos161641838337GTR+I+G pos2616322226527421GTR+I+G pos3616608607604596GTR+I+GMaximum probability (ML) ML analyses were performed using Randomized Accelerated Maximum Probability in RAxML 7.2.6 (Stamatakis et al., 2005; Stamatakis, 2006). For each partition layout, he ran 50 independent ML infies (using 50 different randomized MP trees) with the gtrgamma model to predict the best topology. We then carried out fast (-f a-x option) with 1000 replicas to evaluate support on different nodes (Stamatakis, 2006; Stamatakis et al., 2008). Maximum probability bootstrap rates (MLBS) ≥70% were considered strong support (Hillis and Bull, 1993; Wilcox et al., 2002). Bayes analysis (MB) Bayes phylgenetic analysis was done with MrBayes 3.2.1 (Huelsenbeck and Ronquist, 2001; Ronquist and Huelsenbeck, 2003) using the Metropolis markov chain Monte Carlo (Metropolis MCMC or MC3) algorithm combined. The most appropriate model of nucleotide evolution was independently predicted for each episode using the AIC test performed in MrModelTest 2.3 (Nylander, 2004), as reported in Table 2. Although the model selected in most sections is GTR+G+I, we also conduct our analysis using a simplified GTR+G model. Bayes analysis was done because MCMC may encounter convergence issues when it tries to meet the intras site substitution rate change using a combination of the immutable sites model (+I) and the gamma distributed speed model (+G). This conflict can cause two regions of high posterior probability by creating clear convergence problems in bayes analysis (Brian Moore, Persian. comm.; Stamatakis 2006). Four independent runs, including four-stage heated chains each, were run for at least 20 million generations. Different partition diagrams require a different number of generations to reach the bead correctly, as reported in Table 3. The sample frequency is adjusted according to the number of generations (Table 3). Using Tracer v.1.5 (Rambaut and Drummond, 2007), we visually assessed the possibility of creating the association against the number of productions and to estimate the effective sample size (ESS>200) of all parameters and compare the performance of four independent analysis. In addition, AWTY (Are We There Yet?, Nylander et al., 2008) is used to draw bidirectional split frequencies for four independent MCMC runs and control the possibilities of posterior covers of trees in the example using comparison and slide commands. After checking the convergence, we summarized the rear distribution of trees removed from the top 10% of generations as combustion. Posterior probability (PP) support values were considered a strong support for individual clades resisting above 0.95 (e.g., Alfaro et al., 2003; Erixon et al., 2003; Huelsenbeck and Rannala, 2004). Summary of model partition comparison (Maximum Probability and Bytes analysis)ModelMaximum ProbabilityBayezian RunGenerationsBurn-inMarginal To assess relative support for competing division models, we compared marginal probability scores for both maximum probability and Bayes analysis (Table 3). We also used the Bayes factors (Kass and Raftery, 1995) to choose the department model, which was better supported by Bayes analysis. As described as (Nylander et al., 2004), we calculated ln (Bayes factor) as the estimated marginal probability difference for model pairs. For Bayes analysis, marginal probabilities from harmonic tools were estimated using Tracer v1.5 (Rambaut and Drummond, 2007), employing a predominant probability bootstrap predictor with the standard error estimated using 1000 bootstrap pseutocecytes (Newton, 1994; Suchard et al., 2001). The results of the partition model comparison reported here are based on the consolidation of post-write data from the two runs that achieve the greatest marginal probabilities, as outlined in Table 3. The similarity of tree topologies resulting from analysis using different departments was evaluated using the TOPD-FMTS version 3.3 program (Puigbò et al., 2007). The six compartments were compared to the maximum un kökted probability for each of the schemes and the Bayes trees (without branch lengths). TOPD-FMTS analysis was carried out under default conditions and there were 100 simulated trees as null models. The analysis was conducted using nodal, splitting, and disagree options. The Nodal method compares the number of nodes separating each taxa tree from the other takara and calculates two-way distance matrices from two input trees using taxa common to both trees (Puigbò et al., 2007). The split option uses a crossover method that takes into account the minimum number of processes required to convert one tree to another, following the algorithm proposed by Robinson and Foulds (1981). Finally, the disagree option compares the two trees and returns taxa to disagree between these trees. It first removes a taxa and calculates the gain (split distance reduction) between the two trees. The most earning taxon is removed for the following iterations. This process is then repeated until the divided distance is zero (Puigbò et al., 2007). Research over the past decade has shown that phylgenetic indices can be affected by systematic errors such as non-phylgenetic signals that can drive phylgenetic results (Phillips et al., 2004; Phillips, 2009). Even nucleotide substitution complex models may not capture the substitution process well enough to reliably ensure an accurate phylgenetic reconstruction (Phillips et al., 2004; Phillips, 2009). This problem may be even more relevant in large concane datasets, where long sequences further worsen the potential for biases (systematic error) to be positively misleading (Phillips et al., 2004: p. 1455). Encoding Nucleotides as purines and pyrimidines (RY-coding) have been proposed as an effective approach to assess compositional biases and non-phylgenetic signal (multiple substitution) effects (Phillips et al., 2004; Phillips, 2009). Previous studies of mitochondrial genomes have shown that RY-coding can increase signal levels based on