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| **Species** | **Source** | **Calibration type** | **Marker** | **Number of samples (ancient + modern + sister species)** | **Time span covered by DNA samples (years)** | **Alignment length (bp)** | **Sister species****with GenBank accession number** | **Divergence time** | **Calibration distribution for the age of the root** | **Best-fitting substitution model** | **Population model** | **Substitution rate estimate and 95% credibility interval****(substitutions/site/year)** | **Calibration time (years)** |
| Adelie penguin (*Pygoscelis adeliae*) | Lambert et al. 2002 | aDNA | d-loop(non-coding) | 96 + 380 + 0 | 0 – 6,424 | 347 | n/a | n/a | n/a | TVM+G | constant | 2.31×10-6(1.59×10-5 – 3.06×10-6) | 6.42×103 |
| Turkey (*Meleagris gallopavo gallopavo*) | Speller et al. 2010 | aDNA | d-loop(non-coding) | 136 + 12 + 0 | 0 – 1,250 | 438 | n/a | n/a | n/a | HKY | constant | 1.71×10-6(7.27×10-7 – 2.80×10-6) | 1.25×103 |
| Arctic fox (*Vulpes lagopus*) | aDNA: Dalén *et al.* 2007; cal: Flynn & Galliano 1982, Wayne et al. 1997 | fossil | d-loop(non-coding) | 8 + 41 +1 | 0 – 16,000 | 294 | Wolf(*Canis lupus lupus)*AM711902 | min 9 Mya (oldest *Vulpes* genus fossil);max 52 Mya (caniform/feliform divergence) | exponential: offset = 9 Mya, 97.5% = 52 Mya | HKY+G | skyride | 3.25×10-9(6.65×10-10 – 8.41×10-9) | 5.20×107 |
| Aurochs(*Bos primigenius*) | Edwards et al. 2007 | aDNA | d-loop(non-coding) | 41 + 0 | 2,000 – 12,300 | 360 | n/a | n/a | n/a | HKY | constant | 8.19×10-7(3.33×10-7 – 1.42×10-6) | 1.23×104 |
| Aurochs(*Bos primigenius*) | aDNA: Edwards et al. 2007; cal: Tedford et al. 1991, Barry at al. 2002 after Ho et al. 2008 | fossil | d-loop(non-coding) | 41 + 0 + 1 | 2,000 – 12,300 | 362 | Bison(*Bison bison)*NC012346 | min 2 Mya (oldest bison fossil);max 8.9 Mya (stem of bovines) | exponential: offset = 2 Mya, 95% = 8.9 Mya | HKY+G | constant | 5.66×10-8(1.56×10-8 – 1.10×10-7) | 8.90×106 |
| Bison(*Bison priscus*) | aDNA: Shapiro *et al*. 2004; cal: Tedford et al. 1991, Barry at al. 2002 after Ho et al. 2008 | fossil | d-loop(non-coding) | 160+22+1 | 0 – 60,400 | 613 | Yak(*Bos grunniens)*GQ464290 | min 2 Mya (oldest bison fossil);max 8.9 Mya (stem of bovines) | exponential: offset=2 Mya, 95% = 8.9 Mya | TrN+G | constant | 2.11×10-7(1.41×10-7 – 2.86×10-7) | 8.90×106 |
| Bowhead whale (*Balaena mysticetus*) | Foote et al. 2013 | aDNA | d-loop(non-coding) | 114 + 69 + 0 | 0 – 51,000 | 252 | n/a | n/a | n/a | HKY+G | constant | 3.64×10-7(1.65×10-7 – 6.12×10-7) | 5.10×104 |
| Brown bear (*Ursus arctos*) | aDNA: Korsten *et al*. 2009; Lindqvist *et al*. 2010;cal: Kurtén 1968, 1976; Hofreiter *et al.* 2002 after Korsten *et al.* 2009 | fossil | d-loop(non-coding) | 47+66+1 | 0 – 120,000 | 193 | Cave bear(*Ursus spelaeus)*EU327344 | Based on fossil evidence for their supposed common ancestor, the Etruscan bear (*Ursus etruscus*) | normal: mean 1.45 Mya, 2.5% = 1.2 Mya, 97.5% = 1.7 Mya | K80+G | constant | 3.92×10-7(2.15×10-7 – 6.13×10-7) | 1.45×106 |
| Cave lion (*Panthera leo spelaea*) | Barnett et al. 2009 | fossil | d-loop(non-coding) | 23+0+1 | 11,925 – 58,200 | 216 | Lion(*Panthera leo leo)*DQ899919 | based on first fossil appearance of *Panthera leo fossilis* – 650 kya | normal: mean 550 kya ± 25 kya | HKY | constant | 7.73×10-8(4.23×10-8 – 1.18×10-7) | 5.50×105 |
