University of South Bohemia in České Budějovice Faculty of Science

# Evolution of life history and behavior in Hominidae: Towards phylogenetic reconstruction of the chimpanzeehuman last common ancestor

RNDr. Thesis

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## Annotation

The origin of the fundamental behavioral differences between humans and our closest living relatives is one of the central issues of evolutionary anthropology. In this study we performed a series of phylogenetic comparative analyses using 65 selected life-history and behavioral characters for all extant hominid species to reconstruct the ancestral character states of the last common ancestors of Hominidae, Homininae and Hominini (the chimpanzee-human last common ancestor). These analyses show that many fundamental behavioral and life-history attributes of hominids (including humans) are evidently ancient and likely inherited from the common ancestor of all hominids. On the other hand, numerous behaviors present in extant great apes represent their own terminal autapomorphies (both uniquely derived and homoplastic). We demonstrate that phylogenetic reconstruction of ancestral states is able to provide a detailed suite of behavioral, ecological and life-history characters for each hypothetical ancestor. The living great apes therefore play an important role for the identification of the traits found in the chimpanzee-human last common ancestor, some of which are likely to represent behaviors of the fossil hominins.

## **Declaration** [in Czech]

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V Českých Budějovicích, 27.2.2017

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Mgr. Pavel Duda

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Pavel Duda is the first and corresponding author of the study. He conceived and designed the study with J. Zrzavý, collected the data, analyzed the data, prepared the artworks and co-wrote the paper with J. Zrzavý.

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prof. RNDr. Jan Zrzavý, CSc., co-author

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## Evolution of life history and behavior in Hominidae: Towards phylogenetic reconstruction of the chimpanzee—human last common ancestor

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### ABSTRACT

The origin of the fundamental behavioral differences between humans and our closest living relatives is one of the central issues of evolutionary anthropology. The prominent, chimpanzee-based referential model of early hominin behavior has recently been challenged on the basis of broad multispecies comparisons and newly discovered fossil evidence. Here, we argue that while behavioral data on extant great apes are extremely relevant for reconstruction of ancestral behaviors, these behaviors should be reconstructed trait by trait using formal phylogenetic methods. Using the widely accepted hominoid phylogenetic tree, we perform a series of character optimization analyses using 65 selected life-history and behavioral characters for all extant hominid species. This analysis allows us to reconstruct the character states of the last common ancestors of Hominoidea, Hominidae, and the chimpanzee-human last common ancestor. Our analyses demonstrate that many fundamental behavioral and life-history attributes of hominids (including humans) are evidently ancient and likely inherited from the common ancestor of all hominids. However, numerous behaviors present in extant great apes represent their own terminal autapomorphies (both uniquely derived and homoplastic). Any evolutionary model that uses a single extant species to explain behavioral evolution of early hominins is therefore of limited use. In contrast, phylogenetic reconstruction of ancestral states is able to provide a detailed suite of behavioral, ecological and life-history characters for each hypothetical ancestor. The living great apes therefore play an important role for the confident identification of the traits found in the chimpanzee-human last common ancestor, some of which are likely to represent behaviors of the fossil hominins.

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#### Introduction

Reconstructing the ethology and ecology of the hypothetical chimpanzee—human last common ancestor ('CHLCA' hereinafter) and early hominins is among the central issues of evolutionary anthropology (e.g., Lovejoy, 1981; <u>Tooby and DeVore, 1987;</u> <u>Stanford and Allen, 1991; McGrew, 2010a</u>). The intense interest in this issue has resulted in several different approaches to modeling the behavior of extinct hominins (<u>Stanford and Allen, 1991</u>).

Non-referential modeling (also referred to as 'conceptual' or 'strategic' modeling) (<u>Tooby and DeVore, 1987; Foley and Lee, 1989;</u> Whiten et al., 2010) attempts to reconstruct the behavior of hypothetical ancestors using rules derived from evolutionary biology and behavioral ecology. These conceptual models are based on the implicit assumption that only a limited number of possible behaviors or strategies exist given the morphology and physiology of the species and the prevailing environmental constraints. Given this assumption, one is able to 'predict' ancestral behavior on the basis of general evolutionary principles (Wrangham, 1987).

By contrast, referential modeling (e.g., <u>McGrew, 1981</u>) explicitly relies on knowledge of the ethology, ecology or cognitive skills of a particular species. Subsequent analyses use this reference species as a template for inferring the traits that are most likely ancestral to the condition of a second extant species. Such referential modeling could be based on homology (similarity through shared descent), e.g., a comparison of human ancestors with chimpanzees (<u>McGrew</u>, <u>1981</u>), or analogy (similarity through shared but independently evolved ecological or social adaptations), e.g., a comparison of human ancestors with savanna baboons and their relatives (<u>DeVore and Washburn, 1963; Jolly, 1970, 2001;</u> Skybreak, 1984) or capuchin monkeys (Fernandes, 1991; Perry, 1997; Perry et al., 2003).

Throughout the last three decades, the gradual accumulation of data on great ape behavior and the full recognition of the human







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phylogenetic position within hominids has led to the extensive utilization of extant great apes, especially chimpanzees, as referential models for the evolutionary origins of human traits (Kinzey, 1987; Di Fiore and Rendall, 1994; Rendall and Di Fiore, 1995; Kappeler and Silk, 2010; Whiten et al., 2010). The sister-group relationship between the chimpanzee–bonobo (Pan) and human (Homo) clades became a logical basis for numerous evolutionary hypotheses (Wrangham and Pilbeam, 2001; Begun, 2004). The opinion that the CHLCA was not only morphologically but also behaviorally very similar to the present-day chimpanzee (Pan troglodytes) became a widely held opinion (Lovejoy, 1981; McGrew, 1981; Tanner, 1981; Sarich, 1992; Pilbeam, 1996; Stanford, 1996, 2012; Wrangham and Pilbeam, 2001; Begun, 2004; Pilbeam and Young, 2004). Indeed, the image of the chimpanzee as a proxy for the early human ancestor even penetrated the popular literature (Diamond, 1992; Wrangham and Peterson, 1996; Dawkins, 2004). While chimpanzee-based models encompassed virtually all aspects of hominization, including positional behavior, reproductive biology, hunting and intergroup violence (Tuttle, 1974; Lovejoy, 1981; Stanford, 1996; Wrangham and Peterson, 1996), bonobos (Pan paniscus) have been conspicuously neglected in this respect, despite being equally relevant for such inferences (De Waal, 1998; Sayers and Lovejoy, 2008). This has been ascribed to an unprecedented wealth of data on *P. troglodytes* and a lack of comparable data on P. paniscus (McGrew, 2010a).

Some researchers, however, promoted the utility of more distantly related great ape species for explaining various aspects of human biology. There have been arguments for gorillas (Geary and Flinn, 2001; Geary et al., 2011) as well as orangutans (Schwartz, 2004, 2005; Grehan, 2006; Crompton et al., 2008) as the best models for understanding the evolution of certain aspects of human behavior. Some studies attempt to choose explicitly between two referential models based on a quantification of human-like characters in two ape species. Wrangham and Pilbeam (2001) assessed the presence/absence of 12 behavioral traits in the two species of Pan and in Homo. These authors concluded that certain behaviors found in chimpanzees are the consequence of intense scramble competition (e.g., lethal raiding, group hunting or male dominance) and that these are good candidates for ancestral traits, whereas other behaviors found in bonobos are a result of relaxed scramble competition (e.g., relaxed intergroup interactions, egalitarian males or friendship among adult females) and are likely to be derived. More recently, Geary et al. (2011) identified modal patterns for 18 traits of life history and socio-ecology in chimpanzees, gorillas and modern human hunter-gatherers and quantified the relative number of changes required for the gorilla-like and the chimpanzee-like common ancestors to achieve the observed patterns of present-day hunter-gatherers. They concluded that the gorilla-like starting point provides a more parsimonious scenario of evolution of hominin behavior and social structure than does the chimpanzee-like one.

Behavioral data on great apes are undeniably of immense value for modeling human origins. As models, extant great apes cannot be replaced by inferences drawn from fossils of purported stem hominins (McGrew, 2010a; Whiten et al., 2010). The chimpanzees play a particularly important role in identifying the shared ecological and behavioral homologies of the *Pan–Homo* clade. It has been argued that the relatedness of chimpanzees to the hominin lineage makes their behaviors "phylogenetically relevant" (Pruetz and LaDuke, 2010: 646). However, it was suggested long ago that the CHLCA had to be biologically unique and therefore not necessarily best understood by direct analogy with any *single* extant species (Tooby and DeVore, 1987; Wrangham, 1987; Marlowe, 2005). Various authors (Rendall and Di Fiore, 1995; Marlowe, 2005; Sayers and Lovejoy, 2008; Lycett et al., 2009; Whiten et al., 2010; <u>Sayers et al., 2012</u>) have suggested that the behaviors of the common ancestors within the Hominoidea should be reconstructed trait by trait using multispecies comparative data and making explicit use of phylogenetic methods, thus allowing the reconstructed ancestor to possess unique traits or combinations of traits.

Phylogenetic reconstruction of ancestral states can be considered a special subcategory of referential modeling (Wrangham, 1987; Moore, 1996; Whiten et al., 2010). It is among the standard tools used to understand the processes of evolutionary adaptation. Ancestral state reconstruction is used to infer the values of a trait for internal nodes of a phylogenetic tree (representing the hypothetical common ancestors) based on the trait values of the terminal (usually extant) species and a tree topology, possibly also with consideration of branch lengths (see Pagel, 1999; Salisbury and Kim, 2001; Mooers, 2004). Application of these methods in primatology and anthropology has been advocated (Rendall and Di Fiore, 1995; Whiten et al., 2010), although their potential has long been overlooked. This is likely to be because of the preconception that behavior may be inherently more prone to homoplasy or subject to different selection regimes than morphological and genetic traits (see Rendall and Di Fiore, 2007, for a review). However, there are numerous case studies (Paterson et al., 1995; McLennan and Mattern, 2001; Stuart and Currie, 2001; Zrzavý and Řičánková, 2004; Lycett et al., 2009) and meta-analyses (e.g., DeQueiroz and Wimberger, 1993) that, using various measures of character fit on phylogeny, demonstrate ecological and behavioral characters to be no less phylogenetically informative than morphological and molecular ones.

To date, there are several examples of the application of formal phylogenetic methods that can be drawn from the study of primate behavior. They include the evolution of social organization (Di Fiore and Rendall, 1994), male-female associations (van Schaik and Kappeler, 1997), color vision and coloration (Fernandez and Morris, 2007; Kamilar et al., 2012), food sharing (Jaeggi and van Schaik, 2011), and diet and seed dispersal abilities (Gómez and Verdú, 2012) in primates as a whole. More taxonomically restricted studies concern the evolution of facial complexity and sociality in New World monkeys (Santana et al., 2012), ovulation signaling in Anthropoidea (Sillén-Tullberg and Møller, 1993) and Old World monkeys (Nunn, 1999), social structure in macaques (Thierry et al., 2000; Balasubramaniam et al., 2012), tickle-induced vocalization in great apes and humans (Davila Ross et al., 2009), and cultural behavior in chimpanzees (Lycett et al., 2007, 2009). Recently, formal phylogenetic methods were applied in a study of fossil hominin behavior and material culture (Lycett, 2007, 2009a,b; Organ et al., 2011). A specific subcategory of these studies is the application of the phylogenetic approach to modern human behavior and material and nonmaterial culture (e.g., Lipo et al., 2006; Jordan et al., 2009; Mace and Jordan, 2011; Walker et al., 2011).

Attempts to use phylogenetic approach for understanding the evolution of hominid behavior are relatively recent. Identifying a plausible suite of behaviors for the CHLCA through the comparison of behaviors of extant African apes has been a primary concern of the pioneering studies by <u>Ghiglieri (1987) and</u> Wrangham (1987). Importantly, these studies did not use formal phylogenetic methods, which were relatively undeveloped at the time. Instead, they reasoned that the traits shared across African apes are likely to have been present in the common ancestor as well because otherwise they must have evolved independently at least twice. The results of these two studies are highly consistent in identifying a similar set of behaviors, which include a polygynous mating system, female dispersal and weak female social bonds or maledominated intergroup encounters. Further attempts to infer behaviors in the common ancestors of the hominid lineage using

similar logic are included in studies by Wrangham and Pilbeam (2001), Begun (2004), McGrew (2010a), and Geary et al. (2011).

Following these suggestions, we created a character set consisting of 65 characters for all seven extant hominid species (including humans) and for 12 outgroup species, including representatives of all hylobatid genera and selected well-studied species of cercopithecoid primates. This character set has been framed to include human attributes that are frequently referred to in studies concerning the origin of human behavior, such as life-history characteristics, socio-sexual behavior, sexual morphology and socio-ecology, along with other behavioral characters such as cultural diversity, tool use, shelter construction and locomotion. We performed a series of maximum-parsimony (i.e., cladistic) and maximum-likelihood character optimization analyses (i.e., mapping the character states on the hominoid phylogenetic tree) in order to determine the best-supported sequences of evolutionary changes across characters. The aim of this study is to assess the amount of evolutionary change that characterizes the extant species and their ancestors, to reconstruct likely (and less likely) behaviors of the ancestors of the hominid (sub)clades with an emphasis on ancestral Hominidae (great apes), ancestral Homininae (African apes) and the CHLCA (the last common ancestor of Panini and Hominini) and to assign extant species attributes to phylogenetic ranks ('phylostrata') in order to evaluate how these ancestral phenotypes contribute to the behavioral suites of extant hominid species.

#### Materials and methods

#### Ingroup and outgroup taxa and adopted phylogeny

All seven extant great ape species (*P. troglodytes*, *P. paniscus*, *Gorilla gorilla*, *Gorilla beringei*, *Pongo pygmaeus* and *Pongo abelii*, plus *Homo sapiens*) were included in the analysis as ingroup terminal taxa. The species-level taxonomy from Groves (2001), Geissmann (2002), and Mootnick and Groves (2005) was used. The phylogenetic tree used for character optimization analyses was modified from Perelman et al. (2011). Two taxa not covered by Perelman et al. (2011) were added in agreement with previous studies: *G. beringei* as a sister species of *G. gorilla* (Shoshani et al., 1996; Groves, 2001) and *Hoolock hoolock* as a sister group of *Hylobates* (Roos and Geissmann, 2001; Chatterjee et al., 2009; Thinh et al., 2010; Wall et al., 2013; but see Israfil et al., 2011; Meyer et al., 2012; Springer et al., 2012).

In the phylogenetic classification adopted here (see <u>Harrison</u>, <u>2010</u>; <u>Wood</u>, <u>2010</u>; <u>Wood</u> and <u>Harrison</u>, <u>2011</u>), all great apes (including humans) form the clade (family) Hominidae ('hominids'), and African ape species (*Gorilla*, *Pan*, *Homo*) form the clade (subfamily) Homininae ('hominines'). *Pan* species form the clade (tribe) Panini ('panins') and *Homo* and related genera fall into the clade Hominini ('hominins'), the latter having been referred to as 'family Hominidae' in older taxonomic conventions (the rest of great apes then having formed the paraphyletic 'family Pongidae'). The last common ancestor of panins and hominins, which is referred to in the literature as the 'chimpanzee–human last common ancestor' (LCA, CLCA, CHLCA or C/H LCA; Moore, 1996; Lovejoy, 2009, McGrew, 2010a), 'panin/hominin MRCA' (Wood and Harrison, 2011), 'concestor 1' (Dawkins, 2004), or '*Pan prior*' (Wrangham, 2001) is referred to here as the 'CHLCA'.

Altogether 12 species were used as outgroup species for the reconstruction of the deeper, namely, hominoid and catarrhine ancestors. The outgroups included four gibbon species (Hominoidea: Hylobatidae) representing all hylobatid genera: *Hylobates lar, H. hoolock, Symphalangus syndactylus* and *Nomascus concolor,* and eight well-sampled species of Old World monkeys

(Cercopithecoidea): three papionins (*Papio anubis*, *Theropithecus gelada*, and *Mandrillus sphinx*), two macaques (*Macaca mulatta* and *Macaca fuscata*), two cercopithecines (*Cercopithecus aethiops* and *Erythrocebus patas*) and one colobine (*Semnopithecus entellus*).