compositional heterogeneity by giving more weight to the slowest developing regions in mitochondrial genomes (Brinkmann and Philippe 1999; Phillips and Penny in 2003; Delsuc, Phillips and Penny 2003; Phillips et al., 2004). Therefore, this approach can reduce the weight of systematic biases by increasing the ratio between historical and non-historical signal. To check for this problem, we used and analyzed three additional datasets: 1) RY [3RY], 2) third cone position in protein coding regions replaced with Y [AGY] along with Cs and Ts, and 3) all nucleotides encoded as purines (R) and pirimidines (Y) [allRY]. For each dataset, the reliance support of internal nodes was evaluated by bootstrap analyses using autoMRE (Majority Rule Criterion), as implemented in RAxML 7.2.6 (Pattengale et al., 2009). Incomplete taxa sampling has been shown as a major problem in phylgenetic reconstructions (Zwickl and Hillis, 2002; Hillis et al., 2003; Plazzi et al., 2010; Townsend and Leuenberger, 2011; Nabhan and Sarkar, 2012). Here we openly test the importance of taxa representation in resolving relationships between primates and the main lineages within colugos. We put together four additional datasets, including different numbers of each primate taxon: 1) only six primate taxa (one for each main lineage within primates: Lemuriformes, Ten taxons used by Chyromyiformes, Lorisiformes, Tarsiiformes, Platyrrhini, Catarrhini), 2) Schmitz et al. (2002a), 3) Arnason et al. (2008) and 4) 26 takson Matsui et al. (2009) used by 14 taxa. We then compared the results obtained by these four datasets with our original dataset with 62 primate types. Phylgenetic analysis was performed using RAxML 7.2.6 as described in full above. Fossil constraints have been carefully selected according to criteria for selecting appropriate calibration points reviewed elsewhere (Raaum et al., 2005; Ho and Phillips, 2009; Parham et al., 2012). We applied seventeen fossil restrictions defined in the literature and previous studies on primate and mammalic phylogeny. Details and references to these fossil calibrations, including age, phylgenetic location, minimum and (putative) maximum limits, are reported in Table 4. The detailed procedure of fossil selection, paleontological details and assignment to alternate nodes for calibration of the molecular clock have been reported entirely as Additional Material B1. Evolutionary speed calibration restrictions (millions fossils1. Homo5.010.0ArdipithecusHaile-Selassie et al., 20015.2OrrorinSenut et al., 20016.0SahelanthropusVignaud et al., 2002; Brunet et al., 20026.0-7.02. Gorilla10.0NAChororapithecus abyssinicusSuwa et al., 2007≈10.03. Pongo12.518.0SivapithecusKelley, 2002≈12.54. Crown Catarrhini21.033.9MorotopithecusGebo et al., 1997>20.6VictoriapithecusPilbeam and Walker, 1968Benefit and McCrossin, 2002≈19.05. Theropithecus3.56.5TheropithecusLeakey, 1993Frost, 2007≈3.56. Macaca5.5NAMacaca libycaDelson 1980Jablonski, 2002≈5.57. Colobinae10NAMicrocolobus tugenensisBenefit and Pickford, 1986; Jablonski, 20029.0-11.08. Aotus12.1NAAotus dindensisSetoguchi and Rosenberger, 1987≈12.19. Saimiri12.1NANeosaimiriHartwig and Meldrum, 2002≈12.110. Crown Anthropoidea31.5NAFaum catarrhinesRasmussen, 2002; Seiffert, 200531.511. Lorisoidea36.9NASaharagalagoKaranisiaSeiffert et al., 2003Seiffert, 2007≈36.9Non-primate fossils12. Cetartyodactyla48.6NAHimalayacetusBajpai And Gingerich, 199853.5PakicetusGingerich and Russel 1981Thewissen et al, 2001>48.613. Mysticeti-Odontoceti33.553.5Llanocetus denticrenatusMitchell, 1989≈3.514. Feliniforma-Caniformia43.063.8TapocyonBenton and Donoghue, 200743.0-46.015. Bovidae18.328.55Eotragus noyiSolounias et al., 1995Benton and Donoghue, 2007≈18.316. Moush/Rattus7.316.0Progonomys hussainiJacobs & Downs, 1994Benton and Donoghue, 200711.1-11.517. Equus/Rhinoceros54.058.0LambdotheriumRose, 2006>50.3 The compliance of these 17 minimum age restrictions was assessed using TheFosil cross-calibration (Near and Sanderson, 2004; Near and near, 2005; Hugall et al., 2007; Rutschmann et al., 2007). Fossil cross-verification includes the use of a fossil at the same time to create age estimates for nodes to which other fossils are assigned; then compares the fossil age with the extracted age in this node. This technique assesses the consistency of date estimates generated from different putative calibration points (Near and Sanderson, 2004; Near and near, 2005). We calculated two different statistics to assess the compatibility of each calibration point. First, by following the method proposed by Near et al., we calculate the average deviation (D) between molecular (MA) and fossil age (FA) estimates for all nodes using a single fossil dated node used as a calibration point, and SS values (SSx= Φi≠xD2) for a particular fossil calibration node. Secondly, we applied the statistics described by Hugall et al. (2007). First of all, we calculate the average deviation D as described above. Next, for each calibration point, we achieved the sum of the absolute values of the differences between estimated and recommended ages for each calibration node. This value (Φ| D|) it is an indication of how compatible it is with the rest of a particular fossil calibration: the smaller its value, the more consistent it is. For these analyses, Topology and branch lengths of the MT39 model tree obtained in our Bayes analysis. This topology has been strongly preferred in the Bayes factor comparison analysis described above (see Table 3). For all the analysis described above, we used the ratio-autocorty Bayesian comfortable molecular clock method applied in the MULTIDIVTIME program package (Thorne and Kishino, 2002). First, the maximum probability parameters for the F84 + G evolution model were estimated by baseml from the PAML package (Yang, 1997, 2007). Later, branch lengths and their variance-covarians matrix were calculated by euddals. Finally, deviation times were calculated by multidivtime using conservative priests and fossil calibrations. Bayesian