| Cow(*Bos taurus*) | Bollongino et al. 2006 | aDNA | d-loop(non-coding) | 36+91+0 | 0 – 8,065 | 410 | n/a | n/a | n/a | HKY+G | skyride | 6.72×10-7(4.53×10-7 – 9.29×10-7) | 8.07×103 |
| Cow(*Bos taurus*) | aDNA: Bollongino et al. 2006;cal: Tedford et al. 1991, Barry at al. 2002 after Ho et al. 2008 | fossil | d-loop(non-coding) | 36+91+1 | 0 – 8,065 | 412 | Bison(*Bison bison)*NC012346 | min 2 Mya (oldest bison fossil); max 8.9 Mya (stem of bovines) | exponential: offset = 2 Mya, 95% = 8.9 Mya | HKY+G | constant | 1.02×10-7(4.71×10-8 – 1.80×10-7) | 8.90×106 |
| Horse(*Equus ferus*) | aDNA: Lorenzen et al 2011; cal: Steiner & Ryder 2011 | fossil | d-loop(non-coding) | 128+0+1 | 2,220 – 43,900 | 349 | Zebra(*Equus zebra)*AY651956 | radiation of modern horses 2-4 Mya | uniform: 2-4 Mya | HKY+G | constant | 2.09×10-7(1.21×10-7 – 3.22×10-7) | 4.00×106 |
| Human(*Homo sapiens*) | Fu et al. 2013 | aDNA | d-loop(non-coding) | 10+54+0 | 0 – 39,475 | 1118 | n/a | n/a | n/a | HKY+G | constant | 1.56×10-7(9.27×10-8 – 2.33×10-7) | 4.00×104 |
| Human(*Homo sapiens*) | aDNA: Fu et al. 2013;cal: Yi *et al.* 2002, Ho *et al*. 2005 | fossil | d-loop(non-coding) | 10+54+1 | 0 – 39,475 | 1124 | Chimpanzee(*Pan troglodytes)*X93335 | Based on Sahelanthropus fossil | normal: mean = 6 Mya, 2.5% = 4.5 Mya, 97.5% = 7.5 Mya | HKY+G | constant | 8.47×10-8(5.18×10-8 – 1.31×10-7) | 6.00×106 |
| Human(*Homo sapiens*) | DNA: Ingman et al. 2000; cal: Kelley 2002 | fossil | d-loop(non-coding) | 0+53+1 | 0 | 1124 | Orangutan (*Pongo pygmaeus*)NC001646 | *Homo*-*Pongo* lineage divergence based on *Sivapithecus* fossil | uniform: 8.5-12.5 Mya | HKY+G | constant | 5.11×10-8(2.63×10-8 – 8.76×10-8) | 1.25×107 |
| Lemming (*Dicrostonyx torquatus*) | Prost et al. 2010 | aDNA | cyt b(coding) | 66+10+0 | 0 – 21910 | 282 | n/a | n/a | n/a | K80 | constant | 1.62×10-7(6.54×10-8 – 2.81×10-7) | 2.19×104 |
| Lemming (*Dicrostonyx torquatus*) | Prost et al. 2010 | aDNA | d-loop(non-coding) | 67+10+0 | 0 – 21910 | 426 | n/a | n/a | n/a | F81+G | constant | 5.24×10-8(8.64×10-9 – 1.14×10-7) | 2.19×104 |
| Muskox (*Ovibos moschatus*) | aDNA: Campos *et al*. 2010b; cal: Vrba & Schaller 2000, paleodb.org | fossil | d-loop(non-coding) | 121+4+1 | 0 – 42,550 | 689 | Bison(*Bison bison)*NC012346 | min 11.61 Mya (first Bovinae fossil);max 20 Mya (first appearance of Bovids) | uniform: 11.61-20 Mya | HKY+G | constant | 5.19×10-8(4.19×10-8 – 6.48×10-8) | 2.00×107 |
| Red fox(*Vulpes vulpes* ) | Teacher et al. 2011 | aDNA | cyt b(coding) | 20+301+0 | 0 – 30,000 | 201 | n/a | n/a | n/a | HKY | constant | 1.64×10-7(5.10×10-8 – 3.38×10-7) | 3.00×104 |
| Red fox (*Vulpes vulpes* ) | aDNA: Teacher et al. 2011;cal: Flynn & Galliano 1982, Wayne et al. 1997 | fossil | cyt b(coding) | 20+301+1 | 0 – 30,000 | 202 | Wolf(*Canis lupus lupus)*AM711902 | min 9 Mya (oldest *Vulpes* genus fossil);max 52 Mya (caniform/feliform divergence) | exponential: offset = 9 Mya, 97.5% = 52 Mya | HKY | constant | 6.85×10-9(3.16×10-9 – 1.07×10-8) | 5.20×104 |
| Red fox (*Vulpes vulpes* ) | Teacher et al. 2011 | aDNA | d-loop(non-coding) | 20+301+0 | 0 – 30,000 | 193 | n/a | n/a | n/a | TIM+G | constant | 6.18×10-7(2.94×10-7 – 1.04×10-6) | 3.00×104 |