Note that any individual taxon could be viewed as an ingroup or outgroup depending on the scale of the analysis (e.g., orangutans are an ingroup for Hominidae but an outgroup for Homininae). The outgroup comparison is a simple method to determine the ancestral ingroup character state when the outgroup character states are invariant. The problem of a heterogenous outgroup was first addressed by Maddison et al. (1984; see also Kitching et al., 1998): If two successive outgroup terminal taxa share the same single character state (forming a 'doublet'), then this character state is decisively present also in the ancestral node uniting ingroups with the nearest outgroup. Outgroups further out will have no effect on the ancestral state reconstruction. Thus, all outgroup character states beyond a nearest 'doublet' are irrelevant for ancestral state reconstruction. For example, the CHLCA is the node uniting the Pan species with their nearest outgroup, Homo. The CHLCA could be reconstructed decisively to include all character states shared by either Pan or Homo with any outgroup 'doublet' (i.e., either Gorilla + *Pongo*, or *Pongo* + Hylobatidae, or Hylobatidae + Cercopithecoidea). Otherwise, the CHLCA ancestral state is reconstructed as equivocal. Since all hominid ancestral nodes (Hominidae, Homininae, the CHLCA, as well as ancestral nodes of extant *Pongo*, *Gorilla* and *Pan*) are rooted by at least two successive outgroups (Cercopithecoidea and Hylobatidae for Hominidae; Cercopithecoidea, Hylobatidae, and Pongo for Homininae, etc.), the ancestral reconstructions can be considered well-founded. The ancestral ground pattern of Hominoidea (rooted exclusively by Cercopithecoidea) is less reliable, and the present character set is not at all suitable for reconstructing the ancestor of catarrhine primates (= Cercopithecoidea + Hominoidea clade).

To test whether reconstructed ancestral states in ingroup ancestral nodes are not affected by selection of particular cercopithecoid species as outgroups, we experimentally modified the outgroup taxon sample. Two analyses were performed using maximum-likelihood optimization, 'binary' character set, tree with all branches equal in length). In the first analysis, the cercopithecoid outgroup was reduced to the three species with the smallest amount of unknown and polymorphic character states, namely, one papionin (*M. mulatta*), one cercopithecin (*C. aethiops*) and one colobine (*S. entellus*), i.e., a taxon set representing one species from each of the three subclades of Cercopithecoidea. In the second analysis, the whole cercopithecoid outgroup was excluded and only the four hylobatid species were used as the outgroup.

#### Character scoring

The character set is based on a large variety of literature sources (see Table 1; see Supplementary Online Material [SOM] for a detailed list of characters, character states and references). Characters were selected in order to cover the hominid 'biological' (i.e., life-history, socio-ecological and behavioral) traits that are particularly emphasized in human evolutionary studies. They included (i) life-history patterns (Mace, 2000; Hawkes and Paine, 2006; Robson and Wood, 2008), e.g., gestation length, neonatal weight, growth rate, infant development, weaning, puberty onset, age at first birth, interbirth interval, breeding seasonality, female post-reproductive lifespan, and maximum lifespan; (ii) sociosexual behavior and sexual morphology (Lovejoy, 1981; Dixson, 1998), e.g., mating system, mating tactics, paternity success, mate choice and mate preferences, copulatory behaviors, sexual dimorphism and sexual adornments, genitalic morphology and reproductive physiology, and post-adolescent dispersal patterns P. Duda, J. Zrzavý / Journal of Human Evolution 65 (2013) 424-446