priests were chosen in the multidisciplinary manual according to J. Thorne's recommendations for multidivtime. The root-end was set at an average of 100.0 Ma, with a standard deviation of 100.0 Ma. The evolutionary rate at the root was 0.009 per nucleotide area per myr, and the standard deviation was 0.009. This is calculated as the median root-to-end branch length is divided by the previous root-to-end average. Brownmean and standard deviation are set at 0.020, so much so that brown is multiplied by an average root-end average equals the previous (100Ma) 2. After a burn period of 100,000 generations, MCMC chains were sampled one in every 100 generations until 10,000 samples were taken. Various runs were carried out with various previous selections to test Priors' impact on posteriors. The results were extremely robust against changes to criminal records. During preliminary analysis, fossil constraints were treated as point calibrations (equal to minimum maximum limits). Based on the results of preliminary analyses in which all 17 fossil calibrations were tested for compatibility, a set of 16 constraints was used to obtain the final chronogram presented in the results. In this latest analysis, we have identified the minimum and maximum restriction (if any) reported in Table 4.A for each fossil calibration. Comparison of tree topologies resulting from analysis has shown that the changing partition scheme has little impact on overall tree topology. For ML trees, zero to six of the 168 possible overlaps were defined between partitions, which was defined only as a difference between 0.00-3.57% (nodal distance: 0-0.474; divided distance: 0-0.036). The differences were mainly represented by two taxa positions: the breed within rodents Havya (Cricetulus sister group / (Mus / Rattus) or dormouse sister taxa, Glis glis) and the position of cercopithecus diana in regard to other cercopithecins. Within mb trees, it detected only 2 possible overlaps in the different partitioning scheme (1.07%; nodal distance: 0-0.331; divided distance: 0-0.0119). C. diana position was the only taxon that was contradictory farklı bölümler arasında. Bayes faktörü karşılaştırmaları, rRNA'lar (12S ve 16S), biri 22 tRNA için ve her protein kodon geninin üç kodon pozisyonu için 36 bölümden oluşan 39 bölümlü (MT39) modeli güçlü bir şekilde destekledi. Bölüm şeması MT39 kuvvetle MT6 (lnBF = 5531.809) üzerinde tercih edildi, MT6 MT5 (lnBF = 1287.011) üzerinde tercih edildi, MT5 kuvvetle MT15 üzerinde tercih edildi (lnBF = 5068.416), MT15 MT4 (lnBF = 996.090) ve MT4 MT0 (lnBF = 1440.723) (Tablo 3) üzerinde tercih edilir. Aynı sonuçlar maksimum olasılık (MT39 <> <> <> <> <MT0). we= therefore= treat= the= mt39= ml= and= bayesian= trees= as= our= "preferred= tree".= tree= topology= comparison= analysis= using= topd-fmts= version= 3.3= showed= identical= topologies= between= ml= and= bayesian= trees= (0/168= nodes;= split= distance= random= [differents/possibles]:= 0.997= +/−= 0.007= [167.46= +/−= 1.195/168= +/−= 0.000]).the= bayesian= clade= credibility= values= (pp)= across= the= entire= tree= were= high,= with= only= two= nodes= below= 0.95:= the= sister= group= relationship= between= c.= diana= and= the= clade= including= erythrocebus= patas= and= c.mitis/c.lhoesti= (pp=0.91), and= the= sister= group= relationship= between= erythrocebus= patas= and= c.mitis/c.lhoesti= (pp=0.80) (figure= 1).= in= contrast= to= the= bayesian= results,= the= maximum= likelihood= bootstrap= (bp)= values= were= quite= low= in= several= nodes= across= the= tree= (figure= 1).= within= primates= several= nodes= were= weakly= supported= in= the= ml= analyses.= for= instance ,= within= the= platyrrhines,= the= sister= relationship= between= ateles= and= the= clade= including= aotus,= saimiri,= cebus,= and= saguinus= was= below= 70%= bootstrap= support= also,= several= nodes= within= cercopithecins= (particularly,= the= position= of= e.= patas= and= c.= diana,= and= the= sister= group= relationship= between= nasalis= and= pygathrix)= showed= bootstrap= support= below= 70%= (figure= 1).= bp= and= pp= values= for= all= the= nodes= within= primates= are= reported= in= supplementary= material= (table= c1).in= order= to= evaluate= the= influence= of= rna= sequences= on= the= topology= and= support= values,= we= also= ran= raxml= and= mrbayes= using= only= the= 12= protein= coding= genes= (11,022= bp).= the= topology= of= the= reduced= dataset= did= not= differ= from= the= one= using= all= data.= similar= to= the= ml= results= described= above ,= bp= values= were= generally= lower= than= pp= in= bayesian= analyses= (see= supplementary= figure= d1–2).all= the= analyses= supported= the= same= topology= and= the= monophyly= of= the= order= primates= (figure= 1).= specifically,= mitochondrial= genome= analyses= supported= the= subdivision= of= primates= into= infraorders= strepsirrhini= and= haplorhini,= with= tarsiers= as= sister= group= of= anthropoidea= (bp=>%70 ve PP>0,95) has been obtained. Furthermore, dermopterans (colugos, represented here by the genus Galeopterus) fell outside primates (BP>70% and PP>0.95), and as in many previous studies using mitochondrial DNA, the sister group of anthropoids (Arnason and Janke, 2002; Arnason et al.,</MT0).> ark.,</MT0).