| Red fox (*Vulpes vulpes* ) | aDNA: Teacher et al. 2011;cal: Flynn & Galliano 1982, Wayne et al. 1997 | fossil | d-loop(non-coding) | 20+301+1 | 0 – 30,000 | 196 | Wolf(*Canis lupus lupus)*AM711902 | min 9 Mya (oldest *Vulpes* genus fossil);max 52 Mya (caniform/feliform divergence) | exponential: offset = 9 Mya, 97.5% = 52 Mya | TIM+G | skyride | 9.29×10-10(1.89×10-10 – 2.25×10-9) | 5.20×107 |
| Woolly mammoth (*Mammuthus primigenius*) | Debruyne et al. 2008 | aDNA | cyt b, trnT, trnP(coding) | 103+0+0 | 5,007 – 55,082 | 416 | n/a | n/a | n/a | HKY | constant | 6.30×10-8(2.72×10-8 – 1.12×10-7) | 5.51×104 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | cyt b, trnT, trnP(coding) | 103+0+1 | 5,007 – 55,082 | 416 | Asian elephant(*Elephas maximus)*NC005129 | min 3 Mya (earliest mammoth fossil);max 8.5 Mya (possibly ancestral *Elephas nawataensis*) | uniform: 3-8.5 Mya | HKY | constant | 6.42×10-10(2.96×10-10 – 1.06×10-9) | 8.50×106 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | cyt b, trnT, trnP(coding) | 103+0+1 | 5,007 – 55,082 | 416 | African elephant(*Loxodonta africana)*NC000934 | min 4.2 Mya (most ancient representative of *Elephas*);max 9 Mya (assuming trichotomy) | uniform: 4.2-9 Mya | HKY | constant | 4.34×10-10(2.36×10-10 – 6.83×10-10) | 9.00×106 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | cyt b, trnT, trnP(coding) | 103+0+1 | 5,007 – 55,082 | 416 | Mastodon(*Mammut americanum)*NC009574 | min 24 Mya (first mammutid fossil);max 30 Mya (common ancestor fossil) | uniform: 24-30 Mya | HKY | constant | 1.78×10-10(1.29×10-10 – 2.35×10-10) | 3.00×107 |
| Woolly mammoth (*Mammuthus primigenius*) | Debruyne et al. 2008 | aDNA | d-loop(non-coding) | 103+0+0 | 5,007 – 55,082 | 297 | n/a | n/a | n/a | HKY+G | constant | 1.99×10-7(8.14×10-8 – 4.04×10-7)d | 5.51×104 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | d-loop(non-coding) | 103+0+1 | 5,007 – 55,082 | 297 | Asian elephant(*Elephas maximus)*NC005129 | min 3 Mya (earliest mammoth fossil);max 8.5 Mya (possibly ancestral *Elephas nawataensis*) | uniform: 3-8.5 Mya | HKY+G | constant | 2.40×10-8(4.07×10-9 – 5.88×10-8) | 8.50×106 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | d-loop(non-coding) | 103+0+1 | 5,007 – 55,082 | 297 | African elephant(*Loxodonta africana)*NC000934 | min 4.2 Mya (most ancient representative of *Elephas*);max 9 Mya (assuming trichotomy) | uniform: 4.2-9 Mya | HKY+G | constant | 2.07×10-8(4.40×10-9 – 5.28×10-8) | 9.00×106 |
| Woolly mammoth (*Mammuthus primigenius*) | aDNA: Debruyne et al. 2008; cal: Rohland et al. 2010 | fossil | d-loop(non-coding) | 103+0+1 | 5,007 – 55,082 | 297 | Mastodon(*Mammut americanum)*NC009574 | min 24 Mya (first mammutid fossil);max 30 Mya (common ancestor fossil) | uniform: 24-30 Mya | HKY+G | constant | 5.15×10-10(2.98×10-10 – 8.70×10-10) | 3.00×107 |
| Woolly rhinoceros (*Coelodonta antiquitatis*) | aDNA: Lorenzen et al 2011; cal: Willerslev et al. 2009; Carroll 1988 | fossil | d-loop(non-coding) | 55+0+1 | 12,460 – 43,850 | 547 | Sumatran rhinoceros(*Dicerorhinus sumatrensis)*FJ905816 | min 16 Mya (*C.antiquitatis* fossils - lower Miocene)no more than 56 Mya (rhinoceroses fossils - begining late Eocene) | exponential: offset = 16 Mya, 95% = 56 Mya | TrN+G | constant | 1.38×10-7(3.60×10-8 – 2.54×10-7) | 5.60×107 |