#### Table 1

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4.         Weaking sige (existion of heastfreeding)         4         2-2 years; approx. 22 years; s2 years           5.         Age at the first molar emption (years)         3         3-3 years; approx. 32 years; s2 years           6.         Age at the first molar emption (years)         1         3-years; approx. 31 years; approx. 31 years; s2 years           7.         Age at the first molar emption (years)         2         years; 51 years; s2 years           7.         Age at the first molar emption (years)         2         years; approx. 31 years; s2 years; approx. 31 years; s2 years; approx. 32 years; s2 years;				
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b.         Desponing first female reproduction         2         Early first reproduction:         1.1. Strict first reproduction           1.         Seasonal breeding         2         Production:         1.1. Strict first reproduction           1.         Seasonal breeding         2         Absent (year-round preeding) (year-or)           1.         Seasonal breeding         2         Absent (year-or)         0.4. Optimized (year-or)           2.         Conjugal finance (integrant)         3         Sinter finance (integrant)         3           3.         Maximi present         3         Sinter finance (integrant)         3           4.         Productions (integrant)         3         Sinter finance (integrant)         4           5.         Conjugal finance (integrant)         3         Absent; present         Absent; present           4.         Male (failer) presence within a group)         Male (failer) is unable to maintain proximity to a group; continuous presence of the mate (prontinuous); polyandry           4.         Productions is system         4         Production (integrant); present (proportunistic)           6.         Social nating system         4         Absent; present (production); portunistic)           7.         Ford conduction is a social nating system         Absent; present (wonasting); polynomistic) <td></td> <td></td> <td></td> <td></td>				
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12.         Protected post-reproductive (post-memoryanal) female lifespan <sup>4</sup> 2         Absent: present           3.         Maximum lifespan <sup>4</sup> 5				prolonged (>8 years)
(post-menopausal) female lifespan <sup>a</sup>				
44.       Philopatry (dispersal patterns)       3*       Strick Emaie philopatry: context-dependent dispersal: strict male philopatry         16.       Social unit beyond family scope       2       Absent; present         16.       Social unit beyond family scope       2       Absent; present         17.       Male (father) presence within a group       2       Male (father) yes unable to maintain proximity to a group; continuous presence of the male (father) within a group         18.       Social mating system       4*       Monegamy; physyr; multimalemultifemale (promiscuous); polyandry         19.       Male matery strength       2       Absent (fremale has a little opportant); to choose the maters); present (female is able to earning existent male);         10.       Forcat Cooption of male rank       2       Absent (fremale has a little opportant); to choose the maters); present (female is able to earning existent male);         10.       Foreating (fop-sinc) ingroup male       3       High (100–813); limited (80–413); low (less than 403)         10.       Sexual dimorphism in adrogen-dependent       2       Absent; present         10.       Sexual dimorphism in adrogen-dependent       2       Absent; present         10.       Sexual dimorphism in adrogen-dependent       2       Absent; present         10.       Realize enterede penist       3       Short (-22); medium (05–2		(post-menopausal) female lifespan <sup>a</sup>		
15.         Conjugat family as a social unit         2         Absent: present           16.         Social unit beyond family sope         2         Absent: present           17.         Male (father) presence within a group         2         Male (father) is unable to maintain proximity to a group: continuous presence of the mail (father) within a group           18.         Social mating system         4 <sup>b</sup> Monogamy: polygyny: multimale-multifemale (promiscuous): polyandry           18.         Social mating system         4 <sup>b</sup> Monogamy: polygyny: multimale-multifemale (promiscuous): polyandry           18.         Social mating system         4 <sup>b</sup> Monogamy: polygyny: multimale-multifemale (promiscuous): polyandry           18.         Social mating system         4 <sup>b</sup> Monogamy: polygyny: multimale-multifemale (promiscuous): polyandry           18.         Social mating system         4 <sup>b</sup> Monogamy: polygyny: multimale-multifemale (properties)         Constraints           21.         Male matter choice (screed preference (for famale sage, frankes: preference (for other), preference (for famale sage, frankes: preference (for famale sage, frankes, frankes) <td< td=""><td></td><td></td><td></td><td></td></td<>				
16.         Social mit beyond family scope         2         Absent: present           17.         Male (father) presence within a group         2         Male (father) within a group           18.         Social mits gystem         4 <sup>b</sup> Monogamy: polygyry: multimale-multifemale (promiscuous); polyandry           19.         Male mating system         4 <sup>b</sup> Monogamy: polygyry: multimale-multifemale (promiscuous); polyandry           10.         Forced copulations (rape)         2         Absent (promet opportunity to choose); present (propted, occurs regularly)           11.         Female mate choice (secret op preference         2         Absent (prende regorted); present (propted, occurs regularly)           12.         Male mate preference (for female age, rank, op aparent male preference reported); present (resoft for older, higher-ramking, parous females); preference for younger (adolescench, nulliparous females)           17.         Top-rafing (fog-sine) ingroup male         3         High (100–813); limited (80–413); low (less than 402)           18.         Secual dimorphism in canine size         3         Insignificant (secual dimorphism in canine size); storeg (1.6:1 to 2.6:1)           17.         Secual dimorphism in androgen-dependent secual dimorphism in canine size         3         Absent; present           18.         Social mit be opinis         3         Absent; present           18.         <	14.			Strict female philopatry; context-dependent dispersal; strict male philopatry
7.       Male (father) is unable to maintain proximity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to a group; continuous presence of the maintain growtimity to provide the growtime of the growtim growtime of the growtime of the growtime of				
<ul> <li>Male mating system</li> <li>Social mating system</li> <li>Male mate choice (exerted preference</li> <li>Absent (ron treported); present (reported), cours regularly)</li> <li>Absent (ron treported); present (reported), cours regularly</li> <li>Male mate preference (for female age, and copulation rate)</li> <li>Positive correlation of male rank</li> <li>Male mate preference for younger (adolescent), nulliparous females</li> <li>Positive correlation of male rank</li> <li>Absent; present</li> <li>Male mate preference for younger (adolescent), nulliparous females</li> <li>Positive correlation of male rank</li> <li>Male mate preference for younger (adolescent), nulliparous females</li> <li>Positive correlation of male rank</li> <li>Absent; present</li> <li>Male mater preference reported; preference reported</li></ul>		U U I		
19.         Male mating strategy         2 <sup>h</sup> Possessive - mate guarding*: consortship*: opportunistic*           0.         Force dopatitions (reported). present (reported)	17.	Male (father) presence within a group		male (father) within a group
20.         Forced copulations (Tape)         2         Absent (for not reported); present (reported; occurs regularly)           21.         Fenale mate choice (exerced preference for particular male(s))         2         Absent (fenale has a little opportunity to choose her mates); present (fenale is able to exert mate choice among resident males)           22.         Male mate choice (exerced preference for particular male(s))         No apparent males (preference for oyounger (adolescent), nulliparous females           32.         Positive correlation of male rank and copulation rate         Absent (female is); limited (80–413); low (less than 40%) paternity success (3)           32.         Sexual dimorphism in canine size; male canines sexual dimorphism in canine size; male canines markedly larger than female canines sexual dimorphism in androgen-dependent sexual dimorphism in androgen-dependent sexual dimorphism of adult males'         Absent; present           23.         Sexual dimorphism in androgen-dependent sexual adornments of adult males'         Absent; present           24.         Absent; present         Absent; present           25.         Sexual dimorphism of adult males' polymorphism of adult males' sexual adornments of adult males' sexual adornments         Absent; present           26.         Mater intels         Absent; present           27.         Sexual dimorphism in adult males         male morph;           28.         Sexual dimorphism of adult males         male morph; <t< td=""><td></td><td></td><td></td><td></td></t<>				
21.         Female mate choice (exerted preference for particular male(s))         Absent (female has a little opportunity to choose her mates); present (female is able to exert mate choice among resident males)           22.         Male mate preference (for female age, rank, or parity)         3 <sup>10</sup> No apparent male preference for older, higher-ranking, parous females; preference for younger (adolescent), nulliparous females           23.         Positive correlation of male rank and copulation rate         2         Absent; present           24.         Top-ranking (top-site) ingroup male paternity success (3)         3         High (100–81%); limited (80–41%); low (less than 40%)           25.         Sexual dimorphism in conine size         3         Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1) (male(female body weight ratio)           26.         Sexual dimorphism in conine size         3         Insignificant sexual dimorphism in canine size; male canines moderately larger than female canines; male canines markedly larger than female canines           27.         Sexual dichromatism         2         Absent; present           38.         Sorual dichromatism         2         Absent; present           39         Morphological -bysiological -bysiol		0 00		
for particular male(s)to exert mate choice among resident males)Male mate preference (for female age, rank, or parity)To aparten male preference for younger (adolescent), nulliparous females females; preference for younger (adolescent), nulliparous femalesPositive correlation of male rank and copulation rateAbsent; present and copulation rateTop-ranking (top-sire) ingroup male paternity success (a)High (100-81%); limited (80-41%); low (less than 40%) paternity success (a)Top-ranking (top-sire) ingroup male paternity success (a)Insignificant sexual dimorphism in canine sizeSexual dimorphism in body weight ratioInsignificant sexual dimorphism in canine size; male canines moderately larger than female canines; male canines moderately larger than sexual adorments of adult males'Sexual dimorphism in androgen-dependent sexual adorments of adult males'Absent; present absent; presentMorphological-behavioral polymorphism of adult malesAbsent; remediant (b)Relative length of erected penis' accessStort (>2); medium (0.5-2); long (<0.5)				
22.     Male mate preference (for female age, rank, or parity)     3 <sup>3</sup> No apparent male preference for outger (adolescent), nulliparous females; preference for younger (adolescent), nulliparous females; preference for younger (adolescent), nulliparous females;       23.     Positive correlation of male rank and copulation rate     2     Absent; present       24.     Top-ranking (top-sire) ingroup male     3     High (100–81%); limited (80–41%); low (less than 40%)       25.     Sexual dimorphism in body weight (indice the sexual adomments of addut males' sexual adomments of addut males'     3     Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1)       26.     Sexual dimorphism in antrogen-dependent sexual adomments of addut males'     2     Absent; present       27.     Sexual dimorphism of adult males'     2     Absent; present       28.     Sexual dimorphism of adult males'     2     Absent; present       29.     Morphological-physiological-behavioral male morph;     present (two distinguishable adult sexually mature male morph;       29.     Absent; present     2     Absent; present       30.     Relative length of erected penisd'     3     Short (-2.2); medium (0.5–2.2); long (-0.5)       31.     Relative length of erected penisd'     3     Absent; present       32.     Copulatory plugs     3     Absent; present archavelly length of avalut males; present (two distinguishpale adult sexually mitiate adult (-0	21.		2	
rank, or parity)       females: preference for younger (adolescent), nulliparous females         2       Positive correlation of male rank and copulation rate       Absent; present         24.       Top-ranking (top-site) ingroup male       3         25.       Sexual dimorphism in body weight       3         26.       Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1) (male:female body weight ratio)         27.       Sexual dimorphism in canine size       3         28.       Sexual dimorphism in androgen-dependent       2         29.       Morphological-physiological-behavioral       2         20.       Morphological-physiological-behavioral       2         21.       Morphological-physiological-behavioral       2         22.       Sexual dimorphism of adult males       Short (-2); medium (0.5-2); long (<0.5)		1 ( ) /		
and copulation rate       3       High (100–81%); limited (80–41%); low (less than 40%)         paternity success (3)       1       Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1)         (materimale body weight ratio)       3       Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1)         (materimale body weight ratio)       3       Insignificant sexual dimorphism in canine size; male canines markedly larger than female canines; male canines markedly larger than female canines         8       Sexual dimorphism in androgen-dependent sexual adomments of addut males       Absent; present         8       Sexual dichromatism       2       Absent; one adult male morphs)         90 Morphological-physiological-behavioral polymorphism of adult males       3       Short (-2:); modium (0.5-2); long (-0.5)         31       Baculum (os penis)       3       Absent; resent         32.       Testes size       4       Size (-2.5); large (1.25-2.5); large (2.5-2.5); arge (2.5-		rank, or parity)		females; preference for younger (adolescent), nulliparous females
paternity success (3)1Sexual dimorphism in oddy weight3Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1)(male-female body weight ratio)3Insignificant sexual dimorphism in canne size; male cannes moderately larger than female canines; male cannes markedly larger than female canines26. Sexual dimorphism in androgen-dependent sexual adornments of adult maless2Absent; present27. Sexual dichromatism2Absent; present28. Sexual dichromatism2Absent; present29. Morphological-physiological-behavioral polymorphism of adult males3Short (-2.2); medium (0.52); long (-0.5)31. Baculum (os penis)3Short (-2.2); medium (0.52); long (-0.5)32. Copulatory plugs3Absent; reduced/shortened; present33. Copulatory plugs2Absent; present34. Ovulation3 <sup>th</sup> Well-detectable/advertized;35. Sexual skin swellings3Absent; or only slight turnescence of circum-vulval area); conspicuous swellings; exagera prolonged or semipermanent swellings36. Mating initiation2Mount usually initiated by female superior; ventro-ventral, female superior37. Copulatory posture (hype)3 <sup>th</sup> Dorso-ventral; ventro-ventral, female superior; ventro-ventral, female superior38. Copulatory posture (hype)3 <sup>th</sup> Brife(-2.05); hrife(-2.05); hrife(-1 mni); prolonged (>1.5 min); prolonged (>5 min)39. Mourt usually initiated by female actinis; duration4Brife(-2.05); hrife(-1 mni); prolonged (>1.5 min); prolonged (>5 min)31. Robustory posture (hype)3 <sup>th</sup> </td <td>23.</td> <td></td> <td>2</td> <td>Absent; present</td>	23.		2	Absent; present
(male:female body weight ratio)26.Sexual dimorphism in canine size327.Sexual dimorphism in canine size327.Sexual dimorphism in androgen-dependent sexual adornments of adult males*228.Sexual dichromatism229.Morphologicalphysiological-behavioral polymorphism of adult males*230.Relative length of erected penisd*331.Short (>2); medium (0.5-2); long (<0.5)	24.		3	High (100-81%); limited (80-41%); low (less than 40%)
26.       Sexual dimorphism in canine size       3       Insignificant sexual dimorphism in canines moderately larger than female canines; male canines markedly larger than female canines;         27.       Sexual dimorphism in admogen-dependent sexual adornments of adult males       Absent; present         28.       Morphological-physiogical-behavioral polymorphism of adult males       Absent; present         30.       Relative length of erected penis <sup>d</sup> 3       Short (>2); medium (0.5-2); long (<0.5)	25.		3	Insignificant (0.9:1 to 1.2:1); moderate (1.2:1 to 1.6:1); strong (1.6:1 to 2.6:1)
27.       Sexual dimorphism in androgen-dependent sexual adomments of adult males       2       Absent; present         28.       Sexual dichromatism       2       Absent; present         29.       Morphological-physiological-behavioral polymorphism of adult males       2       Absent; new and morphs; male morphs;         30.       Relative length of erected penis <sup>d</sup> 3       Short (>2); medium (0.5–2); long (<0.5)	26.		3	
29.       Morphological-physiological-behavioral polymorphism of adult males       Absent (one adult male morphs); present (two distinguishable adult sexually mature morphs)         30.       Relative length of erected penis <sup>d</sup> 3       Short (>2); medium (0.5-2); long (<0.5)	27.		2	Absent; present
polymorphism of adult malesmale morphs)30.Relative length of erected penisd331.Baculum (os penis)332.Testes size <sup>a</sup> 433.Copulatory plugs234.Ovulation3 <sup>b</sup> 35.Sexual skin swellings236.Mating initiation237.Copulatory posture (type)3 <sup>b</sup> 38.Our only slight tumescence of circum-vulval area); conspicuous swellings; exaggera37.Copulatory posture (type)3 <sup>b</sup> 38.Copulatory posture (type)3 <sup>b</sup> 39.Copulatory posture (type)3 <sup>b</sup> 30.Copulatory posture (type)3 <sup>b</sup> 31.Copulatory posture (type)3 <sup>b</sup> 32.Copulatory posture (type)3 <sup>b</sup> 33.Copulatory posture (type)3 <sup>b</sup> 34.Ovulation calls (as a device of235.Sexual skin swellings236.Mating initiation437.Copulatory posture (type)3 <sup>b</sup> 39.Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior31.Copulatory posture (type)3 <sup>b</sup> 32.Dorso-ventral; ventro-ventral, flexible33.Copulatory posture (type)3 <sup>b</sup> 39.Dorso-ventral; relativel (as a device of40.Intromission duration441.Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)41.Nocturnal copulations/mate guarding342.Mean (hou	28.		2	Absent; present
31.       Baculum (os penis)       3       Absent; reduced/shortende; present         32.       Testes size <sup>6</sup> 4       Small (<0.25; medium (0.25-1.25); large (1.25-2.5); very large (>2.5)         32.       Opulatory plugs       2       Absent; present         34.       Ovulation       3 <sup>b</sup> Well-detectable/advertized; likelihood of ovulation advertized, exact timing concealed; concealed/non-advertized         35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by approach or courtship behavior         37.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral; female superior; ventro-ventral, female superior         38.       Copulatory posture (flexibility)       2       Fixed (invariably dorso-ventral; ventro-ventral; female superior         39.       Copulatory posture (flexibility)       2       Single intromission; multiple intromission         41.       (Post/copulation calls (as a device of female social signaling)       4       Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)         41.       Notcurnal copulations/mate guarding       3       Absent; consortships occasionally continues at night, mates maintain proximit	29.		2	male morphs)
31.       Baculum (os penis)       3       Absent; reduced/shortened; present         32.       Testes size <sup>6</sup> 4       Small (<0.25; medium (0.25-1.25); large (1.25-2.5); very large (>2.5)         32.       Ovulation       3 <sup>b</sup> Well-detectable/advertized; likelihood of ovulation advertized, exact timing concealed; concealed/non-advertized         34.       Ovulation       3 <sup>b</sup> Well-detectable/advertized; likelihood of ovulation advertized, exact timing concealed; concealed/non-advertized         35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by approach or courtship behavior         37.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral; female superior; ventro-ventral, female superior         38.       Copulatory posture (flexibility)       2       Fixed (invariably dorso-ventral; ventro-ventral; female superior         39.       Copulatory posture (law prime       4       Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)         41.       (Post; copulation als (as a device of escal signaling)       4       Absent; consortships occasionally continues at night, mates maintain proximity; present         42.       Mean (hourly) copu	30.	Relative length of erected penisd	3	Short (>2); medium (0.5–2); long (<0.5)
33.       Copulatory plugs       2       Absent; present         34.       Ovulation       3 <sup>b</sup> Well-detectable/advertized; likelihood of ovulation advertized exact timing concealed; concealed/non-advertized         35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by mal approach or courship behavior         37.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior         38.       Copulatory pattern       2       Single intromission; multiple intromission         30.       Intromission duration       4       Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)         31.       Nocturnal copulatory frequency       4       <0.01; <0.1; >0.1; >1         31.       Nocturnal copulations/mate guarding (sleepting together)       3 <sup>b</sup> Possibly paternity confusion + exchange for favors; paternity confusion + female plotting         45.       Female intragroup relations, degree of cooperation among female intragroup relations, male coalitions       3 <sup>b</sup> Weak male bonds, on male coalitions of two or more males occur occasionally; strong male bonds, on paparent dominane of new sex over another; females domin males (and male status is	31.	Baculum (os penis)	3	
33.       Copulatory plugs       2       Absent; present         34.       Ovulation       3b       Well-detectable/advertized; likelihood of ovulation advertized exact timing concealed; concealed/non-advertized         35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by mal approach or courtship behavior         37.       Copulatory posture (type)       3b       Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior         38.       Copulatory pattern       2       Single intromission; multiple intromission         30.       Intromission duration       4       Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)         31.       Nocturnal copulatory frequency       4       <0.01; <0.1; >0.1; >1         31.       Nocturnal copulations/mate guarding (sleeping together)       3b       Possibly paternity confusion + tendae long, only close kin support; significant cooperation among female intragroup relations, degree of cooperation among female intragroup relations, degree of cooperation among female bonds, on male coalitions of two or more males occur occasionally; strong male bonds, on male coalitions of two or more males occur occasionally; strong male bonds, on male coalitions of two or more males occur occasionally; strong male bonds, no ma	32.	Testes size <sup>e</sup>	4	Small (<0.25); medium (0.25–1.25); large (1.25–2.5); very large (>2.5)
34.       Ovulation       3 <sup>b</sup> Well-detectabl/advertized, likelihood of ovulation advertized, exact timing concealed; concealed/non-advertized         35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by mal approach or courtship behavior         37.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior         38.       Copulatory posture (flexibility)       2       Fixed (invariably dorso-ventral); flexible         39.       Copulatory posture (flexibility)       2       Single intromission multiple intromission         40.       Intromission duration       4       Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)         41.       (Post)copulations/mate guarding       Absent; (not reported); present       (prevailing and fundamental)         42.       Mean (hourly) copulatory frequency       4       <0.01; <0.1; >0.1; >0.1       >1         43.       Norcurnal copulations, mate guarding       3 <sup>b</sup> Absent; consortships occasionally continues at night, mates maintain proximity; present (prevailing and fundamental)         44.       Non-conceptive sexuality (functions)       3 <sup>b</sup>	33.	Copulatory plugs	2	
35.       Sexual skin swellings       3       Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggera prolonged or semipermanent swellings         36.       Mating initiation       2       Mount usually initiated by female approach or solicitation; mount usually initiated by mal approach or courtship behavior         37.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior         38.       Copulatory posture (flexibility)       2       Fixed (invariably dorso-ventral); flexible         39.       Copulatory posture (type)       3 <sup>b</sup> Dorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior         31.       (Post)copulation calls (as a device of female social signaling)       2       Single intromission; multiple intromission         42.       Mean (hourly) copulatory frequency       4       <0.01; <0.1; >0.1; >1         43.       Nocturnal copulations/mate guarding (sleggether)       3 <sup>b</sup> Possibly paternity confusion; paternity confusion + exchange for favors; paternity confusion; paternity confusion + female plotting         44.       Non-conceptive sexuality (functions)       3 <sup>b</sup> Possibly paternity confusion; paternity confusion + exchange for favors; paternity confusion; paternity confusion or hemale plotting         45.       Female intragroup relations, male coalitions       3       Weak male bonds, no male coalitions of two or more mal	34.		3 <sup>b</sup>	
36.Mating initiation2Mount usually initiated by female approach or solicitation; mount usually initiated by mal approach or courtship behavior37.Copulatory posture (type)3bDorso-ventral; ventro-ventral, male superior; ventro-ventral, female superior38.Copulatory posture (flexibility)2Fixed (invariably dorso-ventral); flexible39.Copulatory pattern2Single intromission; multiple intromission40.Intromission duration4Brief (<20 s); brief (<1 min); prolonged (>1.5 min); prolonged (>5 min)41.(Post)copulation calls (as a device of female social signaling)Absent; consortships occasionally continues at night, mates maintain proximity; present (prevailing and fundamental)42.Mean (hourly) copulatory frequency4<0.01; <0.1; >0.1; >0.1; >143.Nocturnal copulations/mate guarding (sleeping together)3bPossibly paternity confusion; paternity confusion + exchange for favors; paternity confusion + female plotting44.Non-conceptive sexuality (functions)3bPossibly paternity confusion, paternity confusion + exchange for favors; paternity confusion + female blotting45.Female intragroup relations, degree of cooperation among females3Weak male bonds, on male coalitions coalitions46.Male intragroup relations, male coalitions3Weak male bonds, no male coalitions47.Intergroup encounters, nature of intergroup relations3bAffiliative <sup>1</sup> ; relatively peaceful <sup>1</sup> ; hostile <sup>k</sup> 48.Intergroup relations3bAffiliative <sup>1</sup> ; relatively peaceful <sup>1</sup> ; hostile <sup>k</sup> </td <td>35.</td> <td>Sexual skin swellings</td> <td>3</td> <td>Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggerated</td>	35.	Sexual skin swellings	3	Absent (or only slight tumescence of circum-vulval area); conspicuous swellings; exaggerated
<ul> <li>37. Copulatory posture (type)</li> <li>3<sup>b</sup></li> <li>Copulatory posture (flexibility)</li> <li>Copulatory posture (flexibility)</li> <li>Copulatory posture (flexibility)</li> <li>Copulatory pattern</li> <li>Copulatory pattern</li> <li>Copulatory pattern</li> <li>Single intromission; multiple intromission</li> <li>Intromission duration</li> <li>(Post)copulation calls (as a device of female social signaling)</li> <li>(Post)copulatory frequency</li> <li>Absent (not reported); present</li> <li>(Post) copulatory frequency</li> <li>Absent; consortships occasionally continues at night, mates maintain proximity; present (prevailing and fundamental)</li> <li>Non-conceptive sexuality (functions)</li> <li>Possibly paternity confusion; paternity confusion + exchange for favors; paternity confusion + female plotting</li> <li>Female intragroup relations, degree of cooperation among females</li> <li>Male intragroup relations, male coalitions</li> <li>Weak male bonds, no male coalitions of two or more males occur occasionally; strong male bonds, characteristic tendency to form coalitions</li> <li>Intergroup encounters, nature of intergroup relations</li> <li>Sex-specific participation in intergroup</li> <li>Sex-specific participation in intergroup</li> <li>Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>	36.	Mating initiation	2	Mount usually initiated by female approach or solicitation; mount usually initiated by male
<ul> <li>38. Copulatory posture (flexibility)</li> <li>2 Fixed (invariably dorso-ventral); flexible</li> <li>39. Copulatory posture (flexibility)</li> <li>40. Intromission duration</li> <li>41. (Post)copulation calls (as a device of female social signaling)</li> <li>42. Mean (hourly) copulatory frequency</li> <li>43. Nocturnal copulations/mate guarding</li> <li>44. Non-conceptive sexuality (functions)</li> <li>45. Female intragroup relations, degree of cooperation among females</li> <li>46. Male intragroup relations, male coalitions</li> <li>47. Intersexual relations</li> <li>48. Intergroup encounters, nature of intergroup</li> <li>49. Sex-specific participation in intergroup</li> <li>42. Fixed (invariably dorso-ventral); flexible</li> <li>43. Sex-specific participation in intergroup</li> <li>44. Sex-specific participation in intergroup</li> <li>45. Female intragroup relations</li> <li>46. Male intragroup relations</li> <li>47. Intersexual relations</li> <li>48. Intergroup encounters, nature of intergroup</li> <li>49. Sex-specific participation in intergroup</li> <li>41. Copulation in intergroup</li> <li>42. Fixed (invariably dorso-ventral); flexible</li> <li>43. Sex-specific participation in intergroup</li> <li>44. Sex and the sex are equally or more involved in intergroup encounters; males are more involved</li> </ul>	37.	Copulatory posture (type)	3 <sup>b</sup>	
<ul> <li>2 Single intromission; multiple intromission</li> <li>4 Brief (&lt;20 s); brief (&lt;1 min); prolonged (&gt;1.5 min); prolonged (&gt;5 min)</li> <li>4. (Post)copulation calls (as a device of female social signaling)</li> <li>4. Mean (hourly) copulatory frequency</li> <li>4. Nocturnal copulations/mate guarding (sleeping together)</li> <li>4. Non-conceptive sexuality (functions)</li> <li>4. Some conceptive sexuality (functions)</li> <li>4. Female intragroup relations, degree of cooperation among females</li> <li>4. Male intragroup relations, male coalitions</li> <li>4. Intergroup necounters, nature of intergroup relations</li> <li>4. Intergroup necounters, nature of intergroup relations</li> <li>4. Sex-specific participation in intergroup</li> <li>4. Some construction among females</li> <li>4. Sex-specific participation in intergroup</li> <li>4. Sex-specific participation in intergroup</li> <li>4. Sex-specific participation in intergroup</li> <li>4. Single intromission; multiple intromission</li> <li>4. Sex-specific participation in integroup</li> <li>4. Single intromission; multiple intromission</li> <li>4. Sex-specific participation in integroup</li> <li>4. Single intromission; multiple intromission</li> <li>4. Sex-specific participation in integroup</li> <li>4. Single intromission; multiple intromission; patternity intromission (see an or involved in integroup encounters; males are more involved in integroup integrat</li></ul>				
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<ul> <li>(sleeping together)</li> <li>(prevailing and fundamental)</li> <li>Non-conceptive sexuality (functions)</li> <li>3<sup>b</sup></li> <li>Possibly paternity confusion; paternity confusion + exchange for favors; paternity confusion + female plotting</li> <li>Female intragroup relations, degree</li> <li>of cooperation among females</li> <li>Male intragroup relations, male coalitions</li> <li>Weak male bonds, no male coalitions (tooperation among females occur occasionally; strong male bonds, characteristic tendency to form coalitions</li> <li>Intersexual relations</li> <li>Intergroup encounters, nature of intergroup relations</li> <li>Sex-specific participation in intergroup</li> <li>Sex-specific participation in intergroup</li> <li>Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>				
<ul> <li>14. Non-conceptive sexuality (functions)</li> <li>3<sup>b</sup> Possibly paternity confusion; paternity confusion + exchange for favors; paternity confusion + female plotting</li> <li>15. Female intragroup relations, degree of cooperation among females</li> <li>16. Male intragroup relations, male coalitions</li> <li>17. Intersexual relations</li> <li>18. Intergroup encounters, nature of intergroup relations</li> <li>19. Sex-specific participation in intergroup</li> <li>2&lt; Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>				
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<ul> <li>Male intragroup relations, male coalitions</li> <li>Weak male bonds, no male coalitions; coalitions of two or more males occur occasionally; strong male bonds, characteristic tendency to form coalitions</li> <li>Intersexual relations</li> <li>Intergroup encounters, nature of intergroup relations</li> <li>Sex-specific participation in intergroup</li> <li>Sex-specific participation in intergroup</li> <li>Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>	15.		3 <sup>b</sup>	Relatively weak female bonds, only close kin support; significant cooperation among
<ul> <li>47. Intersexual relations</li> <li>3<sup>b</sup> Males dominate females; no apparent dominance of one sex over another; females dominate dominate of one sex over another; females dominate dominate status is acquired through female(s))</li> <li>48. Intergroup encounters, nature of intergroup relations</li> <li>49. Sex-specific participation in intergroup</li> <li>2 Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>	46.		3	Weak male bonds, no male coalitions; coalitions of two or more males occur occasionally;
<ul> <li>Intergroup encounters, nature of intergroup relations</li> <li>Sex-specific participation in intergroup</li> <li>Sex-specific participation in intergroup</li> <li>Females are equally or more involved in intergroup encounters; males are more involved</li> </ul>	47.	Intersexual relations	3 <sup>b</sup>	Males dominate females; no apparent dominance of one sex over another; females dominate
49. Sex-specific participation in intergroup 2 Females are equally or more involved in intergroup encounters; males are more involved	48.	<b>0</b>	3 <sup>b</sup>	
encounters/territorial defense in intergroup encounters and play major role in territorial defense	19.	Sex-specific participation in intergroup	2	