> 2008; Schmitz et al., 2002a). Using three additional datasets (3RY, AGY and allRY), we assessed the impact of compositional biases and the non-phylgenetic signal level. All analytics are strongly supported (BP>70%) The monophyly of primates (with colugos other than primates) and two datasets (3RY and AGY) also strongly supported the sister group relationship between tarsiers and anthropoids. When all nucleotides are encoded as RY (allRY), the monophyly of haplorhines (tarsiers+anthropoids) is only poorly supported (BP= 57%). (Additional Figures E1-3). Relations between the main lineages within primates are well supported by lemuriformes and lorisoids in strepsirrhines, platyrrhines and catarrhines, ercoppithecoids (Cercopithecinae and Colobinae) within anthropoids, and hominoids in corteges (Figure 1). Two major discrepancies between our results and widely accepted relationships within primates have been found in phylgenetic relationships within lorisoids and papionines. As the old clade, the division between galagids and lorisids was not supported by our mitogenomic data. In all the analysis carried out here, African loricyds were identified as a clade sister group consisting of Asian loricydes and African galagids. However, while their Bayesanaliz strongly supports this topology (PP>0.95), bootstrap values were relatively low in all analyses (BP<70%). within= the= tribe= papionini,= our= results= did= not= support= the= presence= of= an= african= clade= (theropithecus/papio/lophocebus/mandrillus/cercocebus).= instead,= the= group= mandrillus/cercocebus= clustered= together= with= the= genus= macaca= (bp=>70% and PP>0.95). The same relationships were found within these two primate groups (lorisoids and papionines) when RY-coded datasets (3RY, AGY and allRY) were analyzed. We analyzed four additional datasets, including a subset of primate taxa, to investigate the impact of taxa sampling in our data set. Interestingly, all data sets (6-taxa, 10-taxa, 14-taxa and 26-taxa) showed no support for the sibling relationship between primates monophyly and tarsiers and anthropoids. All reduced data sets are supported in the sibling relationship between colugos and anthropoids instead and between strepsirrhines and tarsiers. However, bootstrap values for both nodes are <70%) across all the analyses: 32–60% for the clade colugos-anthropoids and 45–68% for the clade tarsiers-strepsirrhines (Supplementary Figures F1–4). The cross-validation results (Table 5) reveal that calibration point 13 (C13: the split between Mysticeti and Odontoceti) is highly inconsistent with the other fossil calibrations. Specifically, when used as the only calibration point, C13 tended to overestimate all the other calibration points used in this study (Dx=23.52). Both statistics used in the study (SS ΣD) across= all= the= analyses:= 32–60%= for= the= clade= colugos-anthropoids= and= 45–68%= for= the= clade= tarsiers-strepsirrhines= (supplementary= figures= f1–4).the= cross-validation= results= (table= 5)= reveal= that= calibration= point= 13= (c13:= the= split= between= mysticeti= and= odontoceti)= is= highly= inconsistent= with= the= other= fossil= calibrations.= specifically,= when= used= as= the= only= calibration= point,= c13= tended= to= overestimate= all= the= other= calibration= points= used= in= this= study= (dx=23.52). both= statistics= used= in= the= study= (ss= and= σd)=></70%) across all the analyses: 32–60% for the clade colugos-anthropoids and 45–68% for the clade tarsiers-strepsirrhines (Supplementary Figures F1–4). The cross-validation results (Table 5) reveal that calibration point 13 (C13: the split between Mysticeti and Odontoceti) is highly inconsistent with the other fossil calibrations. Specifically, when used as the only calibration point, C13 tended to overestimate all the other calibration points used in this study (Dx=23.52). Both statistics used in the study (SS and ΣD) > düşüktü (BP</70%).> (BP</70%).> this result (Table 5). All other fossil calibrations used in this study offer reasonable age estimates that are within range of other calibrations. That's why we used 16 calibration points (excluding C13) listed in Table 4 for all date analysis. Cross-validation deviation of candidate calibration points. (Dx: the average average deviation between molecular and fossil age estimates for all existing nodes based on fossil calibration in node x; SS: the sum of the square differences between molecular and fossil age estimates in all other fossil-dated nodes; ΣD: sum of the absolute values of differences between the estimated and proposed ages for each calibration node)CPdivergenceagenode DxSSΣDC1C2C3C4C5C6C7C8C9C10C11C12C13C14C15C16C17C1Homo5.0-7.011.921.14.58.114.510.09.628.121.725.711.827.113.711.127.5−5.602277.0130.5C2Gorilla10.07.2-17.030.46.511.620.914.413.840.631.437.117.039.219.816.039.7−0.931099.6110.94C3Pongo12.55.47.5-21.94.88.515.210.410.029.022.326.211.927.713.911.328.1−6.382181.2127.77C4Crown Catarrhini21.05.37.412.2-4.68.114.610.09.627.721.325.111.426.513.310.826.9−5.212387.5133.29C5Theropithecus3.54.25.89.716.8-6.311.58.07.722.317.220.49.321.510.98.821.8−9.753489.7166.78C6Macaca5.53.75.18.515.03.1-10.27.16.820.115.618.58.419.59.88.019.8−11.564051.0182.05C7Colobinae10.03.65.08.414.53.15.6-6.96.619.214.817.57.918.59.37.518.7−11.324336.2188.3C8Aotus12.16.69.215.226.35.710.218.3-11.735.027.132.214.833.917.213.934.4−2.711373.5110.84C9Saimiri12.16.99.615.927.45.910.619.012.6-36.228.133.115.134.917.614.235.4−1.881306.1110.76C10Crown Anthropoidea31.56.08.413.923.95.29.316.711.310.9-24.328.913.230.415.312.530.8−4.921772.1117.83C11Lorisoidea36.99.613.422.137.98.314.826.518.017.449.7-44.820.547.323.819.348.14.811599.1139.06C12Cetartyodactyla48.610.815.024.742.49.316.529.720.319.555.442.2-22.152.025.721.452.78.052393.3168.76C13Mysticeti-Odontoceti33.515.521.535.661.513.423.842.729.228.181.162.373.5-77.639.131.978.723.5211026.8383.95C14Felis/Catus43.08.812.320.335.07.613.624.416.716.045.935.141.118.8-21.917.943.88.061313.0125.72C15Ovis/Bos18.37.310.216.829.06.311.220.213.813.338.229.334.415.736.3-14.836.8−0.581251.1113.95C16Mus/ Rattus7.34.05.69.316.03.56.211.67.321.016.119.18.820.210.2-220.5−1 0.293836.8174.83C17Equus/Rhinoceros54.011.115.425.443.69.617.030.520.820.00.000.000.000.000.000.000.000 057.143.551.123.453.453527.222.3-9.212694.5180.89 Because the relative position of fossil calibrations in the tree may affect the sensitivity of the historicalization estimates for the node of interest, the estimated and recommended for each calibration node of the absolute values of the deviation between the recommended ages, we tested whether it was related to branch lengths (nodal distance) between the calibration point used in each run and the remaining 16 nodes. We did a