427

#### Table 1 (continued)

#### P. Duda, J. Zrzavý / Journal of Human Evolution 65 (2013) 424-446

	Character	Number of character states	Character states
50.	Stable all-male units (non-breeding groups)	2	Absent (all-male non-breeding groups have not been reported); present (all-male non-breeding or 'bachelor' groups have been reported)
51.	Multimale bisexual groups (inter-male tolerance)	2	Absent; present
52.	'Opposite-sex friendship' (special relationships between male and female)	2	Absent; present
53.	Infant (pre-weaning) mortality <sup>a</sup>	3	Up to 20%; 20–40%; over 40%
54.	Male-led infanticide <sup>a</sup>	4	Absent; rare (reported, occurs rarely); occasional (reported repeatedly, occurs occasionally); frequent (occurs regularly)
55.	Paternal care: protective function of an adult male	2	Infants receives no direct paternal protection; male (father) actively defends his offspring
56.	Paternal care: male—infant interactions	3	Virtually no male—infant interactions; occasional affiliation (play, some food sharing etc.); substantial paternal care <sup>l</sup>
57.	Paternal care: male (possible father) adopts weaned infant if mother dies	3	Absent; occasional; present
58.	Feeding/foraging pattern	2	Group foraging (members of the group maintain proximity during foraging and feeding); solitary foraging (group disperse during feeding and foraging)
59.	Diet	3 <sup>b</sup>	Folivorous (arboreal leaves or terrestrial herbaceous vegetation); frugivorous (ripe fruit); omnivorous <sup>m</sup>
60.	Meat proportion in diet/hunting of animal prey	4 <sup>b</sup>	Absent; occasional hunting or scavenging; present (cooperative arboreal hunting); present (cooperative terrestrial tool-assisted hunting)
61.	Cultural diversity (population-specific behavioral traditions)	2	Absent; present (local differences in tool use, plant use, vocal behavior etc.)
62.	Tool use <sup>a</sup>	4	Absent; simple (e.g., stone-handling, tool-assisted locomotion); sophisticated <sup>n</sup> ; elaborate <sup>o</sup>
63.	Shelter construction (nest building)	3	Shelter construction (nest building) absent; shelter construction (in form of overnight nest) present; construction of elaborate, semipermanent shelters
64.	Habitat	2	Mostly arboreal; mostly terrestrial
65.	Type of bipedalism	5 <sup>b</sup>	Obligate quadrupedalism; occasional bipedalism (semiplantigrade); occasional bipedalism ('midfoot/heel plantigrade'); occasional bipedalism (heel-strike plantigrade); obligate terrestrial bipedalism (and capability of running)

<sup>a</sup> = non-additive/unordered character.

<sup>b</sup> = scoring based exclusively on data from free-ranging populations.

<sup>c</sup> = beard, mane, pelage, 'flanges', colored skin etc.

<sup>d</sup> = head-body length [cm]:pars libera length [mm] ratio.

<sup>e</sup> = mean combined testes weight [g]:mean body weight [kg] ratio.

<sup>f</sup> = a male monopolizes a female within group.

- <sup>g</sup> = a male forms a short-term bond with a female, leaving the social group for some time.
- <sup>h</sup> = a male opportunistically mates with within-group females without restricting others to do so.
- $^{i}$  = intergroup tolerance, peaceful intermingling, feeding, mating and infantine play etc.
- <sup>j</sup> = limited amount of non-lethal aggressive behaviors (agonistic interactions).
- <sup>k</sup> = harsh intergroup competition, lethal aggression (intercommunity killings) and genocide.
- <sup>1</sup> = strong affiliation, carrying, play, grooming and social learning etc.
- $^{m}$  = plant foods, mostly fruits, seeds and storage organs and animal foods.
- <sup>n</sup> = tool kits including tool sets, tool composites and compound tools present.

 $^{\rm o}~=$  containers, complex tools and meta-tools present.

(philopatry); and (iii) socio-ecology (McGrew et al., 1996; <u>Kappeler</u> and Silk, 2010), e.g., social system, paternal investment, adoption, infanticide, intersexual and intrasexual relations, and coalitions and intragroup interactions. Several other characters that are of particular relevance for human evolutionary studies, such as cultural diversity (Wrangham et al., 1994; <u>Lycett et al., 2009; Kappeler</u> <u>et al., 2010</u>), tool use (McGrew, 2010a,b), shelter construction (<u>Groves and Pi, 1985;</u> Fruth and Hohmann, 1996; <u>Anderson, 1998</u>), feeding, diet, habitat use (<u>Doran, 1996;</u> Moore, 1996; <u>Kaplan et al., 2000</u>), and locomotion (<u>Lovejoy, 1988;</u> <u>Crompton et al., 2008</u>), were analyzed as well, in order to roughly characterize the ecology of the hypothetical ancestors.

Several traits that cannot be hypothesized as structurally homologous among the considered species (e.g., sexual adornments of adult males, concealed ovulation in females, cooperative hunting of animal prey and nest building) were also included in the character set. This was because they could represent nonhomologous morphological-physiological-behavioral responses to identical selective pressures (see <u>Ghiglieri, 1987</u>; Wrangham, 1987, for similar treatment of various aspects of social organization as homologous phylogenetic characters; and Fernandez and Morris, 2007, for treatment of sexually selected aspects of primate morphology as homologous phylogenetic characters). Since the characters are not to be used for tree construction but for reconstruction of the ancestral ground patterns, they do not have to be fully logically independent. The parallel alternative formulation of partially overlapping characters could, in fact, be reciprocally illuminative: compare, e.g., #18 Social mating system and #19 Male mating strategy; #25 Sexual dimorphism in body weight and #26 Sexual dimorphism in canine size; #34 Ovulation and #35 Sexual skin swellings; #53 Infant mortality and #54 Male-led infanticide; #62 Tool use, and #63 Shelter construction (nest building) (see SOM for details).

Data from free-ranging populations of apes and monkeys were preferred over data from semi-free-ranging and captive groups. The behavior and life-history patterns exhibited by apes in captivity can differ from those observed in their free-ranging counterparts, showing a variety of behavioral abnormalities (<u>Pazol and Bloomsmith, 1993; Lukas, 1999; Lukas et al., 2002; Birkett and</u> Newton-Fisher, 2011). Different species are likely to respond in different ways to captive environments, and no uniform response pattern should be expected across all primate species that are kept in zoos and laboratories (Hosey, 2005). For eight characters (#8 Age at the first female reproduction, #10 Interbirth interval, #12 Protracted post-reproductive female lifespan, #13 Maximum lifespan, #53 Infant mortality, #54 Male-led infanticide, #61 Cultural diversity, and #62 Tool use), the scoring of a 'prominent' character state in the 'monomorphic' character set was based exclusively on data from free-ranging populations. However, data derived from captive populations were taken into account and used for scoring of 'alternative' character states (see Alternative character sets below). Female life-history traits are subject to great variation in captivity in comparison with free-ranging populations. Captive females may exhibit life-history features not characteristic for free-ranging populations, such as post-reproductive lifespan (Atsalis and Margulis, 2006, 2008; see Walker and Herndon, 2008 for a review). Some behaviors are precluded by captive group management (e.g., infant mortality and infanticide) but may occur for different reasons (e.g., social stress due to overcrowding and lack of space). Moreover, cultural behavior and tool use are often stimulated by captive management (e.g., by different kinds of enrichment) and might be affected by interactions with a human audience.

For humans, data from foraging societies were considered along with the data from agricultural and industrial societies, as the modern foragers might not be useful models for the ancestral populations of *H. sapiens* (Lee and DeVore, 1968; Foley, 1988). Observed intraspecific diversity was covered using polymorphism coding (see below). No a priori hypotheses concerning evolutionary polarity of character states (plesiomorphic or apomorphic) were reflected in character scoring (e.g., '0' or '1') and the '0s' were, when applicable, used merely for absence of the trait in question, either ancestral or derived.

Direct human-ape comparison is problematic. Attempts to find ape homologs of human behavioral traits (such as controlled use of fire, language or artistic expression) can be misleading due to the extraordinary human capabilities for generating behavioral diversity without corresponding genetic change (Smith, 2011). Therefore, an alternative approach was chosen. Comparative biological data have been collected for all species of nonhuman great apes (and selected outgroups), and potential human homologs of these characters have been identified post hoc. However, the numbers of human phenotypic traits that have been analyzed from the phylogenetic point of view are beyond count (see, e.g., Varki and Altheide, 2005; Smith, 2011). As such, various hominid traits that might have played a role in framing the human condition are missing from the character set. Such traits might include, for example, 'capacity for self-recognition and self-awareness' (Gallup, 1982), 'propensity to contagious yawning' (Campbell and De Waal, 2011; Norscia and Palagi, 2011), 'conceptualization of fire' (Pruetz and LaDuke, 2010) and 'sibling availability and sibling relationships' (Geary et al., 2011).

The life-history characters were not scaled to body mass prior to analysis. Regressing traits of interest to body mass and using residuals as data in phylogenetic comparative analysis to uncover relationships between them necessarily makes the analysis biased (one of the 'deadly sins of comparative analysis' according to Freckleton, 2009). Moreover, different scaling methods tend to produce different results (Deaner et al., 2000). It is necessary to interpret the results of any character optimization analyses cautiously, and in the light of possible body mass effects.

The character set has been designed to reflect hominid life history and behavioral diversity, and character states of outgroup taxa were scored only to determine evolutionary polarity of hominid traits. Consequently, some character states for outgroup species (e.g., aspects of social organization) were scored as polymorphic (due to overlap of character states defined primarily for hominids), or considered unknown or inapplicable (see SOM for details).

#### Alternative character sets

Primate species express substantial behavioral diversity and plasticity at both individual and population levels (Kappeler and van Schaik, 2002; <u>Chapman and Rothman, 2009</u>). Not surprisingly, this yields a high incidence of character polymorphism in character sets such as the ones used here. To begin to solve the problem of high intraspecific polymorphism and to mitigate the risks of spurious character state definition and character scoring, six character sets were created and analyzed separately.

- (1) In the basic 'polymorphic' character set, all character states reported by various studies for a given species were scored regardless of their quantitative distribution. This was done using the polymorphic scoring convention. The resulting character set comprised 25 binary and 40 multistate characters (see Tables 1 and 2). Of the multistate characters, 27 were additive (i.e., ordered; using Wagner optimization) and 13 nonadditive (i.e., unordered; using Fitch optimization).
- (2) In the 'monomorphic' character set, only the most frequent (common or prominent) character state was selected (see Table 2). Consider, for example, character #37 Copulatory posture for H. sapiens (Fig. 2). In the 'polymorphic' character set, all defined character states were scored, to reflect the entire cross-cultural and/or individual behavioral flexibility expressed by the human species. By contrast, in the 'monomorphic' character set, only the character state that is most common both cross-culturally and/or individually was scored (i.e., ventro-ventral copulation with a male on top; Kinsey et al., 1948; Ford and Beach, 1952; Dixson, 1998). The 'character polymorphism' does not always imply high intraspecific behavioral diversity. Sometimes the character state only reflects the diversity of previous authors' opinions (see SOM for 'prominent' and 'alternative' character states). So-called 'prominent' character states were identified based on the number of studies in support, year of publication (more recent studies were considered more reliable), nature of populations studied (free-ranging populations preferred) and polymorphism proportions (the character states most common cross-culturally and/or individually were selected).

In order to test the influence of preconceived opinions concerning hominoid evolution on the inferred evolutionary pattern, three 'biased' character sets were created using various permutations of the character scoring.

- (3) In the '*Pan*-like' character set, humans and common chimpanzees (*P. troglodytes*) were scored as similar as possible (i.e., their observed intraspecific polymorphisms were limited to minimize the differences between the two species).
- (4) In the '*Gorilla*-like' character set, interspecific polymorphisms in humans and western lowland gorillas (*G. gorilla*) were resolved to make the human–gorilla differences minimal.

For example, humans are polymorphic in character #48 Intergroup encounters. Human intergroup interactions range from invariably hostile intergroup encounters with occasional lethal violence (<u>Nishida and Hiraiwa-Hasegawa, 1985; Goodall, 1986;</u> Boesch et al., 2007; <u>Sherrow and Amsler, 2007</u>), shared with common chimpanzees (Wrangham, 1999; Wrangham et al., 2006;

Species	Characters	
	1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60	61 62 63 64 65
Homo sapiens	3 2 3 0 2 2 2 3 1 0 0 1 3 1 1 1 1 1 1 1 2 1 0 1 0 1 0 7 1 0 7 1 0 0 0 7 1 1 0 2 1 1 2 1 1 2 1 1 1 1 * 3 1 2 2 0 2 3	13214
Gorilla beringei	2 2 3 2 1 1 1 2 1 2 0 0 2 2 0 1 - 2 2 0 0 1 1 1 1 1 0 0 0 2 1 3 1 0 2 1 0 0 0 0 1 2 1 1 0 2 0 2 1 1 1 7 1 2 0 1 1 1 2 2	1 2 1 1 3
Pan paniscus	3 1 3 2 1 1 1 2 1 1 0 7 2 2 0 1 - 2 2 0 7 2 1 1 1 1 0 0 0 2 1 3 7 1 2 1 0 1 0 1 2 7 2 2 0 2 0 0 1 7 0 0 0 1 0 1 1 1 0 0 1 1 1	1 1 1 ? 3
Gorilla gorilla	3 0 2 2 1 1 1 1 0 1 0 0 2 1 1 0 1 1 0 1 3 0 2 1 1 0 1 0 2 0 0 0 0 0 0 0 0 0 0 0 0	1 1 1 1 3
Gorilla beringei	3 0 2 1 1 1 1 1 0 1 0 0 2 1 1 0 1 1 0 1 1 0 2 1 1 0 1 0	? ? 1 1 3
Pongo pygmaeus	3 1 3 3 1 1 1 3 1 3 0 0 3 1 1 0 0 1 1 1 1	1 1 1 0 3
Pongo abelii	31331113140031100111111112110112107001030*100-0000000111	1 1 1 0 3
Hylobates lar	1 2 3 0 0 0 1 1 1 1 1 2 7 1 1 0 1 0 0 0 1 7 1 0 0 0 0 0 0 0 0 1 7 1 0 1 0	? ? 0 0 2
Hoolock hoolock	1 ? ? 0 0 0 1 1 ? 1 1 ? ? ? 1 0 1 0 0 0 ? ? 1 ? 0 0 1 1 0 1 2 ? 0 ? ? 1 * 1 0 1 1 ? 0 ? 1 * 1 0 ? ? ? 1 1 1 ? 0 1 0	? ? 0 0 2
Nomascus concolor	0 2 3 0 3 3 1 1 3 0 3 3 3 3 1 0 1 0 0 0 1 3 1 3	??002
Symphalangus syndactylus	۰۰ 2 * 2 1 1 0 1 1 1 1 1 1 7 7 1 1 0 1 0 0 0 7 7 1 7 0 0 1 0 0 0 2 1 0 7 1 7 0 1 0 1 7 0 7 7 - 7 1 1 7 0 0 7 0 0 1 2 7 0 0 0 0	??002
Papio anubis	1 2 1 0 1 0 0 0 0 0 0 1 1 0 ? 1 ? 2 2 0 1 1 1 2 2 1 0 0 1 2 3 0 1 2 ? 0 0 0 1 1 ? 1 1 1 ? 1 0 0 1 1 0 2 1 2 1 0 2 1	0 0 0 1 1
Theropithecus gelada	1 1 1 0 0 0 0 0 0 0 0 1 7 0 0 1 1 1 1 0 0 1 1 1 7 2 2 1 0 0 1 2 1 0 0 2 1 0 0 0 1 1 2 7 0 1 0 0 0 1 1 0 7 0 2 1 0 0 0 2 0	0 0 0 1 1
Mandrillus sphinx	0 2 1 0 * 0 0 0 0 0 1 7 0 0 1 1 1 2 2 0 0 1 1 1 2 2 1 0 1 1 2 2 0 0 1 0 0 0 0	0 0 0 1 0
Macaca mulatta	0 2 1 0 0 0 0 0 0 0 1 1 0 0 7 1 7 2 2 0 1 1 1 1 2 1 0 0 1 2 3 0 0 1 0 0 0 1 0 1 2 7 0 1 1 0 1 7 1 1 * 1 7 1 1 0 0 0	0 0 0 1 1
Macaca fuscata	0 2 1 0 0 0 0 0 0 0 1 1 0 0 7 1 7 2 2 0 1 1 1 2 1 2 1 0 0 1 2 3 0 0 1 0 0 1 0 1 7 7 0 1 1 0 0 1 1 1 * 1 7 1 1 0 2 0	1 1 0 1 1
Erythrocebus patas	0 3 0 0 0 0 0 0 0 0 1 7 0 0 1 * * 1 2 ? 0 0 1 2 0 0 1 2 1 0 0 1 0 0 0 1 ? 2 ? 0 1 0 0 2 1 1 0 ? 1 1 ? 0 0 0 0 0	0 0 0 1 1
Chlorocebus aethiops	0 3 0 0 0 0 0 0 * 0 1 ? 0 0 0 1 - 2 2 0 1 ? 1 0 1 2 1 0 0 1 2 3 0 2 1 0 0 0 0 1 ? ? ? 0 1 0 0 1 0 1 1 ? 1 1 ? 1 0 0 2 0	1 0 0 * 1
Semnonithecus entellus	1 1 1 1 1 0 0 * 2 0 1 1 0 1 * * 1 2 0 1 1 1 1 2 2 0 0 1 2 1 0 2 0 1 0 1	0 0 0 1 0

P. Duda, J. Zrzavý / Journal of Human Evolution 65 (2013) 424-446

- (5) Additionally, in the 'uniquely-human' character set, precedence was given to an idea of human uniqueness. Polymorphisms in *H. sapiens, P. troglodytes* and *G. gorilla* were resolved to make the two nonhuman species as similar as possible and humans most distinct from both. In this character set, *H. sapiens* was consciously scored as an exceedingly aberrant hominid with, for example, extremely delayed first reproduction at the age of 21 or more (<u>Barrett et al., 2002</u>), polyandrous mating system (Ford and Beach, 1952; <u>Dixson, 1998</u>; <u>Baker and Bellis, 2007</u>) ventro-ventral, female superior copulations (<u>Dixson, 1998</u>) and highly restricted female mate choice (Wilson and Daly, 1992; Betzig, 1995; Barrett et al., 2002).
- (6) In order to assess whether phylogenetic inference is not biased by the use of multistate characters, a binary version of the character set was created. The 40 multistate characters were recoded as binary characters as follows: (i) Each additive multistate character was simplified to include only two character states ('0' and '1') using the most important gaps between original character states (only the 'prominent' character states were considered). (ii) Each nonadditive multistate character was split into a number of binary characters. All character states describing intraspecific behavioral diversity were considered. There were a few exceptions to these rules, which concerned characters #14 Philopatry (dispersal patterns), #47 Intersexual relations, #59 Diet, and #60 Meat proportion in diet/hunting of animal prey (see SOM for details). If there were two or more possible ways to translate a multistate character into binary one(s), the character scoring leading to the emergence of a possible synapomorphy shared by two or more species was preferred to scoring leading to emergence of single species autapomorphy (compare for example scoring of characters #62 Tool use and #63 Shelter construction using multistate and binary scoring; see SOM). For the remaining 25 characters that were binary even in the 'multistate' character sets, only 'prominent' character states were scored in the binary character set.

In summary, the five 'multistate' character sets of 19 terminal taxa and 65 characters included overall 1235 character states. In the 'polymorphic' matrix, there were 149 polymorphic character states, in the 'monomorphic' matrix the number of unresolved polymorphisms was reduced to 20 and in the three 'biased' character sets ('*Pan*-like', '*Gorilla*-like', and 'uniquely-human') there were 19 unresolved polymorphisms. The overall amount of ambiguous (i.e., polymorphic, unknown or inapplicable) character states varied from 24 to 14% in various 'multistate' character sets. The 'binary' character set included 19 terminal taxa and 77 characters, i.e., 1463 character states of which 11% were ambiguous.

Two measures of character fit on phylogeny (the consistency index [ci] and retention index [ri]) were calculated for each character in the 'polymorphic' and 'monomorphic' character set and for both character sets as a whole (ensemble CI and RI) using NONA 2.0 (Goloboff, 1999) and Mesquite 2.75 (Maddison and Maddison, 2011). The ensemble CI of the character set is a sum of the minimal number of steps across all characters divided by tree length. A maximum CI of 1 indicates that a tree includes no homoplastic

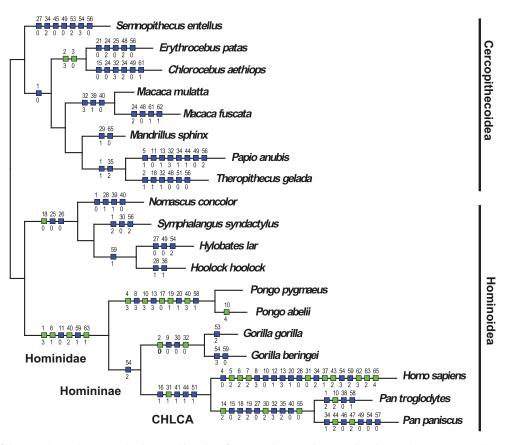


Figure 1. The amount of character change along internal and terminal branches of a tree (evolutionary derivation) based on maximum-parsimony character optimization and the 'unambiguous' optimization routine and the 'monomorphic multistate' character set (for results of optimization of other character sets see SOM). Blue rectangles represent homoplastic (parallel, convergent or reversal) apomorphies, green rectangles represent uniquely derived apomorphies. Numbers above each rectangle indicate character numbers, numbers below indicate character states (see Table 1 and List of characters in SOM). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

changes (i.e., shared character state due to causes other than common descent). The ensemble RI of the character set indicates the degree to which potential synapomorphies are exhibited on the internal branches of a tree, thus supporting the tree topology (Farris, 1989a,b; Kitching et al., 1998).

#### Evolutionary derivation

The six character sets were optimized on the widely accepted hominoid phylogeny (see Ingroup and outgroup taxa and phylogeny) using maximum-parsimony optimization, as implemented in NONA 2.0 (Goloboff, 1999). This allowed us to infer the amount of character change occurring along each internal and terminal branch of a tree (see Table 3; see Fig. 1 for visualization of amount of character change on a tree). This amount of change is hereinafter referred to as 'evolutionary derivation' (Miles and Dunham, 1993; compare 'derivation load' sensu Brinck, 1977; Andersen, 1979; see also Lovejoy et al., 2009, for itemizing evolutionary derivations of hominioid clades concerning skeletal morphology). The 'unambiguous' optimization routine was applied for inferring evolutionary derivations (UNAM: the character states are reconstructed as 'ambiguous' ('?') in cases when 'slow' and 'fast' optimization routines provide for different but equally parsimonious scenarios).

#### Phylogenetic reconstruction of ancestral states

Ancestral states for all 65 characters (from the 'multistate' character sets) and 77 characters (from the 'binary' character set)

were reconstructed using the widely accepted phylogenetic tree (see Ingroup and outgroup taxa and phylogeny) and the maximumparsimony character optimization, utilizing three optimization routines: 'fast' (ACCTRAN: the character changes are placed as close to the root of the tree as possible, i.e., the number of parallelisms and convergences is minimized), 'slow' (DELTRAN: the character changes are assigned along branches as close to the tips as possible,

#### Table 3

Inferred amount of character change (evolutionary derivation) of individual species and their hypothetical ancestors, based on maximum-parsimony character optimization of the 'polymorphic' (a), 'monomorphic' (b), 'Pan-like' (c), 'Gorilla-like' (d), 'uniquely-human' (e) and 'binary' (f) character set, using the 'unambiguous' optimization routine. Number of homoplasies/true homologies that constitute evolutionary derivations is indicated in parentheses.

	a	b	с	d	e	f
Hominoidea	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)
Hylobatidae	2 (1/1)	3 (2/1)	3 (2/1)	3 (2/1)	3 (3/0)	3 (2/1)
Hominidae	5 (1/4)	6 (2/4)	5 (1/4)	6 (2/4)	6 (2/4)	6 (2/4)
Pongo	10 (5/5)	9 (5/4)	9 (4/5)	9 (4/5)	8 (3/5)	8 (6/2)
Pongo pygmaeus	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)	0 (0/0)
Pongo abelii	1(0/1)	1 (0/1)	1(0/1)	1 (0/1)	1 (0/1)	0 (0/0)
Homininae	1 (1/0)	1 (1/0)	1 (1/0)	1 (1/0)	1 (1/0)	1 (1/0)
Gorilla	5 (3/2)	4 (2/2)	5 (3/2)	3 (1/2)	5 (3/2)	2 (2/0)
Gorilla gorilla	0 (0/0)	1 (1/0)	1 (1/0)	0 (0/0)	1(1/0)	1 (1/0)
Gorilla beringei	1 (1/0)	2 (2/0)	1 (1/0)	2 (2/0)	2 (2/0)	1 (1/0)
Hominini	5 (4/1)	5 (4/1)	9 (7/2)	5 (4/1)	7 (5/2)	5 (4/1)
Homo sapiens	12 (5/7)	19 (10/9)	13 (6/7)	13 (6/7)	23 (12/11)	14 (10/4)
Pan	9 (6/3)	10 (7/3)	8 (6/2)	12 (8/4)	6 (5/1)	8 (7/1)
Pan troglodytes	5 (4/1)	4 (3/1)	3 (3/0)	5 (4/1)	6 (6/0)	5 (5/0)
Pan paniscus	7 (5/2)	7 (5/2)	12 (8/4)	8 (6/2)	9 (6/3)	6 (3/3)

i.e., the number of reversals is minimized) and 'unambiguous' (see above).

In addition, the ancestral states of characters from the 'multistate monomorphic' and 'binary' character sets were reconstructed using maximum-likelihood character optimization, as implemented in Mesquite 2.75 (Maddison and Maddison, 2011). The Markov *k*-state 1 parameter model (Mk1) that assumes an equal rate of change between all character states (Lewis, 2001) was used. The topology of the tree used in this analysis was combined from various sources based on different kinds of data, therefore no comparable branch lengths were available. As such, two alternative sets of branch lengths were used for maximum-likelihood optimization (SOM Table S.1): (i) all branch lengths were considered equal, the length of all branches having been arbitrarily set to 1 ('all-equal' hereinafter), (ii) branch lengths were based on maximum-likelihood estimates of nucleotide divergence, accepted from Perelman et al. (2011) ('molecular-calibrated' hereinafter). The lengths of branches leading to H. hoolock and to G. beringei (absent in Perelman et al., 2011) were arbitrarily set as equal to the lengths of branches leading to their sister taxa, i.e., to H. lar (a representative of the Hylobates spp.) and G. gorilla, respectively. The point of divergence of *G. beringei* was arbitrarily set to the midpoint of the branch leading to G. gorilla (see SOM Table S.1 for alternative sets of branch lengths and 'molecular-calibrated' branch lengths). Overall, four series of reconstructions were recovered, resulting from combinations of the two character sets ('monomorphic multistate' and 'binary') and two alternative sets of branch lengths ('all-equal' and 'molecular-calibrated').

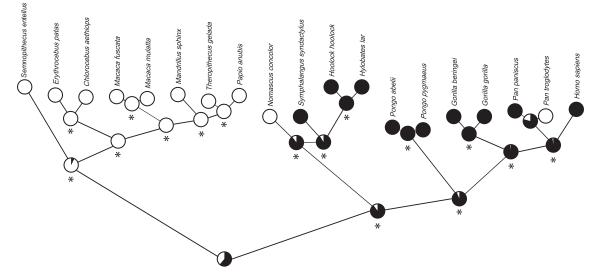
The metric tree (phylogram) with 'molecular-calibrated' branch lengths has been preferred here to the time-calibrated ultrametric tree (chronogram) as an alternative to the tree with equal (= 1)branch lengths. Litsios and Salamin (2012) argued that inferring ancestral character states on time-calibrated trees could have deceiving results as it may not appropriately represent the evolution of species traits. Time-calibrated chronograms inherently include the false assumption that all sister taxa on the tree exhibit substitution rate homogeneity (i.e., identical rates of molecular evolution). Molecular-calibrated phylograms have been found most suitable for accurate reconstruction of ancestral states in various groups including primates (<u>Litsios and Salamin, 2012</u>), possibly because molecular substitution rates are a function of many variables relating to life history (Fontanillas et al., 2007; <u>Nikolaev</u> et al., 2007; Thomas et al., 2010).

The statistical support for the ancestral state reconstructions was determined using a likelihood decision threshold of T = 2(Schluter et al., 1997), indicating support at least 7.4 times greater for the character state in question than for the alternative character state(s). The reconstructed ancestral states in multistate characters were classified into four confidence categories as follows: (i) 'confident': a character state has a statistically significant support (P < 0.05) for its presence in an ancestor, based on the likelihood threshold of T = 2 (Schluter et al., 1997); (ii) 'likely': a character state has a nonsignificant support for its presence, being more supported than the sum of all alternatives; (iii) 'debatable': a character state has a nonsignificant support for its presence, being more supported than any single alternative (note that the confidence categories 'likely' and 'debatable' merge in binary characters); (iv) 'unknown/speculative': a character state unknown due to terminal polymorphism or data deficiency, equal support of two or more contradicting character states, or logical inconsistency between ancestral states inferred from various optimization analyses (Table 4; Figs. 2 and 3; SOM Table S.2).

#### Behavioral phylostratigraphy

Finally, the reconstructed ancestral states were used to assign individual attributes of extant species to nested 'phylostrata' that correspond to the successive phylogenetic nodes (= common ancestors). A 'phylostratum' (modified from <u>Domazet-Lošo et al.</u>, <u>2007</u>) can be considered a set of attributes of a species emerging in one of its successive common ancestors, giving phylogenetic (temporal) rank to every attribute in the character set (Fig. 4).

The evolution of the 65 characters present in four well-sampled extant species (*H. sapiens, P. troglodytes, G. gorilla* and *P. pygmaeus*) was reconstructed using the 'monomorphic multistate' character set and 'fast', 'slow' and 'unambiguous' MP optimization routines. The characters were then distributed into four 'phylostrata', representing the common ancestors of Hominidae, Homininae, the CHLCA and the species' own apomorphies. Character states of an extant species not matching any reconstructed ancestral state were considered novel (autapomorphic) in the given species. Only



**Figure 2.** Reconstruction of ancestral states from the 'binary' character set, using maximum-likelihood character optimization, exemplified by character #37b Copulatory posture (ventro-ventral, male superior) with two character states: white = absent, black = present. Branch lengths were derived from the tree with 'molecular-calibrated' branch lengths. Areas of the pie charts indicate relative support for ancestral states. Significantly supported ancestral states are asterisked.

#### Table 4

The suite of selected life-history, socio-sexual and socio-ecological traits that characterized key common ancestors in Hominoidea, classified into four confidence categories based on maximum-likelihood support. Note that the reconstruction of the common ancestor of Hominoidea is less reliable (regardless of its statistical support) because only one outgroup (Cercopithecoidea) was used to determine the evolutionary polarity of character states.