mantel test to check the relationship between the matrix of deviations | D| (directory error) and nodal distancesmatry in the term branch length (R Development Core Team, 2009). The Mantel test, based on 10,000 copies, produced a positive correlation (p value: 0.038) with r=0.265. To assess the impact size of this corral, we calculated the slope estimate from a linear regression. The β=4.7.Dating analyses showed a positive relationship with the above-described preliminary analyses, as selected by the MT39 partitioning strategy conducted with multidivtime. Estimates of parent nodes within primates can be reported in Table 6 with 95% HPD ranges. Kronogram traces the origin of crown primates to 74.1 Ma (95% HPD=68.2-81.2; Figure 2 and Table 6). Crown strepsirrhines and crown haplorhines were found to be of Late Cretacene, 66.3 Ma (95% HPD=61.1-72.8) and 70.0 Ma (95% HPD=64.3-76.7), respectively. Living platyrrhines are estimated to have experienced the latest common ancestor 20.9 Ma (95% HPD = 17.9-24.4), while crown catalyst occurred much earlier, about 32.1 Ma (95% HPD=29.4-33.8). Homo sapiens and Neanderthals moved away with about 680,000 years ago (95% HPD=490-926,000), while the history of the latest common mitochondrial ancestor among Denisovans, Neanderthals and modern humans was estimated at about 1.39 Ma (95% HPD=1.06-1.83). Estimates of all nodes within primates are reported in Additional Material (Table C1). Comparison of deviation time estimates (posterior mean and 95% reliable range per millions of years) between this study and recent studies on primates. Divergence (node)This studyArnason etal., 2008c, dMatsui etal., 2009dFabre et al.,2009eChatterjeeet al., 2009 ePerelmanet al., 2011fWilkinsonet al., 2011fJameson etal., 2011fSpringer etal., 2012eFinstermeieret al., 2013dCrown Primates (61)74.1 (68.2–81.2)80.076.0 (69.3–82.5)78.8 (69.9–88.4)63.7 (58.3–68.7)87.2 (75.9–98.6)84.5 (69.2–103.5)72.6 (69.6–76.9)67.8 (61.0–76.7)66.2 (59.6–73.6)Crown Strepsirrhini (60)66.3 (61.1–72.8)70.064.5 (57.2–71.7)67.1 (60.2–74.5)51.6 (47.7–55.7)68.7 (58.8–76.6)49.8 (35.9–72.0)52.4 (47.0–57.2)54.2 (48.8–57.2)56.9 (50.5–64.1)Crown Lorisiformes (59)40.3a (37.1–46.3)N/A35.4 (28.5–43.1)39.5 (38.0–41.8)37.5 (36.9–38.7)40.3 (35.2–45.6)N/AN/A34.7 (27.9–38.2)34.5 (30.2–39.0)Lemuriformes-Chiromyiformes (55)59.6 (54.3–65.9)64.055.3 (47.7–63.0)59.6 (53.3–66.7)46.2 (41.3–50.8)58.6 (38.6–76.8)N/AN/A50.0 (45.2–53.8)47.1 (40.9–53.6)Crown Lemuriformes (54)43.5 (37.5–50.1)N/AN/A47.3 (37.9–50.8)32.4 (28.6–33.6)38.6 (26.4–50.0)34.4 (23.5–49.1)N/AN/A31.8 (26.7–36.6) 35.5 (30.4-40.4)Crown Haplorrhini (46)70.0 (64.3-76.7)N/A70.1 (63.2-76.7)7N/AN/A81.3 (69.5-95.8)N/A68.6 (65.6-72.7)61.2 (57.6-69.6)63.1 Anthropoidea (44)46.7a (42.4–50.8)55.045.3 (39.4–51.3)37.7 (33.3–42.7)42.8 (40.1–45.0)43.5 (38.6–48.4)47.2 (38.9–56.5)40.0 (37.3–43.1)40.6 (33.6–49.5)45.3 (40.7–50.1)Crown Platirrhini (43)20.9 (17.9–24.4)N/AN/A14.5 (9.7–19.9)26.6 (23.5–30.0)24.8 (20.6–29.3)25.1 (20.1–31.0)N/A23.3 (19.2–27.5)22.0 (19.2–24.4)Crown Catarrhini (38)32.1b (29.4–33.8)39.030.5 (28.8–35.3)23.9 (23.1–25.9)29.3 (28.0–30.0)31.6 (25.7–37.9)31.0 (25.1–37.7)25.4 (23.7–27.6)25.1 (19.7–32.8)31.9 (28.3–35.7)Crown Cercopithecoidea (37)20.8a (18.6–22.9)N/AN/A13.3 (11.6–14.7)23.4 (21.9–24.9)17.6 (13.9–21.5)14.1 (11.0–17.7)N/A13.2 (8.9–18.3)22.8 (20.0–25.6)Crown Colobinae (36)14.1 (12.0–16.3)N/AN/A8.7 (7.3–10.4)18.4 (16.8–20.1)12.3 (9.4–15.1)N/AN/A8.9 (6.3–12.0)15.5 (13.4–17.8)Crown Cercopithecinae (29)14.1 (12.2–15.8)N/AN/A9.1 (7.7–10.0)18.6 (16.5–20.5)11.5 (9.2–13.9)10.3 (8.1–13.0)N/A8.4 (5.4-11.6)14.9 (12.9-16.8)Crown Hominoidea (12)22.3 (20.5-23.) 9)N/A19.9 (16.7-23.0)18.6 (17.1-20.5)21.5 (18.9–24.3))20.3 (16.6-24.2)19.2 (15.1-24.1)N/A17.4 (N/A17.4 (15.1-24.1)12.4-23.9)20.3 (17.4-23.5)In this study, primate phylgenetic relationships and deviation dates were evaluated using full mitochondrial genome data. We compiled one of the largest mitogenomic datasets for primates and performed a fossil cross-verification procedure to identify and select the most suitable set of fossils to calibrate the molecular primate tree. All the large lineages in the primate order were included in our analysis and it became clear that it was monophyletic. Unlike previous mitogenomic studies, our analysis suggests monophyletic Primates with colugos as sister groups within Euarchontoglires. Previous mitogenomic studies hypothesis of a sibling relationship between anthropoid primates and colugos (Dermoptera), order primates making parafiletics (e.g., Arnason and Janke, 2002; Arnason et al., 2002; Schmitz et al., 2002a; Kjer and Honeycutt, 2007). Arnason et al. (2002) proposed the name Dermosimii for this assembly (Arnason and Janke, 2002; Arson et al., 2002, 2008). However, it has been claimed that this group is a work of a similar nucleotide composition of mitochondrial genomes, rather than reflecting true evolutionary history (Schmitz et al., 2002a; Schmitz and Zischler, 2003; Raina et al., 2005; Zischler, 2007). Unlike mitochondrial results, the monophyly of primates is actually strong morphological studies (Silcox et al., 2007) but is also supported by nuclear sequences (Jameson et al. 2011); Meredith et al., 2011; Perelman et al., 2011) and passable elements (Schmitz et al., 2002a). In this study, we suggest that this structure may also be the result of taxa sampling and the small internode distance between Dermoptera and Primates. Missing or biased taxa phylgenetics is a major problem in studies and can provide misleading results in the rebuilding of phylgenetic relations (Zwickl and Hillis, 2002; Hillis et al., 2003; Plazzi et al., 2010; Townsend and Leuenberger, 2011; Nabhan and Sarkar, 2012) and increased taxa sampling have been shown to be an effective way to improve overall phylgenetic accuracy (Zwickl and Hillis, 2002). Here, a large taxa sampling within primates shows that it supports the invalidity of phylgenetic relationships consistent with morphological and nuclear data and primates monophyly and taxa Dermosimii. When only one subset of primate takara was included in the analyses, the position of the cotgos and tarsiers was poorly supported, and all analyses revealed the sibling relationship between colugos and anthropoites similar to previous studies (e.g., Arnason and Janke, 2002; Arnason et al., 2002; Schmitz et al., 2002a; Kjer and Honeycutt, 2007), thus stating that inadequate taxa sampling mitochondria are likely to cause inconsistency found between DNA and other lines of evidence (e.g., Schmitz et al., 2002a; Silcox et al., 2007; Jameson et al., 2011; Meredith et al., 2011; Perelman et al., 2011)The difficulty of finding primate one foot using mitochondrial sequences is somely confirmed by lower support in ML bootstrap analyses compared to Bayeasian posterior probabilities. Theoretical and empirical studies have shown that the probability of Bayes posterior tends to be significantly higher than the relevant ML bootstrap frequencies. In particular, bootstrap analyses have shown to be particularly sensitive to a small number of characters and may underestimate confidence in tree topologies compared to the possibility of Bayesian posterior in short internodes (Alfaro, 2003; Erixon et al., 2003; Rothfels et al., 2012). The low amount of phylgenetic signaling in the mitochondrial genome for these nodes is shown between the relatively short branch length of the internod between Dermoptera and primates, and between Strepsirrhini and Haplorhini (Figure 1). Within the primates, a well-supported division was found between strepsirrhines (including lorises, galagids and Malagasy lemurs) and haplorhines (including tarsiers and anthropoids). Overall, support values during the entire primate tree were high with only a few exceptions. Within Cercopithecoids, the sister group relationship between C. diana and The Clade, including the sister group relationship between Erythrocebus patas and C.mitis/C.lhoesti and Erythrocebus patas and C.mitis/C.lhoesti, was poorly supported in both Bayes and ML analysis. Within platyrrhines, most of the nodes showed low bootstrap support (but high Bayespp support), agreement with previous studies employing full mitochondrial genomes (Hodgson et al., 2009; Chiou et al., 2011). Phylogenetic the new sequencing of cytocondrial genomes was consistent with previous studies. Aye-aye (Daubentonia madagascariensis) is considered the most basal deviation in lemurs, while Mirza (a member of the Cheirogaleidae family) is captured as a sister group of sporty lemurs (Perelman et al., 2011; Springer et al., 2012). In Cercopithecoidea, phylgenetic positions of five guenon genomes (Allenopithecus nigroviridis, Cercopithecus diana, C. lhoesti, C. mitis and Erythrocebus patas) were the same as those recommended in a larger mitogenomic study for guenons (Guschanski et al., 2013), but unlike nuclear data (Perelman et al., 2011; but see Guschanski et al., 2013). Despite representing large taxa in this study, the primate was either phygenetic relationships that could not overcome some well-known problems affecting mitochondrial-based reconstructions. For example, two well-supported taxonomic groups, African papionines and lorisyds, could not determine that they were monofiletic in our study. In the old group, our mitogenomic tree clusters with clade including Papio, Theropithecus and Lophocebus instead of Mandrillus and Cercocebus Macaca. In Lorisoids, our mitogenomic tree places Asian lorisids as a sister group of African galagids instead of the African lorisid Perodicticus. Both lorisyds and papionines are well supported by morphological data and nuclear sequences, and previous studies using mitochondrial sequences have shown similar difficulty in recovering such clades (Papionini: Disotell et al., 1992; Harris, 2000; Finstermeier et al., 2013; Lorisidae: Roos et al., 2004; Masters et al., 2007; Matsui et al., 2009; Finstermeier et al., 2013; Pozzi et al., admission). The mitochondrial genome represents a single locus and may be different from the species as a result of various events such as phylgenetic history, gene flow, hybridization or incomplete genealogy sequencing (Maddison, 1997; Degnan and Rosenberg, 2006; Maddison and Knowles, 2006; Edwards, 2009). Although mitochondrial genomes are still a powerful source for predicting phylogeny and phylogeny (Moore, 1995), results based on a single marshmallow should always be done with caution (Edwards, 2009; Ting and Sterner, 2013; Pozzi et al., 2014). For our information, this is the first study to investigate the practice of fossil cross-verification within primates. Primate fossil records are highly fragmented and incomplete, and some studies estimate that only 4-7% of all primate species are known from the fossil record (Tavaré et al., 2002; Soligo and Martin, 2006; Martin et al., 2007). The degree of lack of fossil records is particularly extreme in some lineages, especially in malagasy lemurs where no fossils are known – but controversial – except for bugtilemur (see: Marivaux et al., 2001, 2006). As a result, most of the molecular studies conducted to date have used a small set of calibration points, representing only a few nodes within the primate tree (e.g., Fabre et al., 2009; Matsui et al., 2009). More recently, Wilkinson et al. (2011) tried to better integrate existing information of fossil records into molecular history estimates. They developed a new methodology to better account for fossil conservation and exploration rates when calibrateing a molecule-based tree. This study ~ 84 Ma de dated origin for crown primates, confirmed a discrepancy between molecular estimates and known fossil records. In this study, we are spleding cross-validation analysis of fossil records to select the most suitable calibration points to be used together with our data set. Our approach consisted of two different steps: 1) We chose a suitable priori putative fossil to be used as a calibration point for our data set according to the criteria proposed by Parham et al. (2012); 2) We