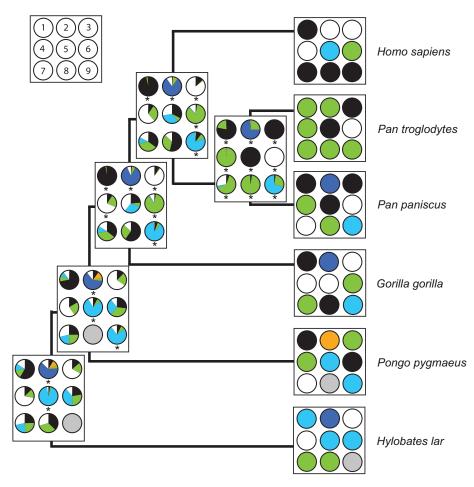
	Hominoidea (last common ancestor of apes)	Hominidae (last common ancestor of great apes)	Homininae (last common ancestor of African apes)	CHLCA (chimpanzee-human last common ancestor)	Panini (last common ancestor of chimpanzee and bonobo)
'Confident'	Slow postnatal growth; first molar eruption at >3 years, last at <8 years; onset of puberty at 6–10 years; first female reproduction at around 10 years (postponed); interbirth interval <5 years; seasonal breeding; both sexes dispersal from natal groups; possessive and opportunistic male mating strategy; forced copulations absent; exerted female mate choice; sexual adornments of adult males present, sexual dichromatism absent; medium-size penis, baculum present medium- size testes; copulatory plugs absent; conspicuous sexual skin swellings; detectable ovulation; female-initiated matings; single intromission; weak male bonds, no male coalitions; multimale groups absent; infant (pre- weaning) mortality <40%; paternal protection present; group foraging; nest building absent	Gestation length >8 months; slow postnatal growth; first molar eruption at 2–5 years, last at 8–12 years; onset of puberty at 6–10 years; first female reproduction at 10–15 years (postponed); interbirth interval <5 years; year-round breeding; male-biased dispersal (female philopatry), both sexes dispersal; single male–multifemale mating system; possessive and opportunistic male mating strategy; exerted female mate choice; male preference for higher-ranking, parous females; strong sexual dimorphism in body and moderate sexual dimorphism in canine size, sexual adornments of adult males present; medium-size penis, baculum present; medium-size testes; copulatory plugs absent; female-initiated matings; flexible copulatory posture; single intromission; male dominance; multimale groups absent; infant (pre-weaning) mortality <40%; group foraging; cultural diversity (behavioral traditions) present, simple tools; nest building present	Gestation length >8 months; slow postnatal growth; first molar eruption at 2–5 years, last at 8–12 years; onset of puberty at 6–10 years; first female reproduction at 10–15 years (postponed); year-round breeding; female post- reproductive lifespan absent; maximum lifespan 40–50 years; female-biased dispersal (male philopatry), both sexes dispersal; single male –multifemale mating system; possessive and opportunistic male mating strategy; forced copulations absent; exerted female mate choice; male preference for higher-ranking, parous females; moderate sexual dimorphism in canine size, sexual adornments of adult males present; medium- size penis, baculum present; medium to small testes; copulatory plugs absent; sexual skin swellings absent or small; flexible copulatory posture; single, prolonged intromission (duration >1.5 min); male dominance; opposite-sex friendship (special relationships) present; infant (pre-weaning) mortality <40%; paternal care and paternal protection present; group foraging; no cooperative hunting; cultural diversity (behavioral traditions) present, simple tools; nest building present	Gestation length >8 months; first molar eruption at 2–5 years, last at 8–12 years; onset of puberty at 6–10 years; first female reproduction at 11–15 years (postponed); interbirth interval <5 years; year-round breeding; maximum lifespan 40 ~50 years; female-biased dispersal (male philopatry), both sexes dispersal; single male—multifemale mating system; possessive male mating strategy; exerted female mate choice; moderate sexual dimorphism in body weight and canine size; medium to long penis, baculum present (possibly reduced); copulatory plugs absent; sexual skin swellings absent or small; flexible copulatory posture; single, prolonged intromission (duration >1.5 min); male dominance; infant (pre- weaning) mortality <40%; paternal care and paternal protection present; group foraging; cultural diversity (behavioral traditions) present, simple tools; nest building present	Gestation length >8 months; slow postnatal growth; weaning at approx. 4–7 years; first molar eruption at 2–5 years, last at 8–12 years; onset of puberty at 6–10 years; first female reproduction at 11–15 years (postponed); year-round breeding; female-biased dispersal (male philopatry); multimale–multifemale (promiscuous) mating system; possessive and opportunistic male mating strategy; forced copulations absent; moderate sexual dimorphism in body weight and canine size, sexual adornments of adult males and male bimaturism absent; relatively long penis with reduced baculum; very large testes; exaggerated sexual swellings; male-initiated matings; single, brief intromission (duration <20 sec); (post)copulation calls present; high copulatory frequency; male dominance; multimale groups present; infant (pre-weaning) mortality <40%; direct paternal protection absent, occasional male–infant affiliation present; group foraging; frugivorous diet (ripe fruit eater); cultural diversity (behavioral traditions) present; nest building present
'Likely'	Medium-size neonates (3 -10% of maternal weight); conjugal families and no semi-cohesive communities; single male -multifemale mating system; positive correlation of male rank and copulation rate; moderate sexual	Medium-size neonates (3–10% of maternal weight); female post-reproductive lifespan absent; maximum lifespan >40 years; female-biased dispersal (male philopatry); conjugal families and no semi-cohesive communities; forced copulations absent; sexual skin	Medium-size neonates (3–10% of maternal weight); weaning at approx. 4–7 years; interbirth interval 3–5 years; conjugal families and no semi-cohesive communities; positive correlation of male rank and copulation rate, high top-sire male mating success (100	Medium-size neonates (3–10% of maternal weight); weaning at approx. 4–7 years; female post-reproductive lifespan absent; conjugal families within semi-cohesive communities; opportunistic male mating strategy; forced copulations absent; positive correlation of	Medium-size neonates (3–10% of maternal weight); interbirth interval 3–5 years; no conjugal families and semi-cohesive communities; positive correlation of male rank and copulation rate, limited male paternity success (100–81%) (80–41%); advertized ovulation

#### Table 4 (continued)

	Hominoidea (last common ancestor of apes)	Hominidae (last common ancestor of great apes)	Homininae (last common ancestor of African apes)	CHLCA (chimpanzee—human last common ancestor)	Panini (last common ancestor of chimpanzee and bonobo)
	dimorphism in canine size; flexible copulatory posture; exchange of favors for sexual access present; moderately hostile intergroup encounters (limited amount of lethal intergroup violence), males more involved in territorial defense; no hunting and no meat in diet	swellings absent or small; positive correlation of male rank and copulation rate; prolonged intromission (duration >1.5 min); weak male bonds, no male coalitions	-81%); strong sexual dimorphism in body weight; detectable ovulation; female- initiated matings; medium copulatory frequency; female (kin) coalitions present, female non-kin coalitions absent; moderately hostile intergroup encounters (limited amount of lethal intergroup violence); regularly occurring infanticide	male rank and copulation rate, high top-sire male mating success (100–81%); sexual adornments of adult males present; medium-size testes; medium copulatory frequency; exchange of favors for sexual access present; moderately hostile intergroup encounters (limited amount of lethal intergroup violence); multimale groups present; regularly occurring infanticide; omnivorous diet	(exact timing possibly concealed due to semipermanent swellings); flexible copulatory posture (ventro-ventral, male superior posture present, female superior absent); occasional hunting of animal prey; simple tools
'Debatable'	Female-biased dispersal (male philopatry); high male paternity success (100 -81%); insignificant to moderate sexual dimorphism in body weight, male bimaturism absent (one adult male morph); brief intromission (duration <1.5 min); low copulatory frequency; stable all-male non- breeding (bachelor) groups absent; infanticide absent or rare	Interbirth interval 1–3 years; maximum lifespan >50 years; high male paterity success (100 –81%); male bimaturism present; low copulatory frequency; stable all-male non- breeding (bachelor) groups absent; infanticide absent or occurs rarely; omnivorous diet; hunting absent or occasional	Male bimaturism present; occasional male coalitions present; stable all-male non- breeding (bachelor) groups present, multimale groups absent; occasional infant adoption by male present; omnivorous diet; hunting absent or occasional	Interbirth interval 3–5 years; concealed ovulation; stable all- male non-breeding (bachelor) groups present; occasional infant adoption by male present; cooperative hunting of animal prey (habitat context unclear)	Strong male bonds, male coalitions present; stable all- male non-breeding (bachelor) groups present; regularly occurring infanticide; occasional infant adoption by male present; regular cooperative arboreal hunting of animal prey
'Unknown/ Speculative'	Gestation length; weaning age; female post- reproductive lifespan; maximum lifespan; male mate preference (for female age, rank, or parity); nature of female intragroup relations (cooperation and coalitions among female kin and non-kin); intersexual relations (intersexual relations (intersexual dominance patterns); opposite-sex friendship (special relationships); paternal care (nature of male—infant interactions); infant adoption by male; dietary specialization; cultural diversity (behavioral traditions); tool use	Weaning age; ovulation detectability; nature of female intragroup relations (cooperation and coalitions among female kin and non- kin); nature of intergroup encounters and sex-specific participation in territorial defense; opposite-sex friendship (special relationships); paternal care and paternal protection; infant adoption by male	Sex-specific participation in territorial defense	Male mate preference; morphological—physiological behavioral polymorphism of adult males (male bimaturism); mating initiation (either female- or male-initiated); nature of female intragroup relations (cooperation and coalitions among female kin and non-kin); sex-specific participation in territorial defense; opposite-sex friendship (special relationships)	Female post-reproductive lifespan; exerted female mate choice; male mate preference; copulatory plugs; nature of female intragroup relations (cooperation and coalitions among female kin and non- kin); nature of intergroup encounters (severity of intergroup violence) and sex- specific participation in territorial defense; opposite- sex friendship (special relationships)

434

P. Duda, J. Zrzavý / Journal of Human Evolution 65 (2013) 424–446



**Figure 3.** Reconstruction of ancestral states of selected characters using maximum-likelihood character optimization (the 'monomorphic multistate' character set and 'molecularcalibrated' branch lengths). The areas of the pie charts indicate relative support for individual ancestral states. Significantly supported ancestral states are asterisked. Selected characters: 1 = #1 Gestation length (white = 5-6 months, light blue = 6-7 months, green = 7-8 months, black = >8 months); 2 = #10 Interbirth interval (white = 1-3 years, light blue = 3-5 years, dark blue = 5-7 years, orange = 6-8 years, black = >8 years); 3 = #19 *Male mating strategy* (white = possessive, green = consortship, black = opportunistic); 4 = #24 Top-ranking (top-sire) ingroup male paternity success (white = high (100-81%), dark blue = limited (80-41%), black = low (less than 40%)); 5 = #32 Testes size (white = small, light blue = medium, green = large, black = very large); 6 = #40 Intromission duration (white = brief (<20 s), dark blue = brief (<1 min), green = prolonged (>1.5 min), black = prolonged (>5 min)); 7 = #54 Male-led infanticide (white = absent, light blue = rare, green = occasional, black = frequent); 8 = #56 Paternal care: male—infant interactions (white = virtually no male—infant interactions, dark blue = occasional affiliation, black = substantial paternal care, gray = unknown or inapplicable); 9 = #62 Tool use (white = absent, light blue = simple, green = sophisticated, black = elaborate, gray = unknown or inapplicable). (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

positive matches between ancestral and extant species character states were considered (i.e., a pair of unknown or inapplicable character states was not considered a match).

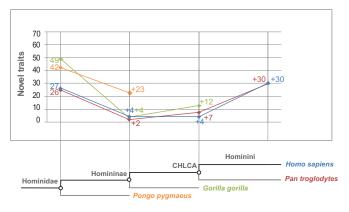
#### **Results and discussion**

# Phylogenetic properties of life-history, behavioral and ecological data

Homology criteria are elusive for life-history, behavioral and ecological traits. This is in part because these traits tend to be viewed as more context-dependent than morphological and molecular traits (Miller and Wenzel, 1995). However, the phylogenetic utility of a character (its 'secondary homology' sensu <u>de Pinna, 1991</u>) need not be speculative as it can be directly measured by indices of character fit on the tree.

Reconstructed evolutionary transitions among character states reveal multiple independent origins and losses of particular character states, suggesting numerous instances of parallel, convergent, and/or reversal character evolution in Hominidae (Fig. 1). However, the ensemble RI of the 'polymorphic' and 'monomorphic' character

sets (RI = 0.67 and 0.62, respectively) falls well within the range of RI values associated with other biological data sets, including those consisting of behavioral traits (Lycett et al., 2009). This suggests that primate (hominid) behavior and socio-ecology do not exhibit higher levels of homoplasy than other biological data sets. The highest possible fit (both consistency index ci = 1 and retention index ri = 1) was found in characters ##6, 7, 14, 17, 31, 43, 47, 55 and 63 (in both the 'monomorphic' and 'polymorphic' character sets), plus ##10, 19 and 45 in the 'polymorphic' character set only. Character state distribution for these characters (e.g., age at the last molar eruption, onset of puberty, presence of baculum and shelter construction) agrees well with phylogeny. These characters exhibited no convergences and/or reversals and their ancestral state reconstructions and thus might be labeled as highly confident. On the contrary, characters ##25, 34, 48 and 49 in both character sets, characters ##36 and 59 in the 'polymorphic' character set only and #45 in the 'monomorphic' character set only have ri = 0, indicating no contribution of these characters to reconstruction of the ancestral ground patterns. Character states for these characters (e.g., mating initiation, ovulation detectability, nature of female intragroup relations and intergroup encounters) exhibit high



**Figure 4.** Phylostratigraphic map of four selected hominid species (*Homo sapiens, Pan troglodytes, Gorilla gorilla* and *Pongo pygmaeus*) describing the amount of evolutionary novelty (number of apomorphies) emerging in each phylostratum and retained in extant species, based on maximum-parsimony character optimization of the 'mono-morphic multistate' character set and the 'slow' optimization routine. Four phylostrata correspond (from left to right) to the hypothetical common ancestors of Hominiae, Homininia and to extant species. For example, out of 65 character states present in *Homo sapiens*, 27 are retained from the last common ancestor of Hominidae, four from the last common ancestor of Hominidae in the human stem lineage after the human–chimpanzee split.

variation even between closely related taxonomic units. These characters exhibit mosaic evolution with a massive amount of homoplasy, due to intraspecific polymorphisms and interspecific variability (SOM Table S.2).

The different reconstruction methods (maximum-parsimony versus maximum-likelihood optimization) do not affect reconstructed ancestral states significantly. The ancestral states based on maximum-parsimony optimization are identical to those that are well supported by maximum-likelihood optimization on the tree with 'all-equal' branch lengths. However, maximum-parsimony reconstructions differ notably from the maximum-likelihood ones inferred from the tree with 'molecular-calibrated' branch lengths. Four characters (##22, 31, 54 and 60) are reconstructed with different ancestral state in the CHLCA (SOM Table S.2). This is due to the ability of maximum likelihood-based methods to take branch lengths into account (changes are more likely to occur on the long branches when their length is proportional to time).

By contrast, accounting for different branch lengths by using maximum likelihood-based methods can have dramatic effects on reconstructed ancestral states (Yang, 1996; Schluter et al., 1997; Cunningham, 1999; Pagel, 1999). When optimizing on the tree with 'all-equal' branch lengths, reconstructed hypothetical ancestors tend to possess the same character state as one of its direct extant descendant species. This is especially true of the last common ancestor of Hominidae, which in several instances possesses reconstructed ancestral states that are identical to character states possessed by orangutans. These states include forced copulations, extended lifespan, greatly prolonged intromission and absence of infanticide, which are rather unlikely to have characterized the common ancestor of all hominids. The reconstructions based on the tree with 'molecular-calibrated' branch lengths generally appear more realistic, although they have less statistical support, and should be considered more reliable given that molecular-calibrated phylograms were found to fit the assumptions of the ancestral character state more accurately (Litsios and Salamin, 2012). The number of characters with confident reconstruction of ancestral state decreased towards the root of the hominoid tree. This tendency was stronger when characters were optimized on the tree with 'molecular-calibrated' branch lengths than on the tree with 'all-equal' branch lengths, owing to long branches of the most basal hominids (orangutans) and their nearest outgroup (gibbons).

Even substantial changes of the outgroup sample have only a marginal impact on the suite of reconstructed ancestral states. Using two alternatives as outgroup samples (three cercopithecoids + hylobatids; hylobatids only), only two and five characters, respectively, were reconstructed with different ancestral states. These differences concerned only the deepest ingroup node, i.e., the ancestral Hominidae (great apes). Given that there are six ingroup ancestral nodes and 77 binary characters, the differences account for 0.43 and 1.01% of ancestral states. Most of these changes occurred when a character state for the outgroup species (gibbons) was unknown, so an outgroup was virtually absent. In some cases, however, the change occurred due to exclusion of an outgroup species with unknown or polymorphic character states, so the ancestral state that could not originally have been reconstructed unambiguously became resolved (see SOM for details).

#### General pattern of character evolution

Mapping the character states on the hominoid phylogenetic tree allowed to infer of the amount of character change along each internal and terminal branch of the hominoid tree (see Fig. 1). Comparison of results of MP character optimization using the 'unambiguous' optimization routine and five character sets revealed that the ratios of evolutionary derivation of individual tree branches remained similar (Table 3; SOM Fig. S.1). The only data set that stands apart is the 'uniquely-human' one (SOM Fig. S.1e). In this data set, the branch leading to *H. sapiens* is more than twice as long as any other branch. However, the 'uniquely-human' character set purposely describes humans as an exceedingly aberrant hominid by scoring only the most distinct human character states, even though the resulting set of character states is not representative of any existing human population.

Most evolutionary transitions occur on the branches leading to the ancestors of the extant hominid genera, not on the deeper branches of the hominoid tree (Fig. 1). Both gorilla species as well as both orangutan species diverged only slightly from the common ancestors of extant Gorillini and Ponginae, respectively. Gorillas are the least derived among the Hominidae. Also, the phylostratigraphic maps show that evolutionary patterns differ for the four hominid lineages (Fig. 4; SOM Fig. S.2). The retained plesiomorphic characters, originating as deep as in the common ancestor of all Hominidae, are still predominant in *P. pygmaeus* and *G. gorilla*, whereas *P. troglodytes* and *H. sapiens* are shown to be more derived (apomorphic) relative to the ancestral ground pattern.