carried out cross-verification analyses aimed at detecting possible outliers in our fossil selection. Since one of the main purposes of this article is to estimate the timing of primate origins, we have included several calibration points in Boreoeutheria (Euarchontoglires and Laurasiatheria). The use of only calibration points within primates can lead to problems in the estimation of dates, especially at the root of the tree (Raaum et al., 2005). In this study, we selected sixteen fossils as calibration points, of which 11 were external primates. The original cross-verification method proposed by Near et al. (2005) has been criticized by many authors for causing various problems in the selection of calibration points, excluding the most informative fossils, except for the most informative fossils, as the method is inconsistent with the majority of remaining calibrations (Marshall, 2008; Ho and Phillips, 2009). Here, we used a conservative approach aimed only at identifying possible outliers in fossil clusters selected in phase a priori. While we agree that the approach used here is not enough to address the complex challenges of calibration (Magallón, 2004; Close and Sanderson, 2004; Near and near, 2005; Hugall et al., 2007; Rutschmann et al., 2007; Pyron, 2010; Wilkinson et al., 2011), we believe our approach allows researchers to better select fossils for use in molecular phylgenetic analysis. For example, this approach can be useful in specifying the correct place of fossils in certain nodes in a tree and excluding fossils that might otherwise be used for miseed in the calibration of molecular phylogens. In addition, new fossils can be tested against a good set of calibration points and settlements locations described here (see also <a0><a1></a1></a0 Pyron, 2010 and Ward et al., 2010). This technique also allows researchers to add more fossils to their analysis, providing a better and much-needed integration between molecular phylogenies and paleontological record. We investigated the relationship between deviation to determine how nodal distance can affect molecular estimates in the tree | Nodal distance for each node selected as D| and putative calibration point. Due to the unfinished nature of the fossil record, there are no calibration points available in many areas of the primate tree (for example, Malagasy lemurs). If evolutionary distance from calibration points was a limiting factor in our ability to accurately predict deviation times, then we would expect a strong correlation between nodal distance and prediction error. The relationship we find in our data set is particularly low, albeit statistically significant. The Mantel test showed poor positive correlation (r=0.265), suggesting that it played a very small role in the error associated with evolutionary distance from calibration points. For example, we found that the difference in the estimated error of the catarrhini deviation date between a near calibration point (Homo/Pan, branch length distance = 0.2588) and a more remote calibration point (Lorisidae/Galagidae, branch length = 0.7788) was only 2.44 million ±. Therefore, our reass confidence in differences away from calibrations will be similar to those closer to calibration points. This result is especially important for some taxonomic groups, where fossil records are particularly few or destroyed. Therefore, despite the negative relationship between nodal distance and accuracy, modern molecular historicalization techniques can successfully provide reliable predictions even in areas where calibration points are not present. The molecular chronogram obtained in this study predicted the crown group origin of the primate order in the late Cretacene (about 74 Ma) in harmony with the latest molecular studies (Arnason et al., 2008; Fabre et al., 2009; Matsui et al., 2009; Jameson et al., 2011; Perelman et al., 2011; Wilkinson et al., 2011). Nuclear estimates appear to provide estimates slightly older than those obtained from mitogenomic data (Perelman et al., 2011; Wilkinson et al., 2011), but to date all molecular data strongly seem to suggest an origin of primates before the K-Pg border. This conclusion agrees with estimates obtained for the other group of mammals from which most recent molecular studies on the diversification of mammals sourced most orders in the Cretacee (Springer et al., 2003; Bininda-Emonds et al., 2007; Meredith et al., 2011). A recent study of mitochondrial genomes, including more than 80 species of primates, recovered more recent origins for the crown group, dated around 66Ma (Finstermeier et al., 2013). This discoordans in our study is particularly interesting given the large overlaps in genome sequences used in both studies. Two main differences may have contributed to the discerning results between the two studies. First, Finstermeier et al. (2013) using calibration points only within primates, problematic age estimates at the root of the tree due to prediction biases (see Raaum et al., 2005). The main differences between finstermeier et al.'s study and ours are limited to deeper nodes in its phylogeny. There may also be an additional source of diskordans caused by the use of controversial calibration points by Finstermeier et al. (2013). Of the nine calibration points used in this study, at least four were either secondary calibrations (molecular history estimates from other molecular analyses) or misinterpretation of fossil records (for example, the use of root fossils to calibrate a crown group) (Graur and Martin 2004; Steiper and Young, 2008; Ho and Phillips, 2009; Pozzi et al., 2011). For example, Finstermeier et al. (2013) calibrated the origin of the crown catalyte using the saadanius hijazensis fossil (Zalmout et al., 2010). However, Saadanius is a root catalyte and probably cannot report decomposed between hominoids and catalytes (see Pozzi et al., 2011). Similarly, a new study by Finstermeier et al. (2013), Steiper and Seiffert (2012) also suggested a newer origin for crown primates, close to the K-Pg limit or possibly the Paleocene. In their study, the authors showed a negative correlation between three different life story variables (body size, absolute endocrinocranial volume, and relative endocranial volume) and molecular ratios in primates. While almost all deviation date estimates for placental mammals based on molecular data are largely consistent with our results, there may be life story factors that all these studies have failed to take into account (Bromham, 2009, 2011; Lanfear et al., 2010; Steiper and Seiffert, 2012). Finally, O'Leary et al. (2013) recently integrated molecular and morphological evidence to support an explosive pattern of evolution for mammals, and most interordinal diversification date back to just after the K-Pg border. According to their analysis, the crown primates are of late Paleocen origin, about 55-56 Ma (O'Leary et al., 2013). But the restructuring proposed by O'Leary et al. (2013) is based on phylgenetic analyses that fail to distinguish between homology and homoplasma, and also means extremely high acceleration in nucleotide substitution rate in early Paleocene mammals (Springer et, 2013). One of the biggest shortcomings of O'Leary et al.'s work is that the oldest known fossil representative was used to the origin of each group. genealogy analysis). As a result, the origin of the crown primates coincides with 55-56 Ma (for example, Teilhardina brandti) (O'Leary et al., 2013) with the first members of the group found in the fossil record. However, the lack of evidence in the fossil record is not necessarily evidence of absence (Ho and Phillips, 2009), and estimates obtained by O'Leary et al. (2013) can be considered minimum deviation times based on minimiseing the ghost lineage rather than actual deviation times (Slater, 2013; Springer et al., 2013; Yoder, 2013; dos Reis et al., 2014). It is estimated that the ancestor of living catalytes (monkeys and Old Earth monkeys) lived about 32 Ma. This result is Zalmout et al. (2012) which deviates from the crown catarrhines to 29 Ma after dates, contrary to what the root catarrhine Saadanius suggested based on hijazensis. Since the root fossils do not provide any information about the time of deviation of a group of crowns, it is not surprising that a date older than 29 Ma was mentioned (Steiper and Young, 2008; Ho and Phillips, 2009); therefore, the origin of saadanius crown catarrhines does not report time (Pozzi et al., 2011). A recent study by Langergraber et al. (2012) revealed a new method of differentiation times within great apes without using fossils as a calibration point. This method is based on recent improvements in the direct measurement of mutation rate in humans (Awadalla et al., 2010; Roach et al., 2010; Sanders et al., 2012; Scally and Durban, 2012) and generational periods within wild populations of chimpanzees and gorillas (Langergraber et al., 2012). Interestingly, the estimates obtained by Langergraber et al. are in line with those reported in this study. The age estimate for the difference between the above study and the single contrast bonobos (Pan paniscus) and the common chimpanzee (Pan troglodytes) dates 1.5 and 2.6 ma langergraber et al. and 2.4-3.8 Ma in our study. Finally, our estimates of 680 ka for Neanderthal and modern humans and ~1.4 Ma for Denisovans and Homo sapiens are older - roughly 1.4x - using even more mitochondrial genomes than those obtained by Krause et al. (2010). We determined the origin of this discrepancy in different use of calibration points used in two studies. Krause et al. actually underted an average decay of human and chimpanzee mtDNAs for 6 million years, while in our study we allowed this node to be between 5 and 10 Ma. This differentiation appeared to be approximately 7.6 Ma (95% HPD=6.7-8.8), significantly above the age used by Krause et al. (2010). When the division between Homo and Pan was determined as 6 Ma, we obtained age estimates that agreed with Krause et al. (H. sapiens-Neanderthal: 530 ka [397-693]; H. sapiens-Denisovans: 1.08 Ma [0.87-1.35]). We claim The deviations obtained in our study are more realistic than what Krause presented in the ancestor al. (2010), since the common ancestor of modern men and chimpanzees is more than 6 Ma old based on both molecular predictions (Jameson et al., 2011; Wilkinson et al., 2011; Springer et al., 2012) and fossil records (Haile-Selassie et al., 2001; Senut et al., 2001; Brunet et al., 2002; Vignaud et al., 2002). Our study applies a fossil cross-verification procedure to identify a number of fossil calibrations that will be used to date a molecular phylogeny within primates. To exclude possible outliers, we used a two-step approach that included priori selection of putative fossils and posteriori cross-verification analysis. The calibration process obtained by such an analysis can then be used to estimate the ages of the nodes of interest. That is why we recommend the use of these fossil calibrations for future studies aimed at estimating the periods of difference within primates. Furthermore, our study showed a poor correlation between nodal distance and accuracy, suggesting that remote calibration points can be used especially for areas of trees where reliable fossil records are particularly few. The results obtained in this study agree with recent studies of primate differentiation dates that support the origin of the order in the Late Cretace. These early primate fossil records most likely show poorly sampled. Although primate evolution contains a slowdown in molecular proportions, most molecular studies to date show that primates - along with the orders of most mammals - are very unlikely to appear after the K-Pg limit. Based on the age obtained in our study, we recommend a short insurance model of primate origin, so relatively little time (<8Myr) order primates passed between origin and large clades, Strepsirrhini, Tarsiiformes and Anthropoidea.

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