H. sapiens is shown as the most derived of all hominid species. However, optimizations of all 'unbiased' character sets (i.e., 'multistate polymorphic', 'multistate monomorphic' and 'binary') show both chimpanzees and bonobos to be similarly distant from the CHLCA as humans (Table 3). Naturally, the actual level of evolutionary derivation (i.e., the amount of character change occurring along terminal branch of a tree) of any species could be manipulated by including numerous singularities (autapomorphies) of the species in question. The point of the present analysis is that some hominid species (chimpanzee, bonobo and human) are consistently indicated as highly derived relative to others (gorillas) when using a character set that includes traits emphasized in human evolutionary studies. Both H. sapiens and P. troglodytes are highly apomorphic, however, these apomorphies represent distinct attributes that evolved only after the Pan–Homo split (Figs. 1 and 4). Most attributes that characterize the *H. sapiens* in the character set are either unique apomorphies of the human lineage or retained plesiomorphies inherited from the last common ancestor of all hominids (Fig. 4). The inferred evolutionary pattern remains unchanged when optimizing various versions of the character set

(Table 3; SOM Fig. S.1), and whilst employing various optimization routines (SOM Fig. S.2). Attributes that have originated in the CHLCA and are still conserved in humans and/or chimpanzees (which would make *H. sapiens* a 'third chimpanzee' [Diamond, 1992] and *P. troglodytes* a suitable model of the CHLCA) are conspicuously less numerous.

The effects of tree topology on the outcome of character optimization are important and nontrivial. The chimpanzee and bonobo novelties are distributed along two successive branches (between CHLCA and Pan ancestor and between Pan ancestor and individual Pan species) whereas a comparable amount of novelties represent H. sapiens itself (see Fig. 1), simply because no other species of the hominin clade survived up to the present. The pectinate (i.e., asymmetrical, imbalanced) tree shape of the hominid phylogeny is indicative of numerous extinction events in the hominid lineage. Such extinction events are indeed known to have occurred in pongines (Harrison, 2010; Wood and Harrison, 2011), in basal African apes (Harrison, 2010) and also in hominins that used to be highly diversified and species-rich until very recently (Foley, 2005; and see Lahr and Foley, 2004; Bokma et al., 2012). Along with species diversity, considerable behavioral diversity has been lost, and we are unable to recover either. This problem is demonstrated by those traits that can be inferred from the fossil record, such as sexual dimorphism in body size. Reduction of sexual dimorphism in body size could have (according to the present analysis, based exclusively on extant species) taken place in the CHLCA or earlier, in the common ancestor of Homininae. The australopithecine fossils suggest, however, that CHLCA and stem hominins may have differed from both the present-day Pan species and modern humans in being highly sexually dimorphic (Lockwood et al., 1996, 2007; Rak et al., 2007; Spoor et al., 2007; Gordon et al., 2008; Van Arsdale and Wolpoff, 2013). This loss of size dimorphism must have occurred at least twice independently, in Pan and in Homo. The problem gets even more complicated if the recently unveiled Ardipithecus ramidus, which is nearly sexually monomorphic, is in fact a stem hominin (Lovejoy, 2009; Harrison, 2010). Patterns of sexual dimorphism and, by inference, the social structure in australopithecines and early Homo are still subject to debate (Kimbel and Delezene, 2009; Plavcan, 2012). Note that some discrepancies between reconstructed ancestral states and behavioral patterns inferred from the fossil record can be caused by a paucity of data and possible misinterpretation of the fossil record. This is possibly the case with dispersal patterns in early hominins and, by implication, in the CHLCA (see Koenig and Borries, 2012).

There are only a few life-history characters that seem to be more or less correlated with body size evolution (length of gestation, age of weaning, age of first reproduction, age of first and last molar eruption), but others (relative neonate body mass, neonate growth rate and interbirth interval) are not. This absence of clear correlation is especially evident for gorillas whose enlarged body size is joined with general life-history acceleration (early first reproduction of females, small neonates and rapid postnatal growth rate).

#### Reconstruction of the deep hominid ancestors

By performing a series of maximum-parsimony and maximumlikelihood character optimizations, all hypothetical ancestors of hominid species and clades have been reconstructed. The emphasis was put on the common ancestors of Hominidae (the great apes), Homininae (the African great apes), Panini (chimpanzees and bonobos) and the CHLCA (the last common ancestor of panins and hominins). The character state of the common ancestor of Hominoidea (apes) has only been reconstructed to provide additional information on the evolutionary polarity of hominid character states. Reconstruction of the hominoid ancestor itself should be considered less reliable since it was rooted exclusively by a single sister clade, namely Cercopithecoidea. Note that, some of the ambiguously reconstructed ('debatable' or 'unknown/speculative') ancestral states could reflect real ancestral polymorphism, not just a lack of information.

According to present reconstructions, the hypothetical common ancestor of Hominidae (great apes) can be characterized by the following suite of life-history traits with significant support (Table 4, Figs. 2 and 3; see SOM Table S.2 for detailed list of ancestral reconstructions): gestation length over eight months accompanied by slow postnatal growth, first molar eruption at two to five years and last at eight to 12 years, puberty onset at six to 10 years, first female reproduction at 10-15 years, interbirth interval less than five (and probably less than three) years, non-seasonal breeding, and post-adolescent dispersal of both sexes depending on social and ecological context. Ancestral hominid socio-sexual and reproductive traits include a one-male/multifemale mating system with males employing possessive and opportunistic mating strategies, exerted female mate choice, male preference for older, higherranking females, strong sexual dimorphism in body weight and moderate sexual dimorphism in canine size, males possessing sexual adornments, medium-size penis with baculum, mediumsize testes, no copulatory plugs, no (or only small) sexual swellings of adult females, female-initiated matings, flexible copulatory posture (see Fig. 2), single intromission and occasional nocturnal mate guarding. The remaining ancestral Hominidae traits in which we can be confident include male dominance, high degree of frugivory, regular shelter (nest) construction and simple tool use (see Fig. 3), as well as presence of cultural diversity (local behavioral traditions in tool use and extractive foraging, etc.).

Several other ancestral hominid traits were reconstructed with a lower degree of certainty. These traits include medium-size neonates (roughly between 3 and 10% of maternal weight), absence of female post-reproductive lifespan, maximum lifespan over 40 years, male bimaturism, female-biased post-adolescent dispersal, and absence of multimale-multifemale communities (i.e., no cohesive social units apart from one male-multifemale groups sensu Rodseth et al., 1991), absence of forced copulations, positive correlation of male rank and copulation rate with high paternity certainty of a top-ranking resident male (see Fig. 3), low copulatory frequency and prolonged intromission (with duration over 1.5 min), weak male bonds, no male coalitions, no stable all-male non-breeding groups, and no or only occasional hunting or scavenging on animal prey. The ancestral states that are uncertain for the last common ancestor of Hominidae include weaning age, ovulation detectability, cooperation and coalitions among female kin and non-kin, nature of intergroup encounters, sex-specific participation in territorial defense, presence of opposite-sex friendships, paternal care and paternal protection, infant adoption by males and degree of arboreality (Table 4).

The last common ancestor of Hominidae likely differed from the preceding common ancestor of Hominoidea (including also Hylobatidae) in possessing prolonged gestation, later weaning, nonseasonal breeding, delayed last molar eruption, male bimaturism, prolonged intromission, possibly less egalitarian intersexual relations (male dominance), higher degree of frugivory and shelter construction (nest building). The changes of life-history characters (gestation, weaning and molar eruption) might be associated with increase in body size.

Reconstructions suggest that the common ancestors of great apes (Hominidae) and African great apes (Homininae) were in most respects similar to each other in their patterns of life history and socio-ecology. The ancestor of the Homininae possibly differed from the preceding common ancestor by displaying female-biased dispersal and moderate sexual dimorphism (with male—female body weight ratio from 1.2:1 to 1.6:1). Novel traits of the hominine ancestor also included higher copulatory frequency, higher intermale tolerance (while the existence of occasional male cooperation is debatable) and stable all-male non-breeding groups. Other likely novel traits included elevated frequency of male-led infanticide accompanied by paternal protection, paternal care (see Fig. 3), and occasional adoption of an infant by a male.

Five character complexes are worth commenting on in some detail:

- (i) Life-history data on Sumatran orangutans (P. abelii) collected by Wich et al. (2004) suggest that, compared with ancestral Hominidae, humans have undergone less of an increase in longevity than commonly assumed. These data also show that humans have experienced selection for earlier cessation of reproduction and shortening of interbirth interval. Our results support this view to some degree. Maximum-likelihood reconstruction of the last common ancestor of Hominidae, and all subsequent common ancestors in the hominid lineage, suggests high longevity (though lifespan below 50 years is more strongly supported than lifespan exceeding 50 years). Our reconstructions also suggest that age at first female reproduction occurs between 10 and 15 years, and that the interbirth interval is less than five years (Table 4 and SOM Table S.2). Thus, postponed age at first female reproduction and greatly prolonged interbirth interval (longer in Sumatran than Bornean orangutans; Wich et al., 2004) appear to be the apomorphies of Pongo. Slow growth and low rate of reproduction in orangutans is consistent with an extremely low rate of energy expenditure, unparalleled in primates (Pontzer et al., 2010). Orangutan life-history patterns can be a consequence of unique adaptive response to severe food shortages in their native Southeast Asian rainforests. (Pontzer et al., 2010; Russon, 2010; see also Harrison and Chivers, 2007).
- (ii) Recently patterns of genetic variation in various orangutan populations have confirmed male-biased dispersal in this species (Morrogh-Bernard et al., 2010; Nater et al., 2011; van Noordwijk et al., 2012), which contrasts to female-biased dispersal observed in African apes. Morrogh-Bernard et al. (2010) hypothesized that female philopatry might represent the ancestral state of early hominoids, since the female philopatry of orangutans is similar to female philopatry in Old World monkey species such as baboons (Papio ssp.) and vervets (Chlorocebus aethiops). To perceive the orangutan social system as a relict, female-retentive system (Ghiglieri, 1987) is tempting but debatable. Firstly, paleontological and paleoclimatological evidence (Harrison and Chivers, 2007), and long-term ethological studies (van Schaik and van Hooff, 1996) suggest that the orangutan social system has evolved only recently from a more or less gorilla-like basis. From this perspective, the ancestral social system of orangutans would have been characterized by higher gregariousness and a more terrestrial lifestyle (Smith and Pilbeam, 1980), accompanied by dispersal patterns more similar to those of African apes. Secondly, orangutans are not, strictly speaking, femalephilopatric. Orangutan females only have shorter average dispersal distances than males (van Schaik and van Hooff, 1996; Morrogh-Bernard et al., 2010; Nater et al., 2011). Importantly, an opposite pattern was found in some species of gibbons, namely the siamang (S. syndactylus; Lappan, 2007), the white-handed gibbon (*H. lar*; Brockelman et al., 1998) and Kloss' gibbon (Hylobates klossii; Tilson, 1981). Genetic evidence suggests that shorter dispersal distances are common in siamang males, who frequently immigrate into groups immediately adjacent to the natal group. In contrast, females

are characterized by longer dispersal distances (Lappan, 2007). Though the exact pattern of philopatry in gibbons and its social and life-history consequences are not clear (Lappan, 2007), both sexes disperse from their natal groups (Leighton, 1987; Brockelman et al., 1998; Reichard and Barelli, 2008). The results of our analyses suggest that the ancestral pattern of the last common ancestor of Hominidae (as well as of Homininae and the CHLCA) has been a context-dependent dispersal of both sexes, likely female-biased (though this was not significantly supported for the common ancestor of Hominidae; see Table 4 and SOM Table S.2). Reconstructed ancestral patterns suggest that while individuals of both sexes have emigrated from their natal groups, females might have had longer dispersal distances than males, whereas some males have stayed in their natal group for their whole life (as in gorillas; Stokes et al., 2003; Robbins et al., 2004; Harcourt and Stewart, 2007). Hence, the ancestral dispersal patterns were likely fluid, with a wider range of strategies employed, while the chimpanzee pattern of strict male-retention is derived (Marlowe, 2004; Koenig and Borries, 2012). This conclusion contrasts with recent tentative reconstructions of dispersal strategies of Plio-Pleistocene hominins. Australopithecus africanus and Paranthropus robustus (Copeland et al., 2011) and Homo neaderthalensis were likely strictly male-philopatric (Lalueza-Fox et al., 2011), based on isotope and DNA analyses, respectively (see Koenig and Borries, 2012, for discussion).

- (iii) A polygynous mating system (associated with possessive mating strategy and high paternity success of the top-ranking male; see Fig. 3) characterizes the whole sequence of ancestors in the hominid lineage, again, with the exception of the common ancestor of panins. The ancestral nature of this mating system is also supported by patterns of sexual dimorphism in extant as well as numerous extinct hominids, including members of the human stem lineage (Lockwood et al., 1996; Harrison and Chivers, 2007; Lockwood et al., 2007; Rak et al., 2007; Spoor et al., 2007; Van Arsdale and Wolpoff, 2013), and by genes associated with sperm competition such as seminal protein genes and the prostate-specific transglutaminase gene (Kingan et al., 2003; Clark and Swanson, 2005; Carnahan and Jensen-Seaman, 2008). These genes are apparently nonfunctional in both gorilla species, suggesting that gorillas have had low sperm competition, and that their current polygynous mating system is therefore ancient. Similarly, orangutans show a longstanding stasis in the genes in question, which may be interpreted as evidence for an unchanging mating system after their divergence from the common ancestor of great apes. Chimpanzees and bonobos, on the other hand, show the fastest rate of evolution in these genes, which is indicative of selection for intense sperm competition (Kingan et al., 2003; Jensen-Seaman and Li, 2003). Genetic data from humans could be interpreted as evidence for fluctuations between different mating systems or as a relaxed functional constraint in these proteins (Carnahan and Jensen-Seaman, 2008). The maintenance of functionality in these genes in the human lineage may also indicate that the ancestral human mating system was neither chimpanzee-like nor purely gorilla-like (Carnahan and Jensen-Seaman, 2008). Testes size, which might serve as a proxy for intensity of sperm competition, was reconstructed here as highly ambiguous in all common ancestors in the hominid lineage (see Fig. 3).
- (iv) The nature of female intragroup relations and the degree of cooperation among females is one of the traits in which the ancestral states are particularly difficult to infer. The only near certain conclusion is the absence of the bonobo-like pattern of

female relationships, which encompasses high cooperation and the affiliation of unrelated females (Idani, 1991; Parish and De Waal, 2000; Furuichi, 2011), strengthened by a frequent socio-sexual behavior (Dixson, 1998) and associated with female social dominance (White, 1996; Parish and De Waal, 2000; Surbeck et al., 2011). Various mutually exclusive characterizations of human female relationships can be found in the literature, ranging from kin-based cooperation (Rodseth et al., 1991) and conspicuous non-kin cooperation (Taylor et al., 2000; Marlowe, 2007) to weak and uncooperative relations (Hrdy, 1981; Benenson et al., 2009). The fundamental nature of female relationships is hard to assess in common chimpanzee due to females' largely solitary lifestyle (Mitani, 2009). The same applies to orangutans (Galdikas, 1984; van Schaik and van Hooff, 1996). Moreover, there are notable differences between study sites in both chimpanzees (Boesch and Boesch-Achermann, 2000; Boesch et al., 2002; Lehmann and Boesch, 2009) and orangutans (compare Knott et al., 2008, and van Noordwijk et al., 2012). In short, females of all hominids tend to express kin-based cooperation or at least greater tolerance towards female kin. This apparently applies to humans (Rodseth et al., 1991), and to some extent gorillas (Bradley et al., 2007) and possibly orangutans (van Noordwijk et al., 2012). In some species, however, female cooperation is effectively precluded by post-adolescent dispersal or a solitary lifestyle.

(v) The presence of tool use and nest building behavior in the common ancestor of Hominidae is congruent with various lines of evidence. Besides P. troglodytes, orangutans are the most skilled tool users (van Schaik and Knott, 2001; van Schaik et al., 2003; Krützen et al., 2011). It is also possible that "their largely arboreal lifestyle curtails their technical expression," because, as in chimpanzees, most tools are used while on the ground (McGrew, 2010b: 580). Fossil evidence, morphology and behavior of present-day orangutans suggest that middle Pleistocene and Pliocene orangutan ancestors "would have been less arboreal, and more chimpanzee-like in their use of terrestrial habitats" (Smith and Pilbeam, 1980: 447). The hvpothesized terrestrial nature of orangutan ancestors could imply more frequent and more complex tool use in the past. Since patterns of tool use and tool production differ markedly among hominid species, some argue that the shared apomorphy of all hominids is not the tool use itself but the general ability for environmental problem solving (McGrew, 1992; Fruth and Hohmann, 1996). Nest building behavior is shared in all great apes (Fruth and Hohmann, 1996) and, since it evinces conserved patterns of construction and function, some authors consider it homologous across hominid species, including humans (Groves and Pi, 1985; Fruth and Hohmann, 1996). Both optimizations of the 'multistate' character set (on the tree with 'all-equal' and 'molecular-calibrated' branch lengths) suggest that nest building, tool use and cultural diversity (characters ##61-63; see Fig. 3) were present in all of the reconstructed common ancestors, but not in the common ancestor of all hominoids, in line with earlier suggestions (Panger et al., 2002; Whiten, 2011). However, the reconstruction that is based on the behavior of free-ranging apes suggests that no ancestor in the hominid lineage, including the last common ancestor of chimpanzees and bonobos, exhibited the extensive technological skills and extensive tool kit (including tool sets, tool composites, and compound tools; McGrew, 2010b) found in present-day chimpanzees (Lycett et al., 2009). The evidence to date has outlined only a much smaller set of multiple-tradition cultures concerning tool use in P. paniscus (Hohmann and Fruth, 2003; Whiten, 2011). On the other hand, studies undertaken in captivity suggest that bonobos are capable of exhibiting technical skills comparable with *Pan troglodytes* (Takeshita and Walraven, 1996; Herrmann et al., 2008; Gruber et al., 2010). It is possible that bonobos have lost tool use in the wild not because they are cognitively incapable but because all relevant food sources can be acquired without the assistance of tools (Hohmann and Fruth, 2003; Gruber et al., 2010). Further research and more precise analyses of technological skills in wild chimpanzee and bonobo communities are warranted (Gruber et al., 2010; Whiten, 2011).

#### Evolutionary novelties of extant great ape genera

Numerous evolutionary novelties were found to originate in the lineages leading to extant hominid genera (see Fig. 1) instead of the deeper branches of the hominoid tree.

For orangutans, these include generally slow postnatal development (i.e., delayed first female reproduction, prolonged interbirth interval, postponed weaning and longer lifespan; Wich et al., 2004), 'consortship' as a prominent male mating strategy (Schürmann, 1982; Utami et al., 2002; Knott et al., 2010), the regular occurrence of forced copulations (MacKinnon, 1974; Knott and Kahlenberg, 2006; Knott, 2009), solitary lifestyle and inability of a dominant male to maintain long-term proximity to females (Smith and Pilbeam, 1980; van Schaik and van Hooff, 1996; Harrison and Chivers, 2007) accompanied by limited paternity certainty of the top-ranking resident male (Utami et al., 2002; Goossens et al., 2006), ventro-ventral copulations (orangutans express, along with humans, the greatest flexibility of copulatory postures; Dixson, 1998) and greatly prolonged intromission (Dixson and Anderson, 2004; Stumpf et al., 2008).

Gorillas are derived in life-history traits such as early first reproduction of females (Harcourt and Stewart, 2007), small neonates and rapid postnatal growth rate (Leigh, 1994; Robson and Wood, 2008) that are tightly linked to higher reliance on vegetative foods (folivorous diet). Other derived traits include small testes (both absolutely and relatively) and a short penis (Dixson and Anderson, 2004) both linked to their social mating system. The origin of gorilla-like sexual dimorphism in body weight (Frayer and Wolpoff, 1985; Shoshani et al., 1996) is uncertain. This trait would be interpreted as plesiomorphic for Hominidae if the evidence of strong sexual dimorphism in some extinct hominins (Lockwood et al., 1996, 2007; Rak et al., 2007; Spoor et al., 2007; Gordon et al., 2008; Van Arsdale and Wolpoff, 2013) was taken into account.

The true apomorphies of the last common ancestor of Pan include strict male philopatry (Ghiglieri, 1987; Rodseth et al., 1991; Stanford, 1998), disintegration of conjugal families (Rodseth et al., 1991; Chapais, 2010), a multimale-multifemale social system and an opportunistic mating strategy (Tutin, 1980; Goodall, 1986; Kano, 1992), limited paternity success of the top-ranking male (Constable et al., 2001; Wroblewski et al., 2009; Newton-Fisher et al., 2010), absence of adult male sexual adornments (Dixson, 1998), an elongated penis with reduced baculum (possibly already reduced in the CHLCA), very large testes (Dixson and Anderson, 2004), exaggerated sexual skin swellings (Dixson, 1998; Nunn, 1999) and advertised or semi-concealed ovulation (Takahata et al., 1996; Nunn, 1999; Pawlowski, 1999; Reichert et al., 2002). Other apomorphies of the Pan ancestor likely included male-initiated copulations (Goodall, 1986; Kano, 1992; Hashimoto and Furuichi, 2006), reduced intromission duration (Tutin, 1980; Dixson and Anderson, 2004) and higher copulatory frequency (Dixson, 1998). The numerous social structures and behavioral patterns of panins lack any clear analogs with other mammalian species (Schwartz, 2004). The remarkable similarity between the social structure of chimpanzees and distantly related taxa such as spider monkeys demonstrates, however, that adaptive responses to the environment can produce remarkably similar social structures and behaviors (Chapman and Rothman, 2009; and see Di Fiore and Rendall, 1994). In the case of spider monkeys and chimpanzees, these include grouping pattern, lethal intergroup violence, femaledirected intragroup aggression, and a reliance on similar food types (Chapman and Rothman, 2009). The number of unique chimpanzee traits as well as their similarities with very distantly related species question the validity of using chimpanzees as models to reconstruct the behavior and social structure of early hominins (Moore, 1996; Schwartz, 2004; Sayers and Lovejoy, 2008; Chapman and Rothman, 2009).

Both species of *Pan* can be further characterized by numerous species-specific apomorphies (Figs. 1 and 4). Apomorphies of the common chimpanzee include shortened gestation (<u>Harcourt et al., 1980; Goodall, 1986; Robson and Wood, 2008</u>), prolonged interbirth interval (<u>Galdikas and Wood, 1990;</u> Wrangham et al., 1996; De Lathouwers and Van Elsacker, 2005; <u>Robson and Wood, 2008</u>), loss of copulatory posture flexibility (<u>Dixson, 1998</u>), increased hostility of intergroup encounters (<u>Goodall, 1986;</u> <u>Wrangham, 1999;</u> <u>Wrangham et al., 2006</u>) and more solitary lifestyle and foraging pattern (Chapman et al., 1994; Wrangham et al., 1996).

There has been a tendency to view P. paniscus as a 'generalized' great ape that might serve as a good model for the 'prototypic ape' (Zihlman et al., 1978; Zihlman, 1996), as well as to see bonobos as the more derived of the two species of Pan (Johnson, 1981; Latimer et al., 1981; and see Stanford, 1998). However, according to the present analyses, bonobos show a level of evolutionary derivation comparable with that of chimpanzees. Apomorphies of the bonobo (Fig. 1; SOM Fig. S.1) encompass exaggerated, semipermanent female swellings and semi-concealed ovulation (Kano, 1992; Wrangham, 1993; Reichert et al., 2002), intense sexual behavior that serves non-conceptive functions (Kano, 1992; Wrangham, 1993; Parish and De Waal, 2000), relatively weak male bonds and no male coalitions (White, 1996; Hohmann, 2001), female collective dominance and equal involvement of both sexes in intergroup encounters (White, 1996; Parish and De Waal, 2000; Surbeck et al., 2011), absence of male-led infanticide (Furuichi et al., 1998; Fowler and Hohmann, 2010; Furuichi, 2011) and absence of infant adoption by males (Geary, 2000).

The differences between chimpanzees and bonobos reflect different evolutionary pathways (Wrangham and Pilbeam, 2001) and could be attributed to selection against male aggression as a consequence of relaxed feeding competition: resulting in juvenilization and 'self-domestication' in the latter species (Wrangham and Pilbeam, 2001; <u>Hare et al., 2012</u>). Humans share important aspects of behavior with both chimpanzees and bonobos (Wrangham and Pilbeam, 2001). This might be entrenched in the species' genomes since incomplete lineage sorting exists between humans, chimpanzees and bonobos (<u>Prüfer et al., 2012</u>).

#### The chimpanzee-human last common ancestor

Our reconstructions suggest that the CHLCA differed from the last common ancestor of Homininae in the presence of communities consisting of less-related individuals, reduced sexual dimorphism in body weight (possibly in contradiction to the fossil evidence; see Lockwood et al., 2007; Rak et al., 2007; Gordon et al., 2008; see above), reduced baculum, presence of female (post)copulation calls, presence of 'consortship' mating strategy, non-conceptive sexuality (e.g., paternity confusion and exchange of favors for sexual access), stronger male bonds and higher degree of male cooperation (male coalitions) and a likely higher proportion of meat in the diet and regular hunting of animal prey.

The ambiguously reconstructed (unknown) ancestral states include degree of ovulation detectability, nature of female intragroup relations, intergroup encounters, presence of female postreproductive lifespan, mating initiation, presence of female mate choice and male mate preference. While the absence of exaggerated sexual skin swellings in the common ancestors within the Hominoidea, including the CHLCA is a near certainty, the extent to which ovulation was concealed in the CHLCA is debatable. It is likely, however, that ovulation has been detectable by small swellings and by behavioral cues throughout the evolutionary history of hominids (Sayers and Lovejoy, 2008). The visual manifestation of ovulation was likely to be more subtle in the CHLCA (Pawlowski, 1999), and advertised ovulation of chimpanzees, semiconcealed ovulation in bonobos (Reichert et al., 2002) and concealed ovulation in humans represent distinct adaptations of the terminal lineages (Sillén-Tullberg and Møller, 1993; Nunn, 1999; Pawlowski, 1999).

The present reconstruction of the CHLCA (and also hominine, hominid, and hominoid ancestors) differs from preceding attempts to apply cladistic reasoning to hominid evolution (Ghiglieri, 1987; Wrangham, 1987). Admittedly, Wrangham's and Ghiglieri's studies identified a similar set of behaviors in the CHLCA, which included a polygynous mating system, female dispersal and weak female social bonds, and male-dominated intergroup encounters. However, the study by Ghiglieri (1987) also lacks data on important traits such as individual life histories and individual mating success, and his results arguably suffer from mischaracterization of several aspects of socio-ecology of particular hominid species. They include interpretation of orangutan social system as a relic, femaleretentive system, similar to that of many Old World monkeys, interpretation of both chimpanzee and human social and mating systems as 'fusion-fission', 'community polygyny' and 'communal breeding', underrated male paternal investment by male gorillas (but likely overrated in bonobos) and likely an underrated role of nepotism in female gorillas as well as in humans (but clearly overrated in orangutans).

#### The process of hominization

Reconstructions suggest that numerous traits characterizing humans are, in fact, ancient and were already present the last common ancestor of Hominidae (some possibly inherited directly from the last common ancestor of Hominoidea; Table 4; Fig. 4; SOM fig. S.2.). These results have possible implications for speculations on the origin of seemingly unique traits of human social and sexual behavior. Various past (and recent) theories regarding the origin of human social and sexual behavior attempt to interpret these traits as adaptations resulting from selection pressures in action during the Plio-Pleistocene, after the split of the Pan-Homo lineages. These theories often rest upon the assumption that human behavior and socio-sexuality have evolved from a more or less chimpanzee-like basis (e.g., a promiscuous mating system and female sexual skin swellings) and then struggle to explain the subsequent transitions in the human lineage, e.g., from promiscuity to pair bonding (Gavrilets, 2012) or from advertised to concealed ovulation (Burley, 1979; Lovejoy, 1981; Daniels, 1983; Diamond, 1992). Some of the traits in question were already present in the CHLCA (Table 4; SOM Table S.2), and their origin likely dates back to the Miocene. Hence, these cannot be explained as adaptations resulting from selection pressures acting during human evolution. These ancient traits include slow postnatal growth rate (Robson and Wood, 2008), postponing the first female reproduction (Leigh, 2001;

Walker et al., 2006), relatively short interbirth interval of less than five years and year-round (non-seasonal) breeding (Hawkes and Paine, 2006), postnatal dispersal of both sexes that was female-biased (Marlowe, 2004, 2005; see above), conjugal families, polygynous mating system, male mate guarding and high paternity certainty (Buss, 2002, 2007; Simmons et al., 2004), sexual dimorphism in androgen-dependent sexual adornments, medium-sized penis and medium-sized testes (Dixson, 1998; Dixson and Anderson, 2004), absence of copulatory plugs (Dixson, 1998; Carnahan and Jensen-Seaman, 2008), absence of exaggerated sexual skin swellings (Nunn, 1999; Pawlowski, 1999), flexible copulatory posture and single, prolonged intromission (Dixson, 1998), paternal care (Hewlett, 1992; Geary, 2000) and cultural diversity (van Schaik et al., 2003; McGrew, 2010a; Whiten, 2011).

Of course, human apomorphies (i.e., traits that have likely originated in the human stem lineage only after *Pan–Homo* split) are also numerous (Figs. 1 and 4) with the long list of unique human adaptations definitely not covered by the present character set (see Varki and Altheide, 2005). Among the characters included in the present character set, the true human novelties encompass early age at weaning (Short, 1994; Sellen, 2001; Kennedy, 2005), delayed eruption of the first molar and completion of the permanent dentition (Smith et al., 1994; Macho, 2001; Robson and Wood, 2008), delayed onset of puberty (Mace, 2000; Parent et al., 2003), shortened interbirth interval (particularly among agricultural and industrialized populations; Short, 1994; Mace, 2000), protracted post-reproductive female lifespan (menopause; Hawkes et al., 1998; Mace, 2000; Hawkes, 2003) and extended lifespan (Kaplan et al., 2000; Mace, 2000; Robson and Wood, 2008). Apomorphic features of socio-sexual behavior include frequent forced copulations (Wrangham and Peterson, 1996; Thornhill and Palmer, 2000; Emery Thompson, 2009; Palombit, 2010), reduction of sexual dimorphism in canine size (Thoren et al., 2006), highly concealed ovulation (though ovulation has not been really advertised in any ancestor in the hominid lineage; Nunn, 1999; Pawlowski, 1999; Geary et al., 2011; see above), frequently employed ventro-ventral copulatory posture (Kinsey et al., 1948; Ford and Beach, 1952; Dixson, 1998), and prevailing nocturnal copulations (Dixson, 1998). Also important are frequent male infanticidal behavior (Daly and Wilson, 1985; Barrett et al., 2002), broadly omnivorous diet (Kaplan et al., 2000), manufacture and use of elaborate tools (Brown, 1991; McGrew, 2010a) and, of course, a unique type of bipedal locomotion (Lovejoy, 1988; Crompton et al., 2008).

#### Conclusions

While the first evolutionists remained intentionally vague concerning characteristics of ape-human ancestors (Huxley, 1863; Darwin, 1871), later researchers enthusiastically used living apes as explicit models for human evolution (see Tuttle, 1974, and Latimer et al., 1981, for review and criticism). The modeling techniques employed so far have been explicitly or implicitly based on preferred referential species and have attempted to answer the question of which extant species is (behaviorally) most similar to the common ancestor. However, as pointed out by Tooby and DeVore (1987) and Sayers and Lovejoy (2008), when an ape species is singled out for modeling human evolution, its similarities to modern humans are likely to be emphasized at the expense of critically important differences. Virtually every great ape species has been suggested to represent a behavioral relic (i.e., highly conserved, possessing retained features present in the last common ancestor of Hominidae) and by implication the single best available model for behavioral evolution of early hominins. This has been said about orangutans (<u>Ghiglieri, 1987;</u> Schwartz, 2004, 2005; <u>Grehan, 2006</u>), gorillas (<u>Geary and Flinn, 2001;</u> Geary et al., 2011), chimpanzees (McGrew, 1981; Tanner, 1981) and bonobos (Zihlman et al., 1978).

In contrast, phylogenetic reconstruction of ancestral states does not use individual species as models. It only utilizes species traits' distribution as an indicator of their plesiomorphic (conserved) or apomorphic (derived) nature. It therefore allows the reconstructed hypothetical hominid ancestors to possess unique combinations of traits rather than assuming that early hominids behaved like a particular extant species (Wrangham, 1987). In addition (unlike non-referential modeling), cladistics treats individual traits independently and avoids relying on unified ecological and behavioral syndromes, the possible existence of which should be tested by independent analyses rather than imposed a priori (<u>Rendall and Di</u> Fiore, 1995).

The present analyses show that studies of living taxa can play an important role in identifying the potential homologies of hypothetical ancestors. Our analyses demonstrate that all extant great ape species are, to a varying extent, apomorphic and their common ancestors possessed unique suites of behaviors unparalleled in extant species. We suggest that the only great apes, if any, that could be viewed as behaviorally relictual are gorillas (in agreement with Geary et al., 2011). We conclude that many fundamental behavioral and life-history attributes of hominids, including humans, are ancient and likely inherited from the common ancestor of all hominids, although numerous behaviors present in extant great apes represent terminal autapomorphies, both uniquely derived and homoplastic. Any evolutionary model that uses a single extant great ape specis as the direct proxy to explain behavioral evolution of early hominins is therefore of limited use. On the contrary, phylogenetic reconstruction is able to provide detailed suites of behavioral, ecological and life-history characters for the hypothetical ancestors (Table 4) that can be tested against independent evidence from the fossil record and behavioral ecology of non-hominoid models.

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#### Appendix A. Supplementary material